GOBP enrichment of MSCs marker genes from UCMSCP0,UCMSCP3,UCMSCP5,UCMSCP5L

sluster	Gene_In_	Description	LogP	Hits
s0	4	muscle contraction	-4.442759279	ACTA2|CALD1|TPM1|TPM2
s0	4	muscle system process	-4.063781647	ACTA2|CALD1|TPM1|TPM2
s0	5	supramolecular fiber organization	-4.006748871	CALD1|COL1A1|TPM1|TPM2|MYL9
s0	4	actin cytoskeleton organization	-3.034291635	CALD1|TPM1|TPM2|MYL9
s0	4	actin filament-based process	-2.864604811	CALD1|TPM1|TPM2|MYL9
s0	3	actin filament organization	-2.833733014	CALD1|TPM1|TPM2
s0	3	wound healing	-2.657825074	SERPINE2|TPM1|MYL9
s0	3	response to wounding	-2.305917105	SERPINE2|TPM1|MYL9
s0	3	cellular response to transforming growth factor beta stimulus	-3.492018016	ACTA2|CDKN2B|COL1A1
s0	3	response to transforming growth factor beta	-3.44605094	ACTA2|CDKN2B|COL1A1
s0	3	connective tissue development	-3.067821813	ACTA2|COL1A1|SELENOM
s0	3	cellular response to growth factor stimulus	-2.139452736	ACTA2|CDKN2B|COL1A1
s0	3	response to growth factor	-2.066018287	ACTA2|CDKN2B|COL1A1
s0	3	blood vessel development	-2.052366378	ACTA2|CALD1|COL1A1
s0	3	vasculature development	-2.008080815	ACTA2|CALD1|COL1A1
s0	3	negative regulation of epithelial cell	-3.416337274	CDKN2B|SPARC|NUPR1
s0	3	regulation of epithelial cell proliferation	-2.352509697	CDKN2B|SPARC|NUPR1
s0	3	response to reactive oxygen species	-3.358992772	COL1A1|TPM1|PRDX5
s0	3	response to oxidative stress	-2.481553642	COL1A1|TPM1|PRDX5
s0	4	muscle structure development	-3.108005139	TAGLN|TPM1|MYL9|NUPR1
s0	3	muscle organ development	-2.68536093	TAGLN|TPM1|NUPR1
s0	3	regulation of actin filament-based process	-2.439018892	ACTA2|TPM1|SYNPO2
s1	6	collagen fibril organization	-11.14184825	COL1A2|COL3A1|COL5A1|COL12A1|LUM|P4HA1

s1	8	extracellular matrix organization	-10.44349218	COL1A2|COL3A1|COL5A1|COL12A1|LUM|MMP2|P4HA1|TGFBI
s1	8	extracellular structure organization	-10.43079343	COL1A2|COL3A1|COL5A1|COL12A1|LUM|MMP2|P4HA1|TGFBI
s1	8	external encapsulating structure	-10.41814252	COL1A2|COL3A1|COL5A1|COL12A1|LUM|MMP2|P4HA1|TGFBI
s1	7	supramolecular fiber organization	-6.48525397	COL1A2|COL3A1|COL5A1|COL12A1|LUM|P4HA1|TNFAIP6
s1	5	skin development	-5.550487565	COL1A2|COL3A1|COL5A1|FGF7|INHBA
s1	3	cellular response to amino acid stimulus	-4.329342171	COL1A2|COL3A1|MMP2
s1	3	cellular response to acid chemical	-4.19884695	COL1A2|COL3A1|MMP2
s1	3	response to amino acid	-3.821104714	COL1A2|COL3A1|MMP2
s1	3	response to acid chemical	-3.676988501	COL1A2|COL3A1|MMP2
s1	3	transmembrane receptor protein serine/threonine kinase signaling pathway	-3.258245784	COL1A2|COL3A1|INHBA
s1	4	skeletal system development	-3.152742662	COL1A2|COL3A1|MMP2|TGFBI
s1	3	connective tissue development	-3.067821813	COL3A1|COL5A1|TGFBI
s1	3	wound healing	-2.657825074	COL3A1|COL5A1|SERPINE2
s1	3	cellular response to growth factor stimulus	-2.139452736	COL1A2|COL3A1|FGF7
s1	3	response to growth factor	-2.066018287	COL1A2|COL3A1|FGF7
s1	4	positive regulation of nitric oxide	-7.5836574	CLU|IL1B|PTGS2|SOD2
s1	4	positive regulation of nitric oxide metabolic	-7.536901736	CLU|IL1B|PTGS2|SOD2
s1	4	regulation of nitric oxide biosynthetic	-6.828977873	CLU|IL1B|PTGS2|SOD2
s1	4	regulation of nitric oxide metabolic process	-6.769007167	CLU|IL1B|PTGS2|SOD2
s1	7	positive regulation of cell migration	-6.515605832	FGF7|IL1B|MMP2|PTGS2|SOD2|SPARC|TNFAIP6
s1	7	positive regulation of cell motility	-6.391270599	FGF7|IL1B|MMP2|PTGS2|SOD2|SPARC|TNFAIP6
s1	7	positive regulation of locomotion	-6.324003025	FGF7|IL1B|MMP2|PTGS2|SOD2|SPARC|TNFAIP6
s1	3	embryo implantation	-5.192255371	IL1B|MMP2|PTGS2
s1	6	multicellular organismal-level homeostasis	-5.044878865	COL3A1|IL1B|INHBA|PTGS2|CXCL6|SOD2
s1	4	response to carbohydrate	-4.878804577	COL6A3|IL1B|PTGS2|SOD2

s1	5	regulation of apoptotic signaling pathway	-4.787690897	CLU|IL1B|INHBA|PTGS2|SOD2
s1	4	multi-organism reproductive process	-4.758475412	IL1B|MMP2|SERPINE2|PTGS2
s1	4	multi-multicellular organism process	-4.671548174	IL1B|MMP2|SERPINE2|PTGS2
s1	4	response to mechanical stimulus	-4.572967944	IL1B|MMP2|SERPINE2|PTGS2
s1	4	negative regulation of apoptotic signaling	-4.34976741	CLU|IL1B|PTGS2|SOD2
s1	5	positive regulation of apoptotic process	-4.156369574	CLU|INHBA|MMP2|PTGS2|SOD2
s1	5	positive regulation of programmed cell	-4.070997703	CLU|INHBA|MMP2|PTGS2|SOD2
s1	3	negative regulation of intrinsic apoptotic signaling pathway	-3.949770429	CLU|PTGS2|SOD2
s1	4	apoptotic signaling pathway	-3.935181578	CLU|IL1B|INHBA|SOD2
s1	4	cellular response to abiotic stimulus	-3.898016806	IL1B|MME|MMP2|PTGS2
s1	4	cellular response to environmental stimulus	-3.898016806	IL1B|MME|MMP2|PTGS2
s1	4	response to lipopolysaccharide	-3.821193764	IL1B|PTGS2|CXCL6|SOD2
s1	4	response to molecule of bacterial origin	-3.719554593	IL1B|PTGS2|CXCL6|SOD2
s1	3	regulation of tube diameter	-3.632448134	MMP2|PTGS2|SOD2
s1	3	blood vessel diameter maintenance	-3.632448134	MMP2|PTGS2|SOD2
s1	3	regulation of tube size	-3.62372949	MMP2|PTGS2|SOD2
s1	3	positive regulation of inflammatory response	-3.581036845	IL1B|PTGS2|NEAT1
s1	4	blood circulation	-3.493056342	COL1A2|MMP2|PTGS2|SOD2
s1	4	response to xenobiotic stimulus	-3.445164469	IL1B|MMP2|PTGS2|SOD2
s1	3	female pregnancy	-3.431103935	IL1B|MMP2|PTGS2
s1	3	regulation of smooth muscle cell	-3.431103935	MMP2|PTGS2|SOD2
s1	4	regulation of inflammatory response	-3.417899081	IL1B|PTGS2|TNFAIP6|NEAT1
s1	3	regulation of blood pressure	-3.317687202	COL1A2|PTGS2|SOD2
s1	3	regulation of intrinsic apoptotic signaling	-3.297548489	CLU|PTGS2|SOD2
s1	4	circulatory system process	-3.159243839	COL1A2|MMP2|PTGS2|SOD2

s1	4	negative regulation of intracellular signal	-2.897013197	CLU|IL1B|PTGS2|SOD2
s1	3	vascular process in circulatory system	-2.861165445	MMP2|PTGS2|SOD2
s1	3	cellular response to chemical stress	-2.811351089	MMP2|PTGS2|SOD2
s1	3	ossification	-2.785043835	COL1A2|MMP2|PTGS2
s1	3	response to hypoxia	-2.785043835	MMP2|PTGS2|SOD2
s1	3	response to decreased oxygen levels	-2.713565456	MMP2|PTGS2|SOD2
s1	3	response to oxygen levels	-2.604644015	MMP2|PTGS2|SOD2
s1	4	response to bacterium	-2.592712949	IL1B|PTGS2|CXCL6|SOD2
s1	3	response to oxidative stress	-2.481553642	MMP2|PTGS2|SOD2
s1	3	response to salt	-2.481553642	IL1B|PTGS2|SOD2
s1	3	positive regulation of defense response	-2.32606235	IL1B|PTGS2|NEAT1
s1	3	positive regulation of protein localization	-2.164245026	IL1B|PTGS2|TNFAIP6
s1	3	regulation of anatomical structure size	-2.082168316	MMP2|PTGS2|SOD2
s1	3	response to inorganic substance	-2.054629643	MMP2|PTGS2|SOD2
s1	6	response to wounding	-5.99571744	COL3A1|COL5A1|FGF7|MMP2|SERPINE2|SOD2
s1	3	collagen metabolic process	-4.719855964	COL1A2|COL5A1|MMP2
s1	4	gland development	-3.437324995	FGF7|MMP2|SERPINE2|SOD2
s1	4	response to radiation	-3.433420161	COL3A1|MME|MMP2|SOD2
s1	3	morphogenesis of an epithelium	-2.226149895	COL5A1|FGF7|MMP2
s1	6	blood vessel development	-5.463321383	COL1A2|COL3A1|COL5A1|MMP2|PTGS2|TGFBI
s1	3	response to angiotensin	-5.458684598	COL3A1|INHBA|PTGS2
s1	6	vasculature development	-5.369783317	COL1A2|COL3A1|COL5A1|MMP2|PTGS2|TGFBI
s1	5	tissue morphogenesis	-4.056531844	COL3A1|COL5A1|FGF7|INHBA|MMP2
s1	5	heart development	-4.049339842	COL3A1|COL5A1|INHBA|MMP2|SOD2
s1	5	cellular response to organonitrogen	-3.968527986	COL1A2|COL3A1|INHBA|MMP2|PTGS2
s1	5	enzyme-linked receptor protein signaling	-3.8877212	COL1A2|COL3A1|FGF7|INHBA|MMP2

s1	5	cellular response to nitrogen compound	-3.845354133	COL1A2|COL3A1|INHBA|MMP2|PTGS2
s1	5	response to hormone	-3.428533474	COL3A1|INHBA|MME|MMP2|PTGS2
s1	4	blood vessel morphogenesis	-3.402532993	COL3A1|MMP2|PTGS2|TGFBI
s1	4	response to peptide	-3.29194893	COL3A1|INHBA|MMP2|PTGS2
s1	4	tube morphogenesis	-2.662954422	COL3A1|MMP2|PTGS2|TGFBI
s1	3	angiogenesis	-2.586229681	MMP2|PTGS2|TGFBI
s1	4	head development	-2.476109061	COL3A1|INHBA|MMP2|SERPINE2
s1	3	response to peptide hormone	-2.458452276	COL3A1|INHBA|PTGS2
s1	3	cellular response to organic cyclic compound	-2.151778231	INHBA|MMP2|PTGS2
s1	3	endodermal cell differentiation	-5.192255371	COL12A1|INHBA|MMP2
s1	3	ovulation cycle process	-5.10506695	INHBA|MMP2|TNFAIP6
s1	3	ovarian follicle development	-4.971773848	INHBA|MMP2|TNFAIP6
s1	3	endoderm formation	-4.922117269	COL12A1|INHBA|MMP2
s1	3	ovulation cycle	-4.61997241	INHBA|MMP2|TNFAIP6
s1	3	endoderm development	-4.424487874	COL12A1|INHBA|MMP2
s1	3	female gonad development	-4.226701178	INHBA|MMP2|TNFAIP6
s1	3	development of primary female sexual	-4.171595549	INHBA|MMP2|TNFAIP6
s1	4	reproductive structure development	-4.023534958	INHBA|MMP2|SERPINE2|TNFAIP6
s1	4	reproductive system development	-4.000983666	INHBA|MMP2|SERPINE2|TNFAIP6
s1	3	female sex differentiation	-3.984120724	INHBA|MMP2|TNFAIP6
s1	3	formation of primary germ layer	-3.883779183	COL12A1|INHBA|MMP2
s1	5	negative regulation of cell differentiation	-3.561883636	COL5A1|IL1B|INHBA|SOD2|TNFAIP6
s1	3	gastrulation	-3.44605094	COL12A1|INHBA|MMP2
s1	3	gonad development	-3.084447605	INHBA|MMP2|TNFAIP6
s1	3	development of primary sexual	-3.056864745	INHBA|MMP2|TNFAIP6
s1	3	rhythmic process	-2.870453273	INHBA|MMP2|TNFAIP6

s1	3	sex differentiation	-2.806925397	INHBA|MMP2|TNFAIP6
s1	3	negative regulation of cell development	-2.780716093	IL1B|INHBA|TNFAIP6
s1	4	chemotaxis	-3.781697552	FGF7|IL1B|MMP2|CXCL6
s1	4	taxis	-3.771976039	FGF7|IL1B|MMP2|CXCL6
s1	3	myeloid leukocyte migration	-3.695263564	IL1B|MMP2|CXCL6
s1	4	locomotion	-3.682498963	FGF7|IL1B|MMP2|CXCL6
s1	3	leukocyte chemotaxis	-3.615071973	IL1B|MMP2|CXCL6
s1	5	cellular response to cytokine stimulus	-3.539882949	IL1B|INHBA|MME|MMP2|CXCL6
s1	3	cell chemotaxis	-3.141591149	IL1B|MMP2|CXCL6
s1	4	cellular response to lipid	-3.055417923	IL1B|INHBA|MMP2|CXCL6
s1	3	leukocyte migration	-2.982854812	IL1B|MMP2|CXCL6
s1	3	cytokine-mediated signaling pathway	-2.442234716	IL1B|INHBA|CXCL6
s1	3	regulation of hormone levels	-2.02117421	IL1B|INHBA|MME
s1	3	molting cycle	-4.185147504	FGF7|INHBA|PTGS2
s1	3	hair cycle	-4.185147504	FGF7|INHBA|PTGS2
s1	5	positive regulation of protein	-3.914274757	CLU|FGF7|IL1B|INHBA|PTGS2
s1	5	positive regulation of phosphorylation	-3.748025137	CLU|FGF7|IL1B|INHBA|PTGS2
s1	4	lipid localization	-3.589205702	CLU|IL1B|INHBA|PTGS2
s1	5	positive regulation of phosphorus metabolic	-3.550850313	CLU|FGF7|IL1B|INHBA|PTGS2
s1	5	positive regulation of phosphate metabolic	-3.550850313	CLU|FGF7|IL1B|INHBA|PTGS2
s1	4	secretion by cell	-3.468924808	FGF7|INHBA|SERPINE2|PTGS2
s1	4	negative regulation of transport	-3.256798955	IL1B|INHBA|SERPINE2|PTGS2
s1	4	export from cell	-3.242963483	FGF7|INHBA|SERPINE2|PTGS2
s1	4	positive regulation of cytokine production	-3.155989741	CLU|IL1B|LUM|PTGS2
s1	4	secretion	-3.064564533	FGF7|INHBA|SERPINE2|PTGS2
s1	3	lipid transport	-2.543203236	CLU|INHBA|PTGS2

s1	4	regulation of epithelial cell migration	-4.023534958	DCN|FGF7|PTGS2|SPARC
s1	3	positive regulation of epithelial cell	-3.394516345	FGF7|PTGS2|SPARC
s1	3	regulation of endothelial cell migration	-3.051423585	DCN|PTGS2|SPARC
s1	3	regulation of epithelial cell proliferation	-2.352509697	FGF7|SPARC|NEAT1
s1	5	cell activation	-3.567425261	CLU|COL3A1|IL1B|SERPINE2|CXCL6
s1	4	inflammatory response	-2.984201417	CLU|IL1B|CXCL6|TNFAIP6
s1	3	gliogenesis	-2.884523455	CLU|COL3A1|IL1B
s1	3	regulation of protein catabolic process	-2.488241231	CLU|IL1B|SERPINE2
s1	3	response to monosaccharide	-3.564365263	COL6A3|PTGS2|SOD2
s1	3	positive regulation of synaptic transmission	-3.564365263	MME|SERPINE2|PTGS2
s1	4	modulation of chemical synaptic	-3.188851317	IL1B|MME|SERPINE2|PTGS2
s1	4	regulation of trans-synaptic signaling	-3.18553275	IL1B|MME|SERPINE2|PTGS2
s1	3	regulation of synaptic plasticity	-3.147457731	MME|SERPINE2|PTGS2
s1	3	positive regulation of neurogenesis	-2.993150752	IL1B|MME|SERPINE2
s1	4	behavior	-2.830288454	MME|SERPINE2|PTGS2|SOD2
s1	3	positive regulation of nervous system	-2.767827981	IL1B|MME|SERPINE2
s1	3	negative regulation of cell adhesion	-2.67742663	MMP2|SERPINE2|TGFBI
s1	4	protein catabolic process	-2.59936034	CLU|MME|MMP2|SERPINE2
s1	3	regulation of neurogenesis	-2.404236072	IL1B|MME|SERPINE2
s1	3	positive regulation of cell development	-2.247585827	IL1B|MME|SERPINE2
s1	3	regulation of nervous system development	-2.189614579	IL1B|MME|SERPINE2
s1	3	lung development	-3.352010521	COL3A1|FGF7|MME
s1	3	respiratory tube development	-3.324474892	COL3A1|FGF7|MME
s1	3	respiratory system development	-3.183269909	COL3A1|FGF7|MME
s1	3	negative regulation of cell migration	-2.458452276	COL3A1|DCN|TNFAIP6
s1	3	negative regulation of cell motility	-2.410480992	COL3A1|DCN|TNFAIP6

s1	3	growth	-2.320269295	COL3A1|FGF7|TNFAIP6
s1	3	developmental growth	-2.320269295	COL3A1|FGF7|TNFAIP6
s1	3	negative regulation of locomotion	-2.305917105	COL3A1|DCN|TNFAIP6
s1	3	negative regulation of immune system	-2.061448291	COL3A1|INHBA|TNFAIP6
s1	4	positive regulation of catabolic process	-2.883422407	CLU|DCN|IL1B|NEAT1
s1	3	regulation of angiogenesis	-2.53968954	DCN|IL1B|SPARC
s1	3	regulation of vasculature development	-2.522281172	DCN|IL1B|SPARC
s1	3	regulation of cellular response to growth factor stimulus	-2.511962069	DCN|IL1B|TNFAIP6
s1	3	positive regulation of cellular catabolic	-2.416760698	DCN|IL1B|NEAT1
s1	3	regulation of small molecule metabolic	-2.582581915	IGFBP4|IL1B|PTGS2
s1	3	regulation of cell growth	-2.32316206	IGFBP4|INHBA|SERPINE2
s1	3	positive regulation of MAPK cascade	-2.169271975	IGFBP4|IL1B|INHBA
s2	16	mitotic cell cycle	-20.99713676	BIRC5|CCNB1|CDC20|CDKN3|CENPF|CKS1B|CKS2|STMN1|CCNB2|DLGAP5|TUBA1B|TUBB4B|TPX2|UBE2S|TUBA1C|CENPW
s2	14	cell division	-18.30070361	BIRC5|CCNB1|CDC20|CENPF|CKS1B|CKS2|STMN1|CCNB2|PTTG1|TUBA1B|TPX2|UBE2S|TUBA1C|CENPW
s2	12	mitotic cell cycle process	-14.59269434	BIRC5|CCNB1|CDC20|CDKN3|CENPF|CKS1B|CKS2|STMN1|CCNB2|DLGAP5|TPX2|UBE2S
s2	10	microtubule cytoskeleton organization	-10.98444427	BIRC5|CCNB1|CDC20|STMN1|CCNB2|DLGAP5|TUBA1B|TUBB4B|TPX2|TUBA1C
s2	11	chromosome organization	-13.28011149	BIRC5|CCNB1|CDC20|CENPF|HMGB1|HMGB3|HSP90AA1|PTTG1|DLGAP5|TPX2|CENPW
s2	5	DNA metabolic process	-3.462277391	CENPF|HMGB1|HMGB3|HSP90AA1|PTTG1
s2	9	nuclear division	-11.65143841	BIRC5|CCNB1|CDC20|CKS2|CCNB2|PTTG1|DLGAP5|TPX2|UBE2S

s2	9	chromosome segregation	-11.44694179	BIRC5|CCNB1|CDC20|CENPF|CCNB2|PTTG1|DLGAP5|TPX2|CENPW
s2	9	organelle fission	-11.3430046	BIRC5|CCNB1|CDC20|CKS2|CCNB2|PTTG1|DLGAP5|TPX2|UBE2S
s2	8	nuclear chromosome segregation	-11.05578249	BIRC5|CCNB1|CDC20|CENPF|CCNB2|PTTG1|DLGAP5|TPX2
s2	7	spindle organization	-10.2392067	BIRC5|CCNB1|CDC20|STMN1|CCNB2|DLGAP5|TPX2
s2	6	mitotic spindle organization	-9.864958035	BIRC5|CCNB1|CDC20|STMN1|DLGAP5|TPX2
s2	6	microtubule cytoskeleton organization involved in mitosis	-9.036724754	BIRC5|CCNB1|CDC20|STMN1|DLGAP5|TPX2
s2	5	regulation of mitotic sister chromatid	-8.916219167	BIRC5|CCNB1|CDC20|CENPF|DLGAP5
s2	6	mitotic nuclear division	-8.444573984	BIRC5|CCNB1|CDC20|DLGAP5|TPX2|UBE2S
s2	5	regulation of chromosome separation	-8.412268403	BIRC5|CCNB1|CDC20|CENPF|DLGAP5
s2	7	non-membrane-bounded organelle assembly	-8.096935213	BIRC5|CDC20|CENPF|CCNB2|DLGAP5|TPX2|CENPW
s2	5	regulation of mitotic metaphase/anaphase	-7.980205975	BIRC5|CCNB1|CDC20|CENPF|DLGAP5
s2	5	regulation of metaphase/anaphase transition of cell cycle	-7.90811183	BIRC5|CCNB1|CDC20|CENPF|DLGAP5
s2	5	regulation of sister chromatid segregation	-7.662896003	BIRC5|CCNB1|CDC20|CENPF|DLGAP5
s2	5	regulation of mitotic nuclear division	-7.386909384	BIRC5|CCNB1|CDC20|CENPF|DLGAP5
s2	5	regulation of chromosome segregation	-7.15933095	BIRC5|CCNB1|CDC20|CENPF|DLGAP5
s2	5	mitotic sister chromatid segregation	-7.077942646	BIRC5|CCNB1|CDC20|DLGAP5|TPX2
s2	5	sister chromatid segregation	-7.015021705	BIRC5|CCNB1|CDC20|DLGAP5|TPX2
s2	4	regulation of mitotic sister chromatid	-6.955624623	BIRC5|CCNB1|CDC20|CENPF
s2	5	regulation of nuclear division	-6.924031571	BIRC5|CCNB1|CDC20|CENPF|DLGAP5
s2	7	regulation of mitotic cell cycle	-6.810387068	BIRC5|CCNB1|CDC20|CENPF|CKS1B|CKS2|DLGAP5
s2	3	positive regulation of mitotic sister chromatid separation	-6.396435688	BIRC5|CDC20|DLGAP5
s2	4	spindle assembly	-5.838876074	BIRC5|CDC20|CCNB2|TPX2

s2	5	regulation of chromosome organization	-5.794136775	BIRC5|CCNB1|CDC20|CENPF|DLGAP5
s2	3	positive regulation of chromosome	-5.747958873	BIRC5|CDC20|DLGAP5
s2	3	mitotic spindle assembly	-5.050072873	BIRC5|CDC20|TPX2
s2	5	regulation of mitotic cell cycle phase	-5.026975511	BIRC5|CCNB1|CDC20|CENPF|DLGAP5
s2	6	regulation of cell cycle process	-4.590059758	BIRC5|CCNB1|CDC20|CENPF|DLGAP5|TPX2
s2	5	regulation of cell cycle phase transition	-4.504814168	BIRC5|CCNB1|CDC20|CENPF|DLGAP5
s2	4	positive regulation of cell cycle process	-4.222783172	BIRC5|CCNB1|CDC20|DLGAP5
s2	3	positive regulation of mitotic cell cycle phase transition	-4.14492185	CCNB1|CDC20|DLGAP5
s2	3	positive regulation of cell cycle phase	-3.894538299	CCNB1|CDC20|DLGAP5
s2	4	positive regulation of cell cycle	-3.816202388	BIRC5|CCNB1|CDC20|DLGAP5
s2	3	positive regulation of mitotic cell cycle	-3.800895221	CCNB1|CDC20|DLGAP5
s2	4	negative regulation of organelle	-3.771976039	CDC20|CENPF|STMN1|TPX2
s2	5	negative regulation of cellular component	-3.584151104	CDC20|CENPF|HMGB1|STMN1|TPX2
s2	7	cell cycle phase transition	-10.06043757	CCNB1|CDC20|CDKN3|CKS1B|CKS2|CCNB2|UBE2S
s2	6	mitotic cell cycle phase transition	-8.428621371	CCNB1|CDKN3|CKS1B|CKS2|CCNB2|UBE2S
s2	7	regulation of transferase activity	-5.976606451	CCNB1|CDC20|CDKN3|HSP90AA1|CCNB2|TPX2|UBE2S
s2	3	regulation of cyclin-dependent protein serine/threonine kinase activity	-4.376020537	CCNB1|CDKN3|CCNB2
s2	3	regulation of cyclin-dependent protein	-4.329342171	CCNB1|CDKN3|CCNB2
s2	5	regulation of protein kinase activity	-4.302197674	CCNB1|CDKN3|HSP90AA1|CCNB2|TPX2
s2	5	regulation of kinase activity	-4.006748871	CCNB1|CDKN3|HSP90AA1|CCNB2|TPX2
s2	3	regulation of protein serine/threonine	-2.789387615	CCNB1|CDKN3|CCNB2
s2	3	kinetochore assembly	-6.746078367	CENPF|DLGAP5|CENPW
s2	3	kinetochore organization	-6.396435688	CENPF|DLGAP5|CENPW
s2	3	centromere complex assembly	-6.003334412	CENPF|DLGAP5|CENPW

s2	3	chromosome localization	-4.14492185	CCNB1|CENPF|DLGAP5
s2	3	protein-DNA complex assembly	-3.073338161	CENPF|DLGAP5|CENPW
s2	3	organelle localization	-2.010251872	CCNB1|CENPF|DLGAP5
s2	4	positive regulation of transferase activity	-3.464939267	CDC20|HSP90AA1|TPX2|UBE2S
s2	3	regulation of protein ubiquitination	-3.232734182	CDC20|HSP90AA1|UBE2S
s2	3	regulation of protein modification by small protein conjugation or removal	-2.987991659	CDC20|HSP90AA1|UBE2S
s2	3	regulation of post-translational protein	-2.793747546	CDC20|HSP90AA1|UBE2S
s2	4	meiosis I cell cycle process	-5.48637854	CDC20|CKS2|CCNB2|PTTG1
s2	4	meiotic cell cycle process	-4.785474783	CDC20|CKS2|CCNB2|PTTG1
s2	4	meiotic cell cycle	-4.295081277	CDC20|CKS2|CCNB2|PTTG1
s2	3	meiosis I	-3.852047877	CKS2|CCNB2|PTTG1
s2	3	meiotic nuclear division	-3.453593415	CKS2|CCNB2|PTTG1
s2	3	regulation of protein-containing complex	-2.317384021	HMGB1|HSP90AA1|STMN1
s2	5	chromatin organization	-3.436265075	H2AZ1|HMGB1|HMGN2|ANP32E|CENPW
s3	17	cell division	-24.24804113	CCNA2|CDK1|CENPE|CENPF|CKS2|AURKA|TOP2A|KIF23|KIF20B|SMC4|UBE2C|TPX2|CKAP2|NUSAP1|ANLN|NCAPG|ASPM
s3	15	mitotic cell cycle process	-20.09841463	CCNA2|CDK1|CENPE|CENPF|CKS2|AURKA|KIF23|SMC4|UBE2C|TPX2|CKAP2|NUSAP1|GTSE1|ANLN|NCAPG
s3	15	mitotic cell cycle	-19.09340589	CCNA2|CDK1|CENPE|CENPF|CKS2|AURKA|KIF23|SMC4|UBE2C|TPX2|CKAP2|NUSAP1|GTSE1|ANLN|NCAPG
s3	14	regulation of cell cycle process	-16.04259221	CDK1|CENPE|CENPF|MKI67|AURKA|KIF23|KIF20B|SMC4|UBE2C|TPX2|NUSAP1|GTSE1|ANLN|NCAPG
s3	13	chromosome organization	-16.82080187	CDK1|CENPE|CENPF|H1-3|H1-5|HMGB2|TOP2A|H4C3|KIF23|SMC4|TPX2|NUSAP1|NCAPG
s3	7	chromosome condensation	-14.56278585	CDK1|H1-3|H1-5|TOP2A|SMC4|NUSAP1|NCAPG

s3	11	nuclear division	-15.29807695	CENPE|CKS2|AURKA|TOP2A|KIF23|SMC4|UBE2C|TPX2|NUSAP1|NCAPG|ASPM
s3	11	organelle fission	-14.91811311	CENPE|CKS2|AURKA|TOP2A|KIF23|SMC4|UBE2C|TPX2|NUSAP1|NCAPG|ASPM
s3	10	nuclear chromosome segregation	-14.8503045	CENPE|CENPF|AURKA|TOP2A|KIF23|SMC4|TPX2|NUSAP1|NCAPG|ASPM
s3	10	chromosome segregation	-13.21125673	CENPE|CENPF|AURKA|TOP2A|KIF23|SMC4|TPX2|NUSAP1|NCAPG|ASPM
s3	8	mitotic nuclear division	-12.22945974	CENPE|AURKA|KIF23|SMC4|UBE2C|TPX2|NUSAP1|NCAPG
s3	7	sister chromatid segregation	-10.76168156	CENPE|TOP2A|KIF23|SMC4|TPX2|NUSAP1|NCAPG
s3	6	microtubule cytoskeleton organization involved in mitosis	-9.036724754	CDK1|CENPE|AURKA|KIF23|TPX2|NUSAP1
s3	6	mitotic sister chromatid segregation	-8.918281865	CENPE|KIF23|SMC4|TPX2|NUSAP1|NCAPG
s3	7	non-membrane-bounded organelle assembly	-8.096935213	CENPE|CENPF|AURKA|KIF23|TPX2|ANLN|ASPM
s3	5	spindle organization	-6.646388898	CENPE|AURKA|KIF23|TPX2|ASPM
s3	7	microtubule cytoskeleton organization	-6.608698358	CDK1|CENPE|AURKA|KIF23|TPX2|NUSAP1|ASPM
s3	4	mitotic spindle organization	-5.962623871	CENPE|AURKA|KIF23|TPX2
s3	4	spindle assembly	-5.838876074	AURKA|KIF23|TPX2|ASPM
s3	4	negative regulation of organelle	-3.771976039	CENPF|TOP2A|TPX2|CKAP2
s3	3	regulation of microtubule-based process	-2.913176302	AURKA|TPX2|CKAP2
s3	4	negative regulation of cellular component	-2.57951135	CENPF|TOP2A|TPX2|CKAP2
s3	11	regulation of mitotic cell cycle	-12.9111676	CDK1|CENPE|CENPF|CKS2|MKI67|AURKA|KIF20B|UBE2C|NUSAP1|GTSE1|ANLN
s3	7	regulation of chromosome segregation	-10.96626498	CDK1|CENPE|CENPF|MKI67|SMC4|UBE2C|NCAPG
s3	7	regulation of chromosome organization	-9.031033127	CDK1|CENPE|CENPF|TOP2A|SMC4|UBE2C|NCAPG
s3	7	regulation of mitotic cell cycle phase	-7.941450248	CDK1|CENPE|CENPF|AURKA|UBE2C|GTSE1|ANLN

s3	7	regulation of cell cycle phase transition	-7.197541482	CDK1|CENPE|CENPF|AURKA|UBE2C|GTSE1|ANLN
s3	3	kinetochore organization	-6.396435688	CENPE|CENPF|SMC4
s3	4	regulation of sister chromatid segregation	-5.80512263	CDK1|CENPE|CENPF|UBE2C
s3	3	regulation of mitotic metaphase/anaphase	-4.255185036	CENPE|CENPF|UBE2C
s3	3	regulation of metaphase/anaphase transition of cell cycle	-4.212697076	CENPE|CENPF|UBE2C
s3	3	regulation of G2/M transition of mitotic cell	-4.068138053	CDK1|CENPF|AURKA
s3	3	regulation of cell cycle G2/M phase	-3.927383626	CDK1|CENPF|AURKA
s3	3	mitotic cell cycle checkpoint signaling	-3.831333894	CDK1|CENPF|GTSE1
s3	3	cell cycle checkpoint signaling	-3.523648003	CDK1|CENPF|GTSE1
s3	3	negative regulation of mitotic cell cycle phase transition	-3.352010521	CDK1|CENPF|GTSE1
s3	3	negative regulation of mitotic cell cycle	-3.046007053	CDK1|CENPF|GTSE1
s3	4	organelle localization	-3.022352764	CENPE|CENPF|NUSAP1|ASPM
s3	3	negative regulation of cell cycle phase	-2.977740027	CDK1|CENPF|GTSE1
s3	3	negative regulation of cell cycle process	-2.763563282	CDK1|CENPF|GTSE1
s3	3	negative regulation of cell cycle	-2.439018892	CDK1|CENPF|GTSE1
s3	3	establishment of organelle localization	-2.358472816	CENPE|CENPF|NUSAP1
s3	3	response to xenobiotic stimulus	-2.320269295	CDK1|CENPF|TYMS
s3	3	muscle structure development	-2.072910004	CDK1|CENPF|H1-5
s3	8	positive regulation of cell cycle process	-10.57319221	CDK1|AURKA|KIF23|KIF20B|SMC4|UBE2C|NUSAP1|NCAPG
s3	8	positive regulation of cell cycle	-9.735158489	CDK1|AURKA|KIF23|KIF20B|SMC4|UBE2C|NUSAP1|NCAPG
s3	3	mitotic chromosome condensation	-6.475380414	SMC4|NUSAP1|NCAPG
s3	4	regulation of chromosome separation	-6.39954084	CENPF|SMC4|UBE2C|NCAPG
s3	3	positive regulation of chromosome	-5.844128555	CDK1|SMC4|NCAPG
s3	3	positive regulation of chromosome	-5.747958873	SMC4|UBE2C|NCAPG

s3	6	positive regulation of organelle organization	-5.550790305	CDK1|AURKA|SMC4|UBE2C|NUSAP1|NCAPG
s3	3	positive regulation of chromosome	-4.007556268	CDK1|SMC4|NCAPG
s3	5	mitotic cell cycle phase transition	-6.67255621	CCNA2|CDK1|CKS2|AURKA|UBE2C
s3	4	animal organ regeneration	-6.655034921	CCNA2|CDK1|AURKA|TYMS
s3	5	cell cycle phase transition	-6.520247366	CCNA2|CDK1|CKS2|AURKA|UBE2C
s3	4	regeneration	-5.160724863	CCNA2|CDK1|AURKA|TYMS
s3	3	G2/M transition of mitotic cell cycle	-5.02343717	CCNA2|CDK1|AURKA
s3	3	cell cycle G2/M phase transition	-4.897994355	CCNA2|CDK1|AURKA
s3	6	DNA metabolic process	-4.538288735	CDK1|CENPF|HMGB2|KPNA2|TOP2A|TYMS
s3	3	positive regulation of mitotic cell cycle	-3.800895221	CDK1|AURKA|UBE2C
s3	3	rhythmic process	-2.870453273	CDK1|TOP2A|TYMS
s3	4	DNA damage response	-2.496598907	CDK1|HMGB2|TOP2A|GTSE1
s3	6	regulation of mitotic nuclear division	-9.291537228	CENPF|MKI67|AURKA|KIF20B|UBE2C|NUSAP1
s3	6	regulation of nuclear division	-8.732369929	CENPF|MKI67|AURKA|KIF20B|UBE2C|NUSAP1
s3	3	positive regulation of mitotic nuclear	-5.192255371	AURKA|UBE2C|NUSAP1
s3	3	positive regulation of nuclear division	-4.783777539	AURKA|UBE2C|NUSAP1
s3	6	protein-DNA complex assembly	-7.585047729	CENPE|CENPF|H1-3|H1-5|HMGB2|H4C3
s3	4	nucleosome assembly	-5.586064622	H1-3|H1-5|HMGB2|H4C3
s3	4	nucleosome organization	-5.315635709	H1-3|H1-5|HMGB2|H4C3
s3	6	chromatin remodeling	-5.028970447	CDK1|H1-3|H1-5|HMGB2|AURKA|H4C3
s3	6	chromatin organization	-4.506524367	CDK1|H1-3|H1-5|HMGB2|AURKA|H4C3
s3	5	regulation of DNA metabolic process	-4.206358843	CCNA2|CDK1|H1-3|H1-5|KPNA2
s3	3	regulation of DNA recombination	-3.723191875	H1-3|H1-5|KPNA2
s3	5	meiotic nuclear division	-6.620544638	CKS2|AURKA|TOP2A|SMC4|ASPM
s3	5	meiotic cell cycle process	-6.378293693	CKS2|AURKA|TOP2A|SMC4|ASPM
s3	5	meiotic cell cycle	-5.759928	CKS2|AURKA|TOP2A|SMC4|ASPM

s3	3	meiotic chromosome segregation	-4.299154553	AURKA|SMC4|ASPM
s3	3	meiosis I	-3.852047877	CKS2|AURKA|TOP2A
s3	3	meiosis I cell cycle process	-3.831333894	CKS2|AURKA|TOP2A
s3	3	female gamete generation	-3.531684362	AURKA|TOP2A|ASPM
s3	4	cellular process involved in reproduction in multicellular organism	-3.29194893	HMGB2|AURKA|TOP2A|ASPM
s3	3	cellular component disassembly	-2.638549683	CDK1|AURKA|TOP2A
s3	4	gamete generation	-2.414450933	HMGB2|AURKA|TOP2A|ASPM
s3	3	growth	-2.320269295	AURKA|TYMS|ASPM
s3	3	developmental growth	-2.320269295	AURKA|TYMS|ASPM
s3	4	mitotic cytokinesis	-6.219597824	KIF23|CKAP2|NUSAP1|ANLN
s3	4	cytoskeleton-dependent cytokinesis	-5.69203559	KIF23|CKAP2|NUSAP1|ANLN
s3	4	cytokinesis	-5.661071319	KIF23|CKAP2|NUSAP1|ANLN
s3	4	regulation of cell division	-4.80372325	AURKA|KIF23|KIF20B|ASPM
s3	3	regulation of cytokinesis	-4.212697076	AURKA|KIF23|KIF20B
s3	3	microtubule-based movement	-2.410480992	CENPE|KIF23|KIF20B
s3	6	protein localization to organelle	-4.596615233	CDK1|H1-5|KPNA2|AURKA|H4C3|KIF20B
s3	3	protein localization to chromosome	-4.19884695	CDK1|H1-5|H4C3
s3	4	regulation of transferase activity	-2.633073944	CCNA2|CENPE|UBE2C|TPX2
s3	3	positive regulation of transferase activity	-2.334808738	CENPE|UBE2C|TPX2
s3	3	regulation of protein kinase activity	-2.098564623	CCNA2|CENPE|TPX2
s4	5	regulation of cell-substrate adhesion	-6.041224272	DAB2|CCN1|SERPINE1|ABI3BP|CCDC80
s4	5	extracellular matrix organization	-5.589134559	CCN1|P4HA1|ADAMTS6|ABI3BP|CCDC80
s4	5	extracellular structure organization	-5.581346446	CCN1|P4HA1|ADAMTS6|ABI3BP|CCDC80
s4	5	external encapsulating structure	-5.573587906	CCN1|P4HA1|ADAMTS6|ABI3BP|CCDC80
s4	4	positive regulation of cell-substrate adhesion	-5.514261658	DAB2|CCN1|ABI3BP|CCDC80

s4	4	positive regulation of cell adhesion	-3.212287666	DAB2|CCN1|ABI3BP|CCDC80
s4	3	response to decreased oxygen levels	-2.713565456	BNIP3|OXTR|PGK1
s4	3	response to oxygen levels	-2.604644015	BNIP3|OXTR|PGK1
s4	3	cytoplasmic translation	-3.852047877	EIF4A2|RPS17|RPS29
s4	3	translation	-2.39802558	EIF4A2|RPS17|RPS29
s4	3	peptide biosynthetic process	-2.311635797	EIF4A2|RPS17|RPS29
s4	3	peptide metabolic process	-2.06831061	EIF4A2|RPS17|RPS29
s4	3	amide biosynthetic process	-2.003751981	EIF4A2|RPS17|RPS29
s4	4	response to mechanical stimulus	-4.572967944	BNIP3|FGF2|TXNIP|USP53
s4	3	response to oxidative stress	-2.481553642	BNIP3|ND3|TXNIP
s4	3	forebrain development	-2.355487286	BNIP3|FGF2|OXTR
s4	3	response to wounding	-2.305917105	BNIP3|FGF2|CCN1
s4	3	positive regulation of apoptotic process	-2.014607346	BNIP3|CCN1|TXNIP
s4	5	blood vessel development	-4.22200512	FGF2|CCN1|SERPINE1|ADAMTS6|CCBE1
s4	5	vasculature development	-4.145015985	FGF2|CCN1|SERPINE1|ADAMTS6|CCBE1
s4	5	positive regulation of cell migration	-4.027925254	DAB2|FGF2|CCN1|SERPINE1|CCBE1
s4	5	positive regulation of cell motility	-3.941206954	DAB2|FGF2|CCN1|SERPINE1|CCBE1
s4	5	positive regulation of locomotion	-3.894324634	DAB2|FGF2|CCN1|SERPINE1|CCBE1
s4	4	angiogenesis	-3.806266687	FGF2|CCN1|SERPINE1|CCBE1
s4	4	regulation of angiogenesis	-3.743166277	FGF2|SERPINE1|PGK1|CCBE1
s4	4	regulation of vasculature development	-3.719554593	FGF2|SERPINE1|PGK1|CCBE1
s4	4	blood vessel morphogenesis	-3.402532993	FGF2|CCN1|SERPINE1|CCBE1
s4	3	positive regulation of angiogenesis	-3.331300651	FGF2|SERPINE1|CCBE1
s4	3	positive regulation of vasculature	-3.331300651	FGF2|SERPINE1|CCBE1
s4	4	tube morphogenesis	-2.662954422	FGF2|CCN1|SERPINE1|CCBE1
s4	4	response to steroid hormone	-4.141317632	DAB2|ND3|OXTR|TXNIP

s4	3	response to salt	-2.481553642	DAB2|OXTR|TXNIP
s4	4	response to hormone	-2.457923253	DAB2|ND3|OXTR|TXNIP
s4	5	enzyme-linked receptor protein signaling	-3.8877212	BDNF|DAB2|FGF2|TXNIP|CRIM1
s4	3	positive regulation of lipid metabolic	-3.641228751	DAB2|FGF2|CCN1
s4	4	transmembrane receptor protein tyrosine kinase signaling pathway	-3.453044003	BDNF|FGF2|TXNIP|CRIM1
s4	4	heart development	-2.944186166	FGF2|CCN1|OXTR|ADAMTS6
s4	4	positive regulation of protein	-2.838136215	BDNF|DAB2|FGF2|CCN1
s4	4	epithelial cell differentiation	-2.791672866	DAB2|FGF2|PGK1|TXNIP
s4	3	positive regulation of nervous system	-2.767827981	BDNF|FGF2|OXTR
s4	4	positive regulation of phosphorylation	-2.707783666	BDNF|DAB2|FGF2|CCN1
s4	3	regulation of ERK1 and ERK2 cascade	-2.673479725	DAB2|FGF2|CCN1
s4	3	regulation of lipid metabolic process	-2.564514794	DAB2|FGF2|CCN1
s4	4	positive regulation of phosphorus metabolic	-2.553473666	BDNF|DAB2|FGF2|CCN1
s4	4	positive regulation of phosphate metabolic	-2.553473666	BDNF|DAB2|FGF2|CCN1
s4	3	regulation of nervous system development	-2.189614579	BDNF|FGF2|OXTR
s4	3	cellular response to growth factor stimulus	-2.139452736	BDNF|DAB2|FGF2
s4	3	response to growth factor	-2.066018287	BDNF|DAB2|FGF2
s4	4	regulation of cellular response to growth factor stimulus	-3.70555601	FGF2|CCN1|CRIM1|CCBE1
s4	3	regulation of osteoblast differentiation	-3.597937022	FGF2|CCN1|CRIM1
s4	3	regulation of transmembrane receptor protein serine/threonine kinase signaling	-2.738296694	DAB2|CCN1|CRIM1
s4	3	generation of precursor metabolites and	-2.346578184	ATP5ME|ND3|PGK1
s4	3	organophosphate biosynthetic process	-2.005914191	ATP5ME|FGF2|ND3

s5	21	DNA metabolic process	-29.65925548	CDC6|DNMT1|FEN1|MSH6|HELLS|MCM3|MCM4|MCM5|MCM6|MCM7|NASP|PCNA|CHAF1A|ORC6|UHRF1|GMNN|GINS2|MCM10|CLSPN|DCTPP1|FAM111B
s5	15	DNA replication	-26.51744835	CDC6|FEN1|MCM3|MCM4|MCM5|MCM6|MCM7|NASP|PCNA|CHAF1A|ORC6|GMNN|GINS2|MCM10|FAM111B
s5	12	DNA-templated DNA replication	-21.7368428	CDC6|FEN1|MCM3|MCM4|MCM5|MCM6|MCM7|PCNA|ORC6|GMNN|GINS2|MCM10
s5	8	DNA replication initiation	-18.72385992	CDC6|MCM3|MCM4|MCM5|MCM6|MCM7|ORC6|MCM10
s5	6	double-strand break repair via break-induced replication	-15.81896282	MCM3|MCM4|MCM5|MCM6|MCM7|GINS2
s5	6	regulation of DNA-templated DNA replication initiation	-15.08593131	MCM3|MCM4|MCM5|MCM6|MCM7|GMNN
s5	12	DNA repair	-14.78471399	FEN1|MSH6|MCM3|MCM4|MCM5|MCM6|MCM7|PCNA|CHAF1A|UHRF1|GINS2|CLSPN
s5	13	DNA damage response	-14.29401068	FEN1|MSH6|MCM3|MCM4|MCM5|MCM6|MCM7|PCNA|CHAF1A|UHRF1|GINS2|MCM10|CLSPN
s5	7	regulation of DNA-templated DNA	-14.19633896	MCM3|MCM4|MCM5|MCM6|MCM7|PCNA|GMNN
s5	6	DNA unwinding involved in DNA	-14.05222489	MCM3|MCM4|MCM5|MCM6|MCM7|GINS2
s5	6	nuclear DNA replication	-13.42574265	FEN1|MCM3|MCM4|MCM6|PCNA|GMNN
s5	8	double-strand break repair via homologous recombination	-13.40193029	FEN1|MCM3|MCM4|MCM5|MCM6|MCM7|UHRF1|GINS2
s5	6	cell cycle DNA replication	-13.31683177	FEN1|MCM3|MCM4|MCM6|PCNA|GMNN
s5	8	recombinational repair	-13.28241577	FEN1|MCM3|MCM4|MCM5|MCM6|MCM7|UHRF1|GINS2
s5	8	regulation of DNA replication	-13.19544158	CDC6|MCM3|MCM4|MCM5|MCM6|MCM7|PCNA|GMNN
s5	9	DNA recombination	-12.68200896	FEN1|MSH6|MCM3|MCM4|MCM5|MCM6|MCM7|UHRF1|GINS2
s5	8	double-strand break repair	-11.34226634	FEN1|MCM3|MCM4|MCM5|MCM6|MCM7|UHRF1|GINS2

s5	6	DNA duplex unwinding	-10.4953829	MCM3|MCM4|MCM5|MCM6|MCM7|GINS2
s5	6	DNA geometric change	-10.2894894	MCM3|MCM4|MCM5|MCM6|MCM7|GINS2
s5	6	DNA conformation change	-10.03837244	MCM3|MCM4|MCM5|MCM6|MCM7|GINS2
s5	9	chromosome organization	-10.01415227	FEN1|MCM3|MCM4|MCM5|MCM6|MCM7|NASP|PCNA|GINS2
s5	9	regulation of DNA metabolic process	-9.663910137	CDC6|MSH6|MCM3|MCM4|MCM5|MCM6|MCM7|PCNA|GMNN
s5	4	DNA strand elongation involved in DNA	-9.311128979	MCM3|MCM4|MCM7|PCNA
s5	4	DNA strand elongation	-8.762172236	MCM3|MCM4|MCM7|PCNA
s5	3	mitotic DNA replication	-6.746078367	MCM3|MCM4|MCM6
s5	6	mitotic cell cycle process	-5.468096933	CDC6|MCM3|MCM4|MCM6|PCNA|CLSPN
s5	6	mitotic cell cycle	-5.085133278	CDC6|MCM3|MCM4|MCM6|PCNA|CLSPN
s5	3	negative regulation of gene expression via CpG island methylation	-7.761455947	DNMT1|HELLS|UHRF1
s5	6	chromatin remodeling	-5.028970447	DNMT1|HELLS|NASP|CHAF1A|DNAJC9|UHRF1
s5	3	heterochromatin formation	-4.61997241	DNMT1|HELLS|UHRF1
s5	6	chromatin organization	-4.506524367	DNMT1|HELLS|NASP|CHAF1A|DNAJC9|UHRF1
s5	3	heterochromatin organization	-4.424487874	DNMT1|HELLS|UHRF1
s5	3	negative regulation of gene expression,	-4.105943284	DNMT1|HELLS|UHRF1
s5	3	epigenetic regulation of gene expression	-3.22643937	DNMT1|HELLS|UHRF1
s5	3	negative regulation of DNA metabolic	-3.632448134	CDC6|MSH6|GMNN
s5	3	negative regulation of cell cycle	-2.439018892	CDC6|GMNN|CLSPN
s5	3	regulation of mitotic cell cycle	-2.059170581	CDC6|GMNN|CLSPN
s5	3	positive regulation of ATP-dependent	-5.285807956	MSH6|DNAJC9|UHRF1
s5	3	regulation of ATP-dependent activity	-4.699242234	MSH6|DNAJC9|UHRF1
s5	4	protein-DNA complex assembly	-4.46499525	NASP|CHAF1A|DNAJC9|GMNN
s5	3	nucleosome assembly	-3.905390999	NASP|CHAF1A|DNAJC9
s5	3	nucleosome organization	-3.704503236	NASP|CHAF1A|DNAJC9

s5	3	response to UV	-3.581036845	FEN1|MSH6|PCNA
s5	3	response to light stimulus	-2.67742663	FEN1|MSH6|PCNA
s5	3	response to radiation	-2.311635797	FEN1|MSH6|PCNA