

Table SI. GO enrichment analysis of differentially expressed genes in hepatocellular carcinoma.

Term ID	Term	Counts	Percentage	P-value
Biological processes				
GO:0045926	Negative regulation of growth	8	6.349206349	4.21x10 ⁻¹¹
GO:0007067	Mitotic nuclear division	16	12.6984127	3.43x10 ⁻¹⁰
GO:0051301	Cell division	16	12.6984127	3.69x10 ⁻⁸
GO:0000281	Mitotic cytokinesis	6	4.761904762	1.93x10 ⁻⁶
GO:0007059	Chromosome segregation	7	5.555555556	9.85x10 ⁻⁶
GO:0071294	Cellular response to zinc ion	7	5.555555556	2.59x10 ⁻⁵
GO:0071276	Cellular response to cadmium ion	6	4.761904762	3.03x10 ⁻⁵
GO:0007062	Sister chromatid cohesion	7	5.555555556	1.05x10 ⁻⁴
GO:0006805	Xenobiotic metabolic process	6	4.761904762	2.58x10 ⁻⁴
GO:0019373	Epoxygenase P450 pathway	4	3.174603175	2.82x10 ⁻⁴
GO:0000086	G ₂ /M transition of mitotic cell cycle	7	5.555555556	4.92x10 ⁻⁴
GO:0051439	Regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	4	3.174603175	5.96x10 ⁻⁴
GO:0000070	Mitotic sister chromatid segregation	4	3.174603175	7.66x10 ⁻⁴
GO:0051436	Negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	5	3.968253968	1.77x10 ⁻³
GO:0097267	Omega-hydroxylase P450 pathway	3	2.380952381	1.82x10 ⁻³
GO:0034501	Protein localization to kinetochore	3	2.380952381	2.27x10 ⁻³
GO:0051437	Positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	5	3.968253968	2.27x10 ⁻³
GO:0031145	Anaphase-promoting complex-dependent catabolic process	5	3.968253968	2.62x10 ⁻³
GO:0007018	Microtubule-based movement	5	3.968253968	2.87x10 ⁻³
GO:0051310	Metaphase plate congression	3	2.380952381	3.29x10 ⁻³
GO:0042738	Exogenous drug catabolic process	3	2.380952381	3.29x10 ⁻³
GO:0042787	Protein ubiquitination involved in ubiquitin-dependent protein catabolic process	6	4.761904762	5.19x10 ⁻³
GO:0008283	Cell proliferation	9	7.142857143	5.27x10 ⁻³
GO:0016477	Cell migration	6	4.761904762	8.43x10 ⁻³
GO:0055114	Oxidation-reduction process	11	8.73015873	1.11x10 ⁻²
GO:0036018	Cellular response to erythropoietin	2	1.587301587	1.45x10 ⁻²
GO:0017144	Drug metabolic process	3	2.380952381	1.63x10 ⁻²
GO:0007052	Mitotic spindle organization	3	2.380952381	1.99x10 ⁻²
GO:0007049	Cell cycle	6	4.761904762	2.11x10 ⁻²
GO:0006890	Retrograde vesicle-mediated transport, Golgi to ER	4	3.174603175	2.19x10 ⁻²
GO:0007093	Mitotic cell cycle checkpoint	3	2.380952381	2.25x10 ⁻²
GO:0007565	Female pregnancy	4	3.174603175	2.70x10 ⁻²
GO:0032355	Response to estradiol	4	3.174603175	2.86x10 ⁻²
GO:0071314	Cellular response to cocaine	2	1.587301587	2.87x10 ⁻²
GO:0007079	Mitotic chromosome movement towards spindle pole	2	1.587301587	2.87x10 ⁻²
GO:0019886	Antigen processing and presentation of exogenous peptide antigen via MHC class II	4	3.174603175	2.94x10 ⁻²
GO:0007080	Mitotic metaphase plate congression	3	2.380952381	2.95x10 ⁻²
GO:0018107	Peptidyl-threonine phosphorylation	3	2.380952381	3.10x10 ⁻²
GO:0000079	Regulation of cyclin-dependent protein serine/threonine kinase activity	3	2.380952381	3.26x10 ⁻²
GO:0000082	G ₁ /S transition of mitotic cell cycle	4	3.174603175	3.82x10 ⁻²
GO:0008202	Steroid metabolic process	3	2.380952381	3.90x10 ⁻²
GO:0034080	CENP-A containing nucleosome assembly	3	2.380952381	3.90x10 ⁻²
GO:0032870	Cellular response to hormone stimulus	3	2.380952381	4.23x10 ⁻²
GO:0016098	Monoterpenoid metabolic process	2	1.587301587	4.28x10 ⁻²
GO:0032873	Negative regulation of stress-activated MAPK cascade	2	1.587301587	4.28x10 ⁻²
GO:0046483	Heterocycle metabolic process	2	1.587301587	4.28x10 ⁻²

Table SI. Continued.

Term ID	Term	Counts	Percentage	P-value
GO:0051988	Regulation of attachment of spindle microtubules to kinetochore	2	1.587301587	4.98x10 ⁻²
GO:0043654	Recognition of apoptotic cell	2	1.587301587	4.98x10 ⁻²
GO:0001867	Complement activation, lectin pathway	2	1.587301587	4.98x10 ⁻²
Cell components				
GO:0030496	Midbody	10	7.936507937	2.09x10 ⁻⁷
GO:0005819	Spindle	8	6.349206349	1.70x10 ⁻⁵
GO:0000776	Kinetochore	7	5.555555556	1.71x10 ⁻⁵
GO:0000777	Condensed chromosome kinetochore	7	5.555555556	2.58x10 ⁻⁵
GO:0031090	Organelle membrane	7	5.555555556	2.58x10 ⁻⁵
GO:0000775	Chromosome, centromeric region	6	4.761904762	3.93x10 ⁻⁵
GO:0005737	Cytoplasm	54	42.85714286	3.34x10 ⁻⁴
GO:0005874	Microtubule	9	7.142857143	1.18x10 ⁻³
GO:0005876	Spindle microtubule	4	3.174603175	3.17x10 ⁻³
GO:0005581	Collagen trimer	5	3.968253968	3.39x10 ⁻³
GO:0000922	Spindle pole	5	3.968253968	6.20x10 ⁻³
GO:0005829	Cytosol	34	26.98412698	9.92x10 ⁻³
GO:0005680	Anaphase-promoting complex	3	2.380952381	1.03x10 ⁻²
GO:0005634	Nucleus	49	38.88888889	1.42x10 ⁻²
GO:0005576	Extracellular region	19	15.07936508	2.11x10 ⁻²
GO:0048471	Perinuclear region of cytoplasm	10	7.936507937	2.37x10 ⁻²
GO:0005813	Centrosome	8	6.349206349	2.46x10 ⁻²
GO:0031262	Ndc80 complex	2	1.587301587	2.65x10 ⁻²
GO:0000942	Condensed nuclear chromosome outer kinetochore	2	1.587301587	2.65x10 ⁻²
GO:0005694	Chromosome	4	3.174603175	3.35x10 ⁻²
GO:0005871	Kinesin complex	3	2.380952381	4.91x10 ⁻²
Molecular function				
GO:0019825	Oxygen binding	5	3.968253968	3.53x10 ⁻⁴
GO:0019901	Protein kinase binding	11	8.73015873	3.76x10 ⁻⁴
GO:0016705	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	5	3.968253968	7.40x10 ⁻⁴
GO:0008017	Microtubule binding	8	6.349206349	7.52x10 ⁻⁴
GO:0004497	Monooxygenase activity	5	3.968253968	7.90x10 ⁻⁴
GO:0020037	Heme binding	6	4.761904762	3.07x10 ⁻³
GO:0005506	Iron ion binding	6	4.761904762	4.90x10 ⁻³
GO:0008392	Arachidonic acid epoxygenase activity	3	2.380952381	5.03x10 ⁻³
GO:0005515	Protein binding	77	61.11111111	1.07x10 ⁻²
GO:0003777	Microtubule motor activity	4	3.174603175	1.98x10 ⁻²
GO:0035173	Histone kinase activity	2	1.587301587	2.84x10 ⁻²
GO:0004866	Endopeptidase inhibitor activity	3	2.380952381	3.33x10 ⁻²

GO, Gene Ontology.