

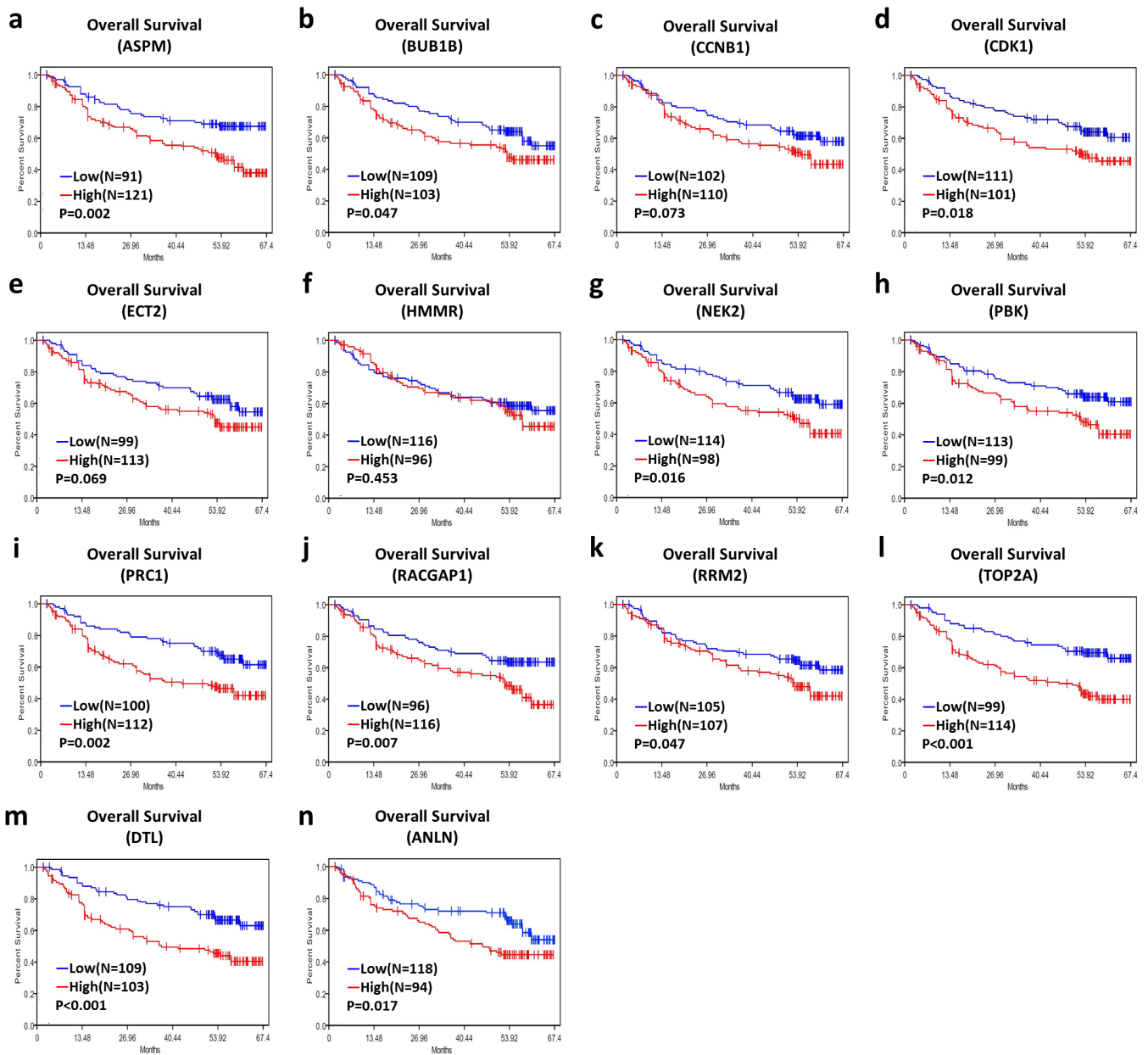
## Supplementary

**Table S1** Gene ontology analysis of up-regulated expressed genes in HBV-associated HCC

Category	Term	Count	P value	FDR
GOTERM_BP_DIRECT	Cell division	8	1.95E-07	2.71E-04
	M phase	8	4.09E-07	5.68E-04
	Mitosis	7	7.65E-07	0.00106
	Nuclear division	7	7.65E-07	0.00106
	M phase of mitotic cycle	7	8.50E-07	0.00118
	Mitotic cell cycle	8	9.04E-07	0.00125
	Organelle fission	7	9.67E-07	0.00134
	Cell cycle process	9	1.11E-06	0.00154
	Cell cycle	9	1.18E-05	0.01634
	Cytoskeleton organization	6	4.51E-04	0.62344
	Regulation of cell cycle	5	0.00151	2.08031
GOTERM_CC_DIRECT	Spindle	6	1.92E-06	0.00213
	Microtubule cytoskeleton	8	8.33E-06	0.00925
	Cytoskeleton	10	6.58E-05	0.073050
	Intracellular non-membrane-bounded organelle	11	0.00177	1.94895
	Non-membrane-bounded organelle	11	0.00177	1.94895
GOTERM_MF_DIRECT	Centrosome	4	0.00418	4.54495
	Microtubule organizing center	4	0.00587	6.32857
	Cytosol	6	0.0407	36.97028
	Protein serine/ threonine kinase activity	4	0.0308	29.05918

**Table S2** Gene ontology analysis of down-regulated expressed genes in HBV-associated HCC

Category	Term	Count	P value	FDR
GOTERM_BP_DIRECT	Oxidation reduction	14	1.20E-06	0.00182
	Secondary metabolic process	6	1.65E-05	0.02527
	Innate immune response	6	2.37E-04	0.36189
	Vitamin metabolic process	5	2.40E-04	0.36594
	Immune response	11	4.06E-04	0.61801
	Cellular amino acid derivative metabolic process	6	5.55E-04	0.84488
	Defense response	10	7.63E-04	1.15976
	Hormone metabolic process	5	8.93E-04	1.35635
GOTERM_CC_DIRECT	Extracellular region	26	4.10E-07	4.64E-04
	Extrinsic to membrane	9	0.00147	1.64552
	Cell fraction	11	0.02026	20.65319
	Insoluble fraction	9	0.03165	30.46864
	Integral to plasma membrane	11	0.03566	33.65317
	Intrinsic to plasma membrane	11	0.04069	37.45891
	Endomembrane system	8	0.05785	48.99586
	Membrane fraction	8	0.06697	54.30599
GOTERM_MF_DIRECT	Electron carrier activity	10	4.51E-07	5.71E-04
	Iron ion binding	10	7.00E-06	0.00886
	Heme binding	7	1.42E-05	0.01801
	Tetrapyrrole binding	7	2.05E-05	0.02594
	Sugar binding	7	2.04E-04	0.25768
	Carbohydrate binding	8	8.64E-04	1.08720



**Figure S1** The overall survival analysis of 14 hub genes by GSE14520 clinical data. Overexpression of 11 genes (*ASPM*, *BUB1B*, *CDK1*, *NEK2*, *PBK*, *PRC1*, *RACGAP1*, *RPM2*, *TOP2A*, *ANLN* and *DTL*) had a significantly worse survival rate ( $P < 0.05$ ).