Discovery of microarray-identified genes correlates with development and prognosis of human hepatocellular carcinomas

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Supplementary Table S1. Biological process and cellular component annotation of the 80 genes associated with HCC development and progression by DAVID online tool

Most highly enriched		P value	No. of genes	
Cell cycle-related (Biological processes)	Mitotic cell cycle	2.09E-06	12	17 genes in total (*AURKA*, *CAP2*, *CDK1*, *CDKN3*, *CKS1B*, *GMNN*, *KPNA2*, *NUSAP1*, *PRC1*, *PSMD4*, *PTTG1*, *RACGAP1*, *RAD21*, *TBCE*, *TOP2A*, *UBE2C*, *ZWINT*)
	Cell cycle process	2.15E-05	13	
	Cell cycle	2.53E-05	15	
	Cell division	1.10E-04	9	
	Cell cycle phase	2.15E-04	10	
	M phase	2.33E-04	9	
	Chromosome segregation	7.26E-04	5	
	Nuclear division	8.16E-04	7	
	Mitosis	8.16E-04	7	
	Microtubule cytoskeleton organisation	8.51E-04	6	
	M phase of mitotic cell cycle	8.97E-04	7	
	Organelle fission	0.001005	7	
	Spindle organisation	0.001482	4	
	Microtubule-based process	0.001675	7	
	Cytoskeleton organisation	0.006138	8	
	Regulation of cell cycle	0.006282	7	
Microtubule cytoskeleton-Spindle	Microtubule cytoskeleton	1.73E-04	11	14 genes in total (*AURKA*, *CCT3*, *CDK1*,
	Spindle	5.35E-04	6	

related	Cytoskeletal component	0.003506	12	*ENAH*, *FCN2*, *HSPB1*,
(Cellular	Spindle microtubule	0.007579	3	*NDRG2*, *NUSAP1*, *PEA15*,
component)	Cytoskeleton	0.008458	14	*PRC1*, *PSMB4*, *RACGAP1*,
				TBCE, *TOP2A*)