Table S8A Gene Ontology (GO) Biological Process Analysis				
GO ID	GO Term	Term P value	No. of Genes	Associated Genes Found
GO:0016071	mRNA metabolic process	6.347E-41	75	[illegible]
GO:0010629	negative regulation of gene expression	7.228E-32	101	[illegible]
GO:0051276	chromosome organization	8.135E-32	78	[illegible]
GO:0000398	mRNA splicing, via spliceosome	6.014E-31	45	[illegible]
GO:0006396	RNA processing	2.013E-30	67	[illegible]
GO:0016032	viral process	4.174E-30	66	[illegible]
GO:0008380	RNA splicing	1.923E-28	47	[illegible]
GO:0006397	mRNA processing	1.619E-27	49	[illegible]
GO:0043933	protein-containing complex subunit organization	4.191E-25	87	[illegible]
GO:0006259	DNA metabolic process	6.636E-25	61	[illegible]
GO:0034622	cellular protein-containing complex assembly	3.015E-24	64	[illegible]
GO:0065003	protein-containing complex assembly	4.271E-24	79	[illegible]
GO:0043044	ATP-dependent chromatin remodeling	6.660E-24	24	[illegible]
GO:0072594	establishment of protein localization to organelle	4.958E-23	47	[illegible]
GO:0000723	telomere maintenance	1.556E-22	28	[illegible]
GO:0006338	chromatin remodeling	4.432E-22	31	[illegible]
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	9.651E-22	72	[illegible]
GO:0006325	chromatin organization	3.295E-21	52	[illegible]
GO:0034080	CENP-A containing nucleosome assembly	3.665E-21	17	[illegible]
GO:0022613	ribonucleoprotein complex biogenesis	5.122E-21	39	[illegible]
GO:0010608	posttranscriptional regulation of gene expression	5.127E-21	47	[illegible]
GO:0034724	DNA replication-independent nucleosome organization	7.575E-21	18	[illegible]
GO:0051253	negative regulation of RNA metabolic process	9.730E-21	68	[illegible]
GO:0006335	DNA replication-dependent nucleosome assembly	1.452E-20	15	[illegible]
GO:0010558	negative regulation of macromolecule biosynthetic process	1.598E-20	71	[illegible]
GO:0019083	viral transcription	1.951E-20	27	[illegible]
GO:0009890	negative regulation of biosynthetic process	2.232E-20	73	[illegible]
GO:0016233	telomere capping	2.232E-20	18	[illegible]
GO:0033365	protein localization to organelle	1.384E-19	55	[illegible]
GO:0040029	regulation of gene expression, epigenetic	1.390E-19	33	[illegible]
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	2.830E-19	21	[illegible]
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	3.696E-19	67	[illegible]
GO:0006974	cellular response to DNA damage stimulus	3.767E-19	51	[illegible]
GO:0034728	nucleosome organization	4.059E-19	26	[illegible]
GO:0006333	chromatin assembly or disassembly	5.117E-19	28	[illegible]
GO:0071824	protein-DNA complex subunit organization	8.054E-19	31	[illegible]
GO:0006281	DNA repair	1.114E-18	41	[illegible]
GO:0006303	double-strand break repair via nonhomologous end joining	3.860E-18	20	[illegible]
GO:0006402	mRNA catabolic process	7.841E-18	33	[illegible]
GO:0006413	translational initiation	2.033E-17	25	[illegible]
GO:0006302	double-strand break repair	3.632E-17	28	[illegible]
GO:0070972	protein localization to endoplasmic reticulum	3.939E-17	22	[illegible]
GO:1903507	negative regulation of nucleic acid-templated transcription	4.730E-17	60	[illegible]
GO:0065004	protein-DNA complex assembly	6.324E-17	27	[illegible]
GO:0045814	negative regulation of gene expression, epigenetic	8.788E-17	20	[illegible]
GO:0071103	DNA conformation change	2.735E-16	31	[illegible]
GO:0043484	regulation of RNA splicing	4.026E-16	22	[illegible]
GO:0045892	negative regulation of transcription, DNA-templated	6.218E-16	57	[illegible]
GO:0060964	regulation of gene silencing by miRNA	8.798E-16	19	[illegible]
GO:0006412	translation	1.036E-15	40	[illegible]
GO:0000956	nuclear-transcribed mRNA catabolic process	1.084E-15	24	[illegible]
GO:0016458	gene silencing	1.699E-15	26	[illegible]
GO:1903311	regulation of mRNA metabolic process	1.790E-15	29	[illegible]
GO:0022618	ribonucleoprotein complex assembly	2.358E-15	23	[illegible]
GO:0034401	chromatin organization involved in regulation of transcription	2.704E-15	21	[illegible]
GO:0031047	gene silencing by RNA	4.999E-15	22	[illegible]
GO:0006886	intracellular protein transport	5.486E-15	54	[illegible]
GO:0044265	cellular macromolecule catabolic process	6.523E-15	53	[illegible]
GO:0031507	heterochromatin assembly	7.426E-15	16	[illegible]
GO:0035195	gene silencing by miRNA	8.429E-15	20	[illegible]
GO:0034655	nucleobase-containing compound catabolic process	2.463E-14	35	[illegible]
GO:0006403	RNA localization	3.672E-14	24	[illegible]
GO:0031497	chromatin assembly	5.035E-14	22	[illegible]
GO:0006612	protein targeting to membrane	1.088E-13	22	[illegible]
GO:0006518	peptide metabolic process	1.473E-13	42	[illegible]
GO:0030518	intracellular steroid hormone receptor signaling pathway	2.564E-13	18	[illegible]
GO:0050684	regulation of mRNA processing	2.695E-13	19	[illegible]
GO:0060249	anatomical structure homeostasis	2.808E-13	32	[illegible]
GO:0031647	regulation of protein stability	3.773E-13	25	[illegible]
GO:0003712	transcription coregulator activity	4.274E-13	35	[illegible]
GO:0042254	ribosome biogenesis	5.785E-13	25	[illegible]
GO:0051052	regulation of DNA metabolic process	9.886E-13	27	[illegible]
GO:0090150	establishment of protein localization to membrane	1.656E-12	26	[illegible]
GO:1904814	regulation of protein localization to chromosome, telomeric region	1.988E-12	8	[illegible]
GO:1900182	positive regulation of protein localization to nucleus	3.643E-12	14	[illegible]
GO:1904851	positive regulation of establishment of protein localization to telomere	6.532E-12	7	[illegible]
GO:0070198	protein localization to chromosome, telomeric region	7.884E-12	10	[illegible]
GO:2001252	positive regulation of chromosome organization	1.248E-11	19	[illegible]
GO:0034502	protein localization to chromosome	1.320E-11	14	[illegible]
GO:0050821	protein stabilization	1.775E-11	19	[illegible]
GO:1904871	positive regulation of protein localization to Cajal body	1.777E-11	7	[illegible]
GO:0006913	nucleocytoplasmic transport	2.174E-11	25	[illegible]
GO:0030521	androgen receptor signaling pathway	3.077E-11	12	[illegible]
GO:0030219	megakaryocyte differentiation	3.673E-11	14	[illegible]
GO:0051054	positive regulation of DNA metabolic process	3.810E-11	19	[illegible]
GO:1903405	protein localization to nuclear body	4.217E-11	7	[illegible]
GO:0034504	protein localization to nucleus	5.573E-11	22	[illegible]
GO:0072657	protein localization to membrane	8.396E-11	33	[illegible]
GO:0070199	establishment of protein localization to chromosome	1.001E-10	9	[illegible]
GO:0032204	regulation of telomere maintenance	1.063E-10	13	[illegible]
GO:1903707	negative regulation of hemopoiesis	2.692E-10	16	[illegible]
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	5.459E-10	12	[illegible]
GO:1904874	positive regulation of telomerase RNA localization to Cajal body	5.828E-10	7	[illegible]
GO:0033044	regulation of chromosome organization	1.061E-09	23	[illegible]
GO:1901796	regulation of signal transduction by p53 class mediator	1.510E-09	17	[illegible]
GO:0072331	signal transduction by p53 class mediator	1.609E-09	20	[illegible]
GO:0030522	intracellular receptor signaling pathway	1.810E-09	20	[illegible]
GO:0071383	cellular response to steroid hormone stimulus	2.692E-09	19	[illegible]
GO:0006352	DNA-templated transcription, initiation	3.230E-09	19	[illegible]
GO:0090671	telomerase RNA localization to Cajal body	3.778E-09	7	[illegible]
GO:2000573	positive regulation of DNA biosynthetic process	4.981E-09	11	[illegible]
GO:0007004	telomere maintenance via telomerase	5.721E-09	11	[illegible]
GO:0071396	cellular response to lipid	7.669E-09	29	[illegible]
GO:1903829	positive regulation of cellular protein localization	8.387E-09	21	[illegible]
GO:0006605	protein targeting	9.850E-09	24	[illegible]
GO:0045637	regulation of myeloid cell differentiation	1.245E-08	18	[illegible]
GO:0003713	transcription coactivator activity	1.427E-08	21	[illegible]
GO:1903312	negative regulation of mRNA metabolic process	1.829E-08	11	[illegible]
GO:0042255	ribosome assembly	2.557E-08	10	[illegible]
GO:0000077	DNA damage checkpoint	2.594E-08	14	[illegible]
GO:0060765	regulation of androgen receptor signaling pathway	3.000E-08	7	[illegible]
GO:0033120	positive regulation of RNA splicing	3.080E-08	8	[illegible]
GO:0044839	cell cycle G2/M phase transition	3.241E-08	18	[illegible]
GO:0000380	alternative mRNA splicing, via spliceosome	3.686E-08	11	[illegible]
GO:0048545	response to steroid hormone	4.179E-08	22	[illegible]
GO:0071407	cellular response to organic cyclic compound	4.552E-08	28	[illegible]
GO:0007339	binding of sperm to zona pellucida	5.714E-08	8	[illegible]
GO:1903827	regulation of cellular protein localization	6.952E-08	26	[illegible]
GO:0000245	spliceosomal complex assembly	7.379E-08	9	[illegible]
GO:0045786	negative regulation of cell cycle	9.690E-08	27	[illegible]
GO:0051168	nuclear export	1.111E-07	15	[illegible]
GO:0051170	import into nucleus	1.377E-07	14	[illegible]
GO:0034248	regulation of cellular amide metabolic process	1.475E-07	23	[illegible]
GO:1903313	positive regulation of mRNA metabolic process	1.479E-07	10	[illegible]
GO:0031396	regulation of protein ubiquitination	1.603E-07	15	[illegible]
GO:0051236	establishment of RNA localization	2.033E-07	15	[illegible]
GO:0003714	transcription corepressor activity	2.198E-07	16	[illegible]
GO:1902749	regulation of cell cycle G2/M phase transition	2.715E-07	15	[illegible]
GO:1904951	positive regulation of establishment of protein localization	2.963E-07	23	[illegible]
GO:0006406	mRNA export from nucleus	3.269E-07	11	[illegible]
GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway	3.410E-07	7	[illegible]
GO:0032986	protein-DNA complex disassembly	3.737E-07	6	[illegible]
GO:0000075	cell cycle checkpoint	4.482E-07	15	[illegible]
GO:0035722	interleukin-12-mediated signaling pathway	5.883E-07	8	[illegible]
GO:0048026	positive regulation of mRNA splicing, via spliceosome	6.416E-07	6	[illegible]
GO:0098761	cellular response to interleukin-7	7.287E-07	7	[illegible]
GO:0006476	protein deacetylation	7.580E-07	10	[illegible]
GO:1903706	regulation of hemopoiesis	8.258E-07	22	[illegible]
GO:1901987	regulation of cell cycle phase transition	8.712E-07	21	[illegible]
GO:0002683	negative regulation of immune system process	8.712E-07	21	[illegible]
GO:0017038	protein import	9.101E-07	14	[illegible]
GO:0060766	negative regulation of androgen receptor signaling pathway	9.478E-07	5	[illegible]
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	1.028E-06	9	[illegible]
GO:0010948	negative regulation of cell cycle process	1.295E-06	18	[illegible]
GO:0030099	myeloid cell differentiation	1.414E-06	20	[illegible]
GO:0042307	positive regulation of protein import into nucleus	1.433E-06	7	[illegible]
GO:0071897	DNA biosynthetic process	1.480E-06	14	[illegible]
GO:0016570	histone modification	1.490E-06	21	[illegible]
GO:1990948	ubiquitin ligase inhibitor activity	1.850E-06	4	[illegible]
GO:0050686	negative regulation of mRNA processing	2.499E-06	6	[illegible]
GO:2001020	regulation of response to DNA damage stimulus	3.010E-06	14	[illegible]
GO:0010389	regulation of G2/M transition of mitotic cell cycle	3.187E-06	13	[illegible]
GO:0031503	protein-containing complex localization	3.468E-06	16	[illegible]
GO:1901990	regulation of mitotic cell cycle phase transition	3.702E-06	19	[illegible]
GO:0015931	nucleobase-containing compound transport	3.825E-06	15	[illegible]
GO:0042752	regulation of circadian rhythm	3.983E-06	10	[illegible]
GO:0046822	regulation of nucleocytoplasmic transport	4.617E-06	10	[illegible]
GO:0042274	ribosomal small subunit biogenesis	5.108E-06	8	[illegible]
GO:0034470	ncRNA processing	6.216E-06	18	[illegible]
GO:0042273	ribosomal large subunit biogenesis	6.250E-06	8	[illegible]
GO:0045292	mRNA cis splicing, via spliceosome	6.263E-06	6	[illegible]
GO:1901988	negative regulation of cell cycle phase transition	6.659E-06	14	[illegible]
GO:0051973	positive regulation of telomerase activity	7.395E-06	6	[illegible]
GO:0034660	ncRNA metabolic process	8.456E-06	20	[illegible]
GO:2000435	negative regulation of protein neddylation	8.523E-06	3	[illegible]
GO:0031397	negative regulation of protein ubiquitination	9.191E-06	8	[illegible]
GO:0009895	negative regulation of catabolic process	1.062E-05	16	[illegible]
GO:0002181	cytoplasmic translation	1.423E-05	9	[illegible]
GO:1902750	negative regulation of cell cycle G2/M phase transition	1.530E-05	9	[illegible]
GO:0042177	negative regulation of protein catabolic process	1.551E-05	10	[illegible]
GO:0034605	cellular response to heat	1.650E-05	10	[illegible]
GO:0017148	negative regulation of translation	1.650E-05	10	[illegible]
GO:0090666	scaRNA localization to Cajal body	2.110E-05	3	[illegible]
GO:0006310	DNA recombination	2.357E-05	15	[illegible]
GO:0007051	spindle organization	3.058E-05	11	[illegible]
GO:0032388	positive regulation of intracellular transport	3.240E-05	13	[illegible]
GO:2000323	negative regulation of glucocorticoid receptor signaling pathway	4.180E-05	3	[illegible]
GO:0000027	ribosomal large subunit assembly	4.527E-05	5	[illegible]
GO:0097193	intrinsic apoptotic signaling pathway	4.688E-05	14	[illegible]
GO:0032868	response to insulin	5.396E-05	14	[illegible]
GO:0031123	RNA 3'-end processing	5.399E-05	10	[illegible]
GO:0090316	positive regulation of intracellular protein transport	5.686E-05	11	[illegible]
GO:2000059	negative regulation of ubiquitin-dependent protein catabolic process	6.143E-05	6	[illegible]
GO:1901991	negative regulation of mitotic cell cycle phase transition	6.204E-05	12	[illegible]
GO:0051984	positive regulation of chromosome segregation	7.183E-05	5	[illegible]
GO:0048268	clathrin coat assembly	7.303E-05	4	[illegible]
GO:0006754	ATP biosynthetic process	7.591E-05	6	[illegible]
GO:0030374	nuclear receptor transcription coactivator activity	8.000E-05	7	[illegible]
GO:0031124	mRNA 3'-end processing	8.731E-05	8	[illegible]
GO:0003720	telomerase activity	9.300E-05	6	[illegible]
GO:0016575	histone deacetylation	1.012E-04	7	[illegible]
GO:0045930	negative regulation of mitotic cell cycle	1.087E-04	14	[illegible]
GO:0006356	regulation of transcription by RNA polymerase I	1.090E-04	5	[illegible]
GO:0042790	nucleolar large rRNA transcription by RNA polymerase I	1.133E-04	4	[illegible]
GO:0009205	purine ribonucleoside triphosphate metabolic process	1.177E-04	7	[illegible]
GO:0006090	pyruvate metabolic process	1.293E-04	10	[illegible]
GO:0032508	DNA duplex unwinding	1.351E-04	8	[illegible]
GO:0070932	histone H3 deacetylation	1.385E-04	4	[illegible]
GO:0061621	canonical glycolysis	1.410E-04	5	[illegible]
GO:0051225	spindle assembly	1.434E-04	8	[illegible]
GO:0051438	regulation of ubiquitin-protein transferase activity	1.493E-04	6	[illegible]
GO:0043488	regulation of mRNA stability	1.617E-04	10	[illegible]
GO:0000028	ribosomal small subunit assembly	1.676E-04	4	[illegible]
GO:0002218	activation of innate immune response	1.754E-04	9	[illegible]
GO:0046364	monosaccharide biosynthetic process	1.916E-04	8	[illegible]
GO:0045815	positive regulation of gene expression, epigenetic	1.942E-04	6	[illegible]
GO:0000387	spliceosomal snRNP assembly	2.019E-04	5	[illegible]
GO:0004407	histone deacetylase activity	2.019E-04	5	[illegible]
GO:0007338	single fertilization	2.030E-04	9	[illegible]
GO:0002833	positive regulation of response to biotic stimulus	2.055E-04	12	[illegible]
GO:0007062	sister chromatid cohesion	2.296E-04	6	[illegible]
GO:0000715	nucleotide-excision repair, DNA damage recognition	2.386E-04	4	[illegible]
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	2.686E-04	7	[illegible]
GO:0031330	negative regulation of cellular catabolic process	2.874E-04	12	[illegible]
GO:0019042	viral latency	3.287E-04	3	[illegible]
GO:0045876	positive regulation of sister chromatid cohesion	3.287E-04	3	[illegible]
GO:0006360	transcription by RNA polymerase I	3.407E-04	6	[illegible]
GO:0032869	cellular response to insulin stimulus	3.433E-04	11	[illegible]
GO:0000819	sister chromatid segregation	3.537E-04	10	[illegible]
GO:2000058	regulation of ubiquitin-dependent protein catabolic process	3.676E-04	9	[illegible]
GO:0006282	regulation of DNA repair	3.818E-04	8	[illegible]