Table SVII. GO and KEGG analysis.

Category	Term	Description	Count	P.adjust
BP	GO:0000070	Mitotic sister chromatid segregation	9	2.13×10^{-13}
BP	GO:0000819	Sister chromatid segregation	9	5.26×10^{-13}
BP	GO:0098813	Nuclear chromosome segregation	9	7.66×10^{-12}
BP	GO:0140014	Mitotic nuclear division	9	1.13×10^{-11}
BP	GO:0022402	Cell cycle process	13	1.99×10^{-11}
CC	GO:0005819	Spindle	8	5.73×10^{-9}
CC	GO:0015630	Microtubule cytoskeleton	10	4.93×10^{-8}
CC	GO:0044430	Cytoskeletal part	11	4.93×10^{-8}
CC	GO:0000775	Chromosome, centromeric region	6	1.27×10^{-7}
CC	GO:0000779	Condensed chromosome, centromeric region	5	3.67×10^{-7}
MF	GO:0019901	Protein kinase binding	6	5.51×10^{-4}
MF	GO:0019900	Kinase binding	6	5.82×10^{-4}
MF	GO:0008017	Microtubule binding	3	1.33×10^{-2}
MF	GO:0019899	Enzyme binding	7	1.84×10^{-2}
MF	GO:0003684	Damaged DNA binding	2	2.24×10^{-2}
KEGG	hsa04110	Cell cycle	3	4.04×10^{-4}
KEGG	hsa04114	Oocyte meiosis	2	1.36×10^{-2}
KEGG	hsa04218	Cellular senescence	2	1.43×10^{-2}

KEGG, Kyoto Encyclopedia of Genes and Genomes; GO, Gene Ontology; MF, molecular function; CC, cellular component; BP, biological process.