Figure S1. WNT signaling pathway map.

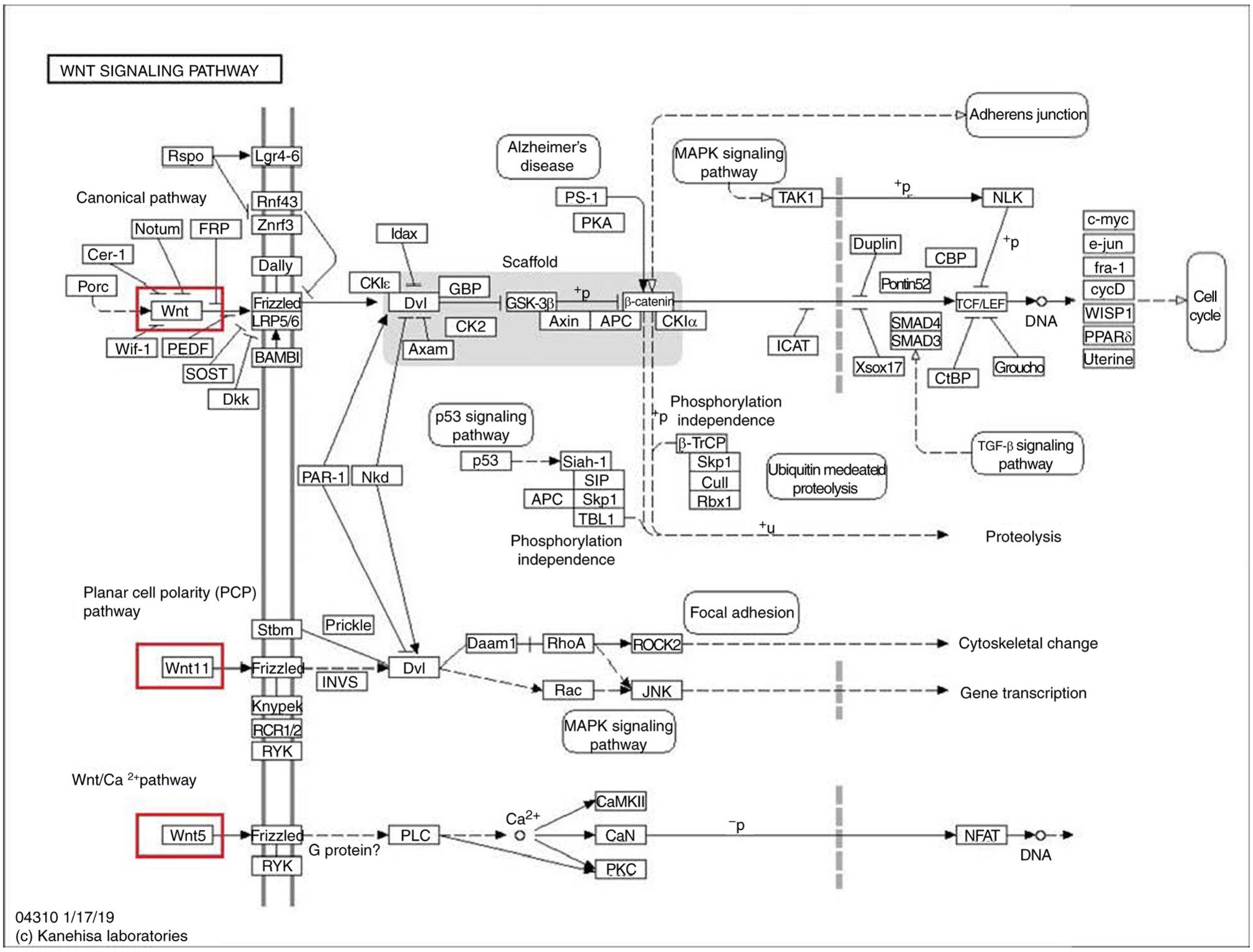

Figure S2. Gene Ontology terms of *WNT* family genes conducted by BiNGO in Cytoscape.

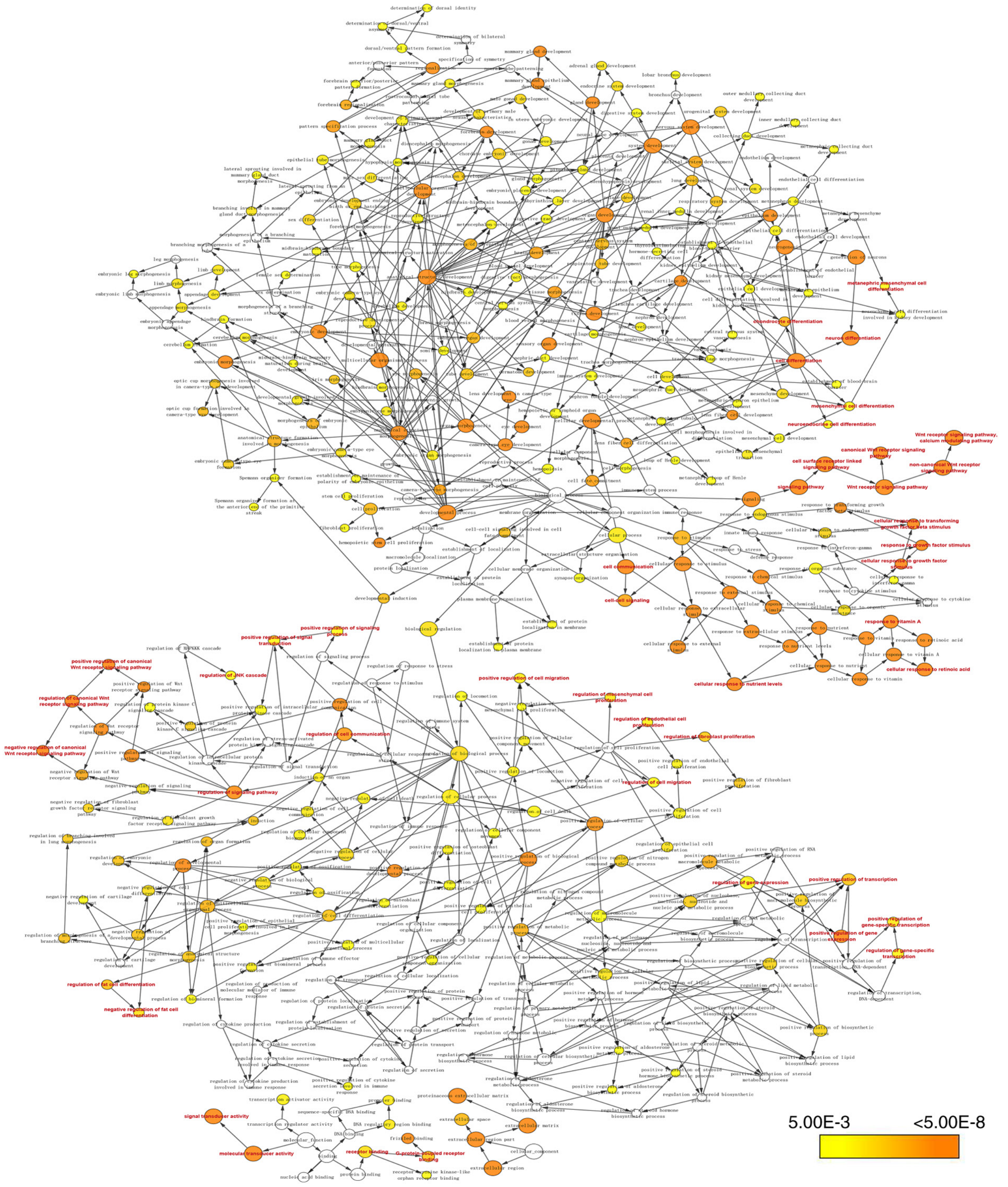

Table SI. Clinical characteristics of HBV-related HCC patients in GSE14520 cohort.

		OS				RFS			
Variables	Patients (n=212)	No. of events	MST (months)	HR (95% CI)	P-value	No. of events	MRT (months)	HR (95% CI)	P-value
Sex									
Female	29	8	NA	1		10	NA	1	
Male	183	74	NA	1.704 (0.821-3.534)	0.152	106	40	2.143 (1.120-4.100)	0.021
Age (years)									
≤60	175	69	NA	1		96	45	1	
>60	37	13	NA	0.864 (0.478-1.564)	0.630	20	48	0.974 (0.602-1.578)	0.916
ALT (U/l)									
≤50	124	46	NA	1		63	53	1	
>50	88	36	NA	1.095 (0.708-1.693)	0.684	53	40	1.241 (0.861-1.788)	0.248
AFP (ng/ml)[a]									
≤300	115	39	NA	1		62	48	1	
>300	94	43	NA	1.546 (1.002-2.385)	0.049	54	35	1.200 (0.833-1.728)	0.328
Cirrhosis									
No	17	2	NA	1		5	NA	1	
Yes	195	80	NA	4.335 (1.065-17.638)	0.041	111	37	2.612 (1.066-6.402)	0.036
Tumor size (cm)[b]									
≤5	137	46	NA	1		73	51	1	
>5	74	36	53	1.975 (1.274-3.060)	0.002	43	28	1.409 (0.966-2.056)	0.075
Number of nodules									
Single	167	59	NA	1		90	49	1	
Multiple	45	23	47	1.607 (0.992-2.604)	0.054	26	28	1.216 (0.785-1.883)	0.382
BCLC stage									
0	20	2	NA	1		6	NA	1	
A	143	48	NA	4.119 (1.001-16.951)	0.050	74	51	2.050 (0.892-4.711)	0.091
B	22	12	46	8.992 (2.005-40.320)	0.004	15	26	4.019 (1.550-10.421)	0.004
C	27	20	13	18.993 (4.419-81.632)	<0.001	21	8	6.163 (2.477-15.333)	<0.001
TNM stage									
I	89	20	NA	1		35	NA	1	
II	76	32	NA	2.214 (1.265-3.873)	0.005	48	28	1.995 (1.289-3.088)	0.002
III	47	30	18	5.197 (2.930-9.218)	<0.001	33	18	3.220 (1.993-5.204)	<0.001

[a] Information on AFP was unavailable in 3 patients. [b] Information on tumor size was unavailable in 1 patient. HBV, hepatitis B virus; HCC, hepatocellular carcinoma; OS, overall survival; RFS, recurrence-free survival; MST, median survival time; MRT, median recurrence time; ALT, alanine aminotransferase; AFP, α-fetoprotein; BCLC, Barcelona Clinic Liver Cancer; TNM, tumor-node-metastasis; HR, hazard ratio; CI, confidence interval; NA, not available.

Table SII. Gene Ontology (GO) terms of *WNT* family genes.

Category	Term	Count	%	P-value	Genes
GOTERM_BP_DIRECT	GO:0045165, cell fate commitment	17	0.534591195	7.97E-41	*WNT5A, WNT10A, WNT16, WNT10B, WNT5B, WNT2B, WNT2, WNT1, WNT7B, WNT4, WNT3, WNT9B, WNT11, WNT9A, WNT6, WNT7A, WNT8B*
GOTERM_BP_DIRECT	GO:0016055, Wnt signaling pathway	19	0.597484277	3.01E-36	*WNT5A, WNT10A, WNT16, WNT10B, WNT5B, WNT3A, WNT2B, WNT2, WNT1, WNT7B, WNT4, WNT3, WNT9B, WNT11, WNT9A, WNT6, WNT7A, WNT8A, WNT8B*
GOTERM_BP_DIRECT	GO:0030182, neuron differentiation	17	0.534591195	4.41E-35	*WNT5A, WNT10A, WNT16, WNT10B, WNT5B, WNT3A, WNT2B, WNT2, WNT7B, WNT4, WNT3, WNT9B, WNT11, WNT9A, WNT6, WNT8A, WNT8B*
GOTERM_BP_DIRECT	GO:0060070, canonical Wnt signaling pathway	14	0.440251572	3.29E-27	*WNT5A, WNT10B, WNT3A, WNT2B, WNT2, WNT1, WNT7B, WNT4, WNT3, WNT9B, WNT11, WNT9A, WNT7A, WNT8A*
GOTERM_BP_DIRECT	GO:0071300, cellular response to retinoic acid	12	0.377358491	8.99E-23	*WNT5A, WNT2, WNT7B, WNT10B, WNT3, WNT5B, WNT3A, WNT9B, WNT11, WNT9A, WNT6, WNT8B*
GOTERM_BP_DIRECT	GO:0007275, multicellular organism development	15	0.471698113	1.75E-18	*WNT5A, WNT10A, WNT16, WNT10B, WNT5B, WNT2B, WNT2, WNT1, WNT7B, WNT4, WNT9B, WNT11, WNT9A, WNT6, WNT8A*
GOTERM_BP_DIRECT	GO:0090263, positive regulation of canonical Wnt signaling pathway	7	0.220125786	2.03E-09	*WNT2, WNT1, WNT4, WNT10B, WNT3A, WNT7A, WNT2B*
GOTERM_BP_DIRECT	GO:0060021, palate development	6	0.188679245	1.36E-08	*WNT5A, WNT3A, WNT9B, WNT11, WNT7A, WNT8A*
GOTERM_BP_DIRECT	GO:0061303, cornea development in camera-type eye	4	0.125786164	5.77E-08	*WNT9B, WNT9A, WNT6, WNT2B*
GOTERM_BP_DIRECT	GO:0061180, mammary gland epithelium development	4	0.125786164	5.77E-08	*WNT2, WNT7B, WNT4, WNT3*
GOTERM_BP_DIRECT	GO:0071560, cellular response to transforming growth factor beta stimulus	5	0.157232704	1.90E-07	*WNT5A, WNT2, WNT10A, WNT4, WNT7A*
GOTERM_BP_DIRECT	GO:0071425, hematopoietic stem cell proliferation	4	0.125786164	3.74E-07	*WNT5A, WNT1, WNT10B, WNT2B*
GOTERM_BP_DIRECT	GO:1904886, beta-catenin destruction complex disassembly	4	0.125786164	1.57E-06	*WNT1, WNT3A, WNT8A, WNT8B*
GOTERM_BP_DIRECT	GO:0061184, positive regulation of dermatome development	3	0.094339623	3.25E-06	*WNT1, WNT4, WNT3A*
GOTERM_BP_DIRECT	GO:0010628, positive regulation of gene expression	6	0.188679245	6.46E-06	*WNT10A, WNT16, WNT3, WNT3A, WNT11, WNT6*
GOTERM_BP_DIRECT	GO:1904954, canonical Wnt signaling pathway involved in midbrain dopaminergic neuron differentiation	3	0.094339623	6.50E-06	*WNT2, WNT1, WNT3*
GOTERM_BP_DIRECT	GO:0002062, chondrocyte differentiation	4	0.125786164	9.23E-06	*WNT10B, WNT5B, WNT7A, WNT2B*
GOTERM_BP_DIRECT	GO:0045893, positive regulation of transcription, DNA-templated	7	0.220125786	1.10E-05	*WNT5A, WNT1, WNT4, WNT3A, WNT11, WNT6, WNT7A*

Table SII. Continued.

Category	Term	Count	%	P-value	Genes
GOTERM_BP_DIRECT	GO:0001658, branching involved in ureteric bud morphogenesis	4	0.125786164	1.16E-05	*WNT1*, *WNT4*, *WNT9B*, *WNT6*
GOTERM_BP_DIRECT	GO:0045599, negative regulation of fat cell differentiation	4	0.125786164	1.16E-05	*WNT5A*, *WNT1*, *WNT10B*, *WNT3A*
GOTERM_BP_DIRECT	GO:1904953, Wnt signaling pathway involved in midbrain dopaminergic neuron differentiation	3	0.094339623	1.62E-05	*WNT5A*, *WNT1*, *WNT3A*
GOTERM_BP_DIRECT	GO:0033278, cell proliferation in midbrain	3	0.094339623	1.62E-05	*WNT2*, *WNT1*, *WNT3A*
GOTERM_BP_DIRECT	GO:0070307, lens fiber cell development	3	0.094339623	2.27E-05	*WNT7B*, *WNT5B*, *WNT7A*
GOTERM_BP_DIRECT	GO:0061072, iris morphogenesis	3	0.094339623	4.86E-05	*WNT2*, *WNT9A*, *WNT2B*
GOTERM_BP_DIRECT	GO:0060071, Wnt signaling pathway, planar cell polarity pathway	4	0.125786164	1.22E-04	*WNT5A*, *WNT1*, *WNT9B*, *WNT11*
GOTERM_BP_DIRECT	GO:0051091, positive regulation of sequence-specific DNA binding transcription factor activity	4	0.125786164	1.81E-04	*WNT2*, *WNT1*, *WNT10B*, *WNT3A*
GOTERM_BP_DIRECT	GO:0048843, negative regulation of axon extension involved in axon guidance	3	0.094339623	3.47E-04	*WNT5A*, *WNT3*, *WNT3A*
GOTERM_BP_DIRECT	GO:0035115, embryonic forelimb morphogenesis	3	0.094339623	5.28E-04	*WNT3*, *WNT9A*, *WNT7A*
GOTERM_BP_DIRECT	GO:0002088, lens development in camera-type eye	3	0.094339623	5.62E-04	*WNT5A*, *WNT2*, *WNT2B*
GOTERM_BP_DIRECT	GO:0001837, epithelial to mesenchymal transition	3	0.094339623	5.97E-04	*WNT5A*, *WNT4*, *WNT11*
GOTERM_BP_DIRECT	GO:0090090, negative regulation of canonical Wnt signaling pathway	4	0.125786164	6.58E-04	*WNT5A*, *WNT4*, *WNT5B*, *WNT11*
GOTERM_BP_DIRECT	GO:0032526, response to retinoic acid	3	0.094339623	8.68E-04	*WNT9B*, *WNT8A*, *WNT8B*
GOTERM_BP_DIRECT	GO:0009267, cellular response to starvation	3	0.094339623	0.001140139	*WNT4*, *WNT9B*, *WNT2B*
GOTERM_BP_DIRECT	GO:0048146, positive regulation of fibroblast proliferation	3	0.094339623	0.0015026	*WNT5A*, *WNT2*, *WNT1*
GOTERM_BP_DIRECT	GO:0045669, positive regulation of osteoblast differentiation	3	0.094339623	0.001851502	*WNT7B*, *WNT4*, *WNT10B*
GOTERM_BP_DIRECT	GO:0007416, synapse assembly	3	0.094339623	0.001913051	*WNT5A*, *WNT3A*, *WNT7A*
GOTERM_BP_DIRECT	GO:0048697, positive regulation of collateral sprouting in absence of injury	2	0.062893082	0.002142793	*WNT3*, *WNT3A*
GOTERM_BP_DIRECT	GO:0072174, metanephric tubule formation	2	0.062893082	0.002142793	*WNT4*, *WNT9B*
GOTERM_BP_DIRECT	GO:0061317, canonical Wnt signaling pathway involved in cardiac muscle cell fate commitment	2	0.062893082	0.002142793	*WNT3A*, *WNT8A*
GOTERM_BP_DIRECT	GO:0060775, planar cell polarity pathway involved in gastrula mediolateral intercalation	2	0.062893082	0.002142793	*WNT5A*, *WNT11*
GOTERM_BP_DIRECT	GO:0007267, cell-cell signaling	4	0.125786164	0.002359008	*WNT2*, *WNT1*, *WNT9B*, *WNT9A*
GOTERM_BP_DIRECT	GO:0030324, lung development	3	0.094339623	0.002951142	*WNT5A*, *WNT2*, *WNT7B*
GOTERM_BP_DIRECT	GO:0003408, optic cup formation involved in camera-type eye development	2	0.062893082	0.003212562	*WNT5A*, *WNT16*
GOTERM_BP_DIRECT	GO:0060492, lung induction	2	0.062893082	0.003212562	*WNT2*, *WNT2B*
GOTERM_BP_DIRECT	GO:0060638, mesenchymal-epithelial cell signaling	2	0.062893082	0.003212562	*WNT5A*, *WNT2B*
GOTERM_BP_DIRECT	GO:0022009, central nervous system vasculogenesis	2	0.062893082	0.004281249	*WNT7B*, *WNT7A*
GOTERM_BP_DIRECT	GO:1904861, excitatory synapse assembly	2	0.062893082	0.004281249	*WNT5A*, *WNT7A*

Table SII. Continued.

Category	Term	Count	%	P-value	Genes
GOTERM_BP_DIRECT	GO:0021871, forebrain regionalization	2	0.062893082	0.004281249	*WNT7B*, *WNT2B*
GOTERM_BP_DIRECT	GO:0048570, notochord morphogenesis	2	0.062893082	0.004281249	*WNT5A*, *WNT11*
GOTERM_BP_DIRECT	GO:0003402, planar cell polarity pathway involved in axis elongation	2	0.062893082	0.004281249	*WNT5A*, *WNT11*
GOTERM_BP_DIRECT	GO:0008584, male gonad development	3	0.094339623	0.004474791	*WNT5A*, *WNT4*, *WNT2B*
GOTERM_BP_DIRECT	GO:0061038, uterus morphogenesis	2	0.062893082	0.005348853	*WNT9B*, *WNT7A*
GOTERM_BP_DIRECT	GO:0072201, negative regulation of mesenchymal cell proliferation	2	0.062893082	0.005348853	*WNT5A*, *WNT11*
GOTERM_BP_DIRECT	GO:0045836, positive regulation of meiotic nuclear division	2	0.062893082	0.005348853	*WNT5A*, *WNT4*
GOTERM_BP_DIRECT	GO:0060028, convergent extension involved in axis elongation	2	0.062893082	0.006415376	*WNT5A*, *WNT11*
GOTERM_BP_DIRECT	GO:1902474, positive regulation of protein localization to synapse	2	0.062893082	0.006415376	*WNT5A*, *WNT7A*
GOTERM_BP_DIRECT	GO:0048341, paraxial mesoderm formation	2	0.062893082	0.006415376	*WNT5A*, *WNT11*
GOTERM_BP_DIRECT	GO:2000049, positive regulation of cell-cell adhesion mediated by cadherin	2	0.062893082	0.007480818	*WNT5A*, *WNT3A*
GOTERM_BP_DIRECT	GO:0000578, embryonic axis specification	2	0.062893082	0.007480818	*WNT1*, *WNT7A*
GOTERM_BP_DIRECT	GO:1904948, midbrain dopaminergic neuron differentiation	2	0.062893082	0.008545182	*WNT2*, *WNT9B*
GOTERM_BP_DIRECT	GO:0090037, positive regulation of protein kinase C signaling	2	0.062893082	0.008545182	*WNT5A*, *WNT11*
GOTERM_BP_DIRECT	GO:0036465, synaptic vesicle recycling	2	0.062893082	0.008545182	*WNT3A*, *WNT7A*
GOTERM_BP_DIRECT	GO:0072089, stem cell proliferation	2	0.062893082	0.008545182	*WNT7B*, *WNT3*
GOTERM_BP_DIRECT	GO:0040037, negative regulation of fibroblast growth factor receptor signaling pathway	2	0.062893082	0.010670676	*WNT5A*, *WNT4*
GOTERM_BP_DIRECT	GO:0007411, axon guidance	3	0.094339623	0.012341195	*WNT5A*, *WNT3*, *WNT3A*
GOTERM_BP_DIRECT	GO:0008284, positive regulation of cell proliferation	4	0.125786164	0.012705871	*WNT2*, *WNT1*, *WNT10B*, *WNT3A*
GOTERM_BP_DIRECT	GO:0021846, cell proliferation in forebrain	2	0.062893082	0.012791867	*WNT3A*, *WNT7A*
GOTERM_BP_DIRECT	GO:0060317, cardiac epithelial to mesenchymal transition	2	0.062893082	0.01385085	*WNT2*, *WNT16*
GOTERM_BP_DIRECT	GO:0021527, spinal cord association neuron differentiation	2	0.062893082	0.01385085	*WNT1*, *WNT3A*
GOTERM_BP_DIRECT	GO:0001701, in utero embryonic development	3	0.094339623	0.016787196	*WNT7B*, *WNT3A*, *WNT9B*
GOTERM_BP_DIRECT	GO:0050768, negative regulation of neurogenesis	2	0.062893082	0.017021368	*WNT3A*, *WNT7A*
GOTERM_BP_DIRECT	GO:0035567, non-canonical Wnt signaling pathway	2	0.062893082	0.018076066	*WNT5A*, *WNT7A*
GOTERM_BP_DIRECT	GO:0045944, positive regulation of transcription from RNA polymerase II promoter	5	0.157232704	0.018348782	*WNT5A*, *WNT2*, *WNT1*, *WNT3A*, *WNT7A*
GOTERM_BP_DIRECT	GO:0036342, post-anal tail morphogenesis	2	0.062893082	0.019129695	*WNT5A*, *WNT3A*
GOTERM_BP_DIRECT	GO:0030325, adrenal gland development	2	0.062893082	0.020182257	*WNT4*, *WNT11*
GOTERM_BP_DIRECT	GO:0002053, positive regulation of mesenchymal cell proliferation	2	0.062893082	0.027520373	*WNT5A*, *WNT2*
GOTERM_BP_DIRECT	GO:0035116, embryonic hindlimb morphogenesis	2	0.062893082	0.029607425	*WNT3*, *WNT7A*

Table SII. Continued.

Category	Term	Count	%	P-value	Genes
GOTERM_BP_DIRECT	GO:0048706, embryonic skeletal system development	2	0.062893082	0.031690247	*WNT5A*, *WNT11*
GOTERM_BP_DIRECT	GO:0030501, positive regulation of bone mineralization	2	0.062893082	0.036878844	*WNT4*, *WNT10B*
GOTERM_BP_DIRECT	GO:0007257, activation of JUN kinase activity	2	0.062893082	0.039979387	*WNT5A*, *WNT7B*
GOTERM_BP_DIRECT	GO:0007223, Wnt signaling pathway, calcium modulating pathway	2	0.062893082	0.041010804	*WNT5A*, *WNT11*
GOTERM_BP_DIRECT	GO:0051496, positive regulation of stress fiber assembly	2	0.062893082	0.044098781	*WNT4*, *WNT11*
GOTERM_BP_DIRECT	GO:0034613, cellular protein localization	2	0.062893082	0.045126018	*WNT5A*, *WNT3A*
GOTERM_BP_DIRECT	GO:0030514, negative regulation of BMP signaling pathway	2	0.062893082	0.047177366	*WNT5A*, *WNT1*
GOTERM_BP_DIRECT	GO:0010595, positive regulation of endothelial cell migration	2	0.062893082	0.048201478	*WNT5A*, *WNT7A*
GOTERM_BP_DIRECT	GO:0042472, inner ear morphogenesis	2	0.062893082	0.054324354	*WNT1*, *WNT3A*
GOTERM_BP_DIRECT	GO:0060548, negative regulation of cell death	2	0.062893082	0.057371823	*WNT16*, *WNT11*
GOTERM_BP_DIRECT	GO:0042733, embryonic digit morphogenesis	2	0.062893082	0.058385583	*WNT5A*, *WNT7A*
GOTERM_BP_DIRECT	GO:0050680, negative regulation of epithelial cell proliferation	2	0.062893082	0.058385583	*WNT5A*, *WNT10B*
GOTERM_BP_DIRECT	GO:0032092, positive regulation of protein binding	2	0.062893082	0.063438959	*WNT5A*, *WNT3A*
GOTERM_BP_DIRECT	GO:0001947, heart looping	2	0.062893082	0.063438959	*WNT5A*, *WNT3A*
GOTERM_BP_DIRECT	GO:0000902, cell morphogenesis	2	0.062893082	0.064446555	*WNT3*, *WNT8A*
GOTERM_BP_DIRECT	GO:0046330, positive regulation of JNK cascade	2	0.062893082	0.067463206	*WNT16*, *WNT7A*
GOTERM_BP_DIRECT	GO:0001938, positive regulation of endothelial cell proliferation	2	0.062893082	0.071471118	*WNT5A*, *WNT2*
GOTERM_BP_DIRECT	GO:0033138, positive regulation of peptidyl-serine phosphorylation	2	0.062893082	0.072470551	*WNT5A*, *WNT3A*
GOTERM_BP_DIRECT	GO:0030216, keratinocyte differentiation	2	0.062893082	0.078445847	*WNT5A*, *WNT16*
GOTERM_BP_DIRECT	GO:0042060, wound healing	2	0.062893082	0.08240916	*WNT5A*, *WNT5B*
GOTERM_BP_DIRECT	GO:0043066, negative regulation of apoptotic process	3	0.094339623	0.084262975	*WNT5A*, *WNT11*, *WNT7A*
GOTERM_BP_DIRECT	GO:0032355, response to estradiol	2	0.062893082	0.09322543	*WNT7A*, *WNT8B*
GOTERM_BP_DIRECT	GO:0030336, negative regulation of cell migration	2	0.062893082	0.097128678	*WNT4*, *WNT11*
GOTERM_BP_DIRECT	GO:0045892, negative regulation of transcription, DNA-templated	3	0.094339623	0.098625276	*WNT5A*, *WNT4*, *WNT11*
GOTERM_CC_DIRECT	GO:0005578, proteinaceous extracellular matrix	19	0.597484277	5.82E-34	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*
GOTERM_CC_DIRECT	GO:0005615, extracellular space	19	0.597484277	3.90E-21	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*

Table SII. Continued.

Category	Term	Count	%	P-value	Genes
GOTERM_CC_DIRECT	GO:0005576, extracellular region	19	0.597484277	9.85E-20	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*
GOTERM_CC_DIRECT	GO:0030666, endocytic vesicle membrane	9	0.283018868	8.08E-16	*WNT5A*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT5B*, *WNT3A*, *WNT6*, *WNT7A*
GOTERM_CC_DIRECT	GO:0005796, Golgi lumen	9	0.283018868	1.85E-14	*WNT5A*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT5B*, *WNT3A*, *WNT6*, *WNT7A*
GOTERM_CC_DIRECT	GO:0005788, endoplasmic reticulum lumen	9	0.283018868	5.24E-12	*WNT5A*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT5B*, *WNT3A*, *WNT6*, *WNT7A*
GOTERM_CC_DIRECT	GO:0009986, cell surface	7	0.220125786	9.21E-06	*WNT5A*, *WNT1*, *WNT4*, *WNT5B*, *WNT3A*, *WNT6*, *WNT7A*
GOTERM_CC_DIRECT	GO:0070062, extracellular exosome	10	0.314465409	6.28E-04	*WNT5A*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT5B*, *WNT3A*, *WNT9A*, *WNT6*, *WNT7A*
GOTERM_CC_DIRECT	GO:0005886, plasma membrane	10	0.314465409	0.009916722	*WNT5A*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT5B*, *WNT3A*, *WNT6*, *WNT7A*
GOTERM_CC_DIRECT	GO:1990909, Wnt signalosome	2	0.062893082	0.010814249	*WNT2*, *WNT3*
GOTERM_CC_DIRECT	GO:0098793, presynapse	2	0.062893082	0.061389051	*WNT3A*, *WNT7A*
GOTERM_MF_DIRECT	GO:0005109, frizzled binding	19	0.597484277	4.73E-51	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*
GOTERM_MF_DIRECT	GO:0048018, receptor agonist activity	9	0.283018868	3.43E-21	*WNT5A*, *WNT2*, *WNT1*, *WNT4*, *WNT10B*, *WNT3*, *WNT3A*, *WNT7A*, *WNT8A*
GOTERM_MF_DIRECT	GO:0005125, cytokine activity	4	0.125786164	8.10E-04	*WNT5A*, *WNT2*, *WNT1*, *WNT7A*
GOTERM_MF_DIRECT	GO:0019904, protein domain specific binding	4	0.125786164	0.001312497	*WNT5A*, *WNT1*, *WNT3*, *WNT3A*
GOTERM_MF_DIRECT	GO:0005110, frizzled-2 binding	2	0.062893082	0.002131501	*WNT5A*, *WNT3A*
GOTERM_MF_DIRECT	GO:0039706, co-receptor binding	2	0.062893082	0.010614673	*WNT3A*, *WNT9B*
GOTERM_MF_DIRECT	GO:0044212, transcription regulatory region DNA binding	3	0.094339623	0.021228971	*WNT5A*, *WNT1*, *WNT11*
GOTERM_MF_DIRECT	GO:0005102, receptor binding	3	0.094339623	0.053518524	*WNT5B*, *WNT3A*, *WNT7A*

BP, biological process; CC, cellular component; MF, molecular function.

Table SIII. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways of *WNT* family genes.

Category	Term	Count	%	P-value	Genes
KEGG_PATHWAY	hsa05217: Basal cell carcinoma	19	0.597484	7.31E-40	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*
KEGG_PATHWAY	hsa04916: Melanogenesis	19	0.597484	1.56E-34	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*
KEGG_PATHWAY	hsa04310: Wnt signaling pathway	19	0.597484	8.20E-32	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*
KEGG_PATHWAY	hsa04550: Signaling pathways regulating pluripotency of stem cells	19	0.597484	1.08E-31	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*
KEGG_PATHWAY	hsa04390: Hippo signaling pathway	19	0.597484	4.60E-31	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*
KEGG_PATHWAY	hsa05205: Proteoglycans in cancer	19	0.597484	9.44E-29	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*
KEGG_PATHWAY	hsa05166: HTLV-I infection	19	0.597484	9.59E-27	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*
KEGG_PATHWAY	hsa05200: Pathways in cancer	19	0.597484	2.67E-23	*WNT5A*, *WNT10A*, *WNT16*, *WNT10B*, *WNT5B*, *WNT3A*, *WNT2B*, *WNT2*, *WNT1*, *WNT7B*, *WNT4*, *WNT3*, *WNT9B*, *WNT11*, *WNT9A*, *WNT6*, *WNT7A*, *WNT8A*, *WNT8B*

Table SIV. Clinical characteristics of HCC patients in the TCGA cohort.

		RFS				OS			
Variables	Patients (n=370)	No. of events	MRT (days)	Crude HR (95% CI)	Log-rank P-value	No. of events	MST (days)	Crude HR (95% CI)	Log-rank P-value
Age (years)					0.81				0.184
≤65	232	87	912	1		73	2,456	1	
>65	138	52	828	1.043 (0.739-1.472)		57	1,423	1.265 (0.893-1.791)	
Sex					0.919				0.261
Female	121	45	893	1		51	1,490	1	
Male	249	94	875	0.982 (0.688-1.401)		79	2,486	0.817 (0.573-1.164)	
BMI[a]					0.909				0.363
≤28	240	86	903	1		83	2,131	1	
>28	94	38	879	0.978 (0.666-1.435)		29	2,116	0.821 (0.537-1.257)	
Alcohol consumption[b]					0.665				0.896
No	234	85	912	1		84	1,694	1	
Yes	117	46	879	1.083 (0.756-1.552)		40	1,624	1.026 (0.703-1.496)	
Ishak fibrosis score[c]					0.931				0.872
0-No Fibrosis	74	30	893	1		30	2,131	1	
1,2-Portal fibrosis	31	11	754	0.866 (0.432-1.736)		9	1,372	0.917 (0.429-1.962)	
3,4-Fibrous septa	28	11	828	1.050 (0.526-2.097)		6	NA	0.682 (0.281-1.654)	
5-Nodular formation and incomplete cirrhosis	9	3	1.432	0.789 (0.240-2.591)		2	1,386	0.750 (0.177-3.167)	
6-Established cirrhosis	69	30	776	1.134 (0.683-1.884)		17	NA	0.766 (0.418-1.403)	
Tumor stage[d]					<0.0001				<0.0001
I	171	45	1.509	1		42	2,532	1	
II	85	34	754	1.914 (1.225-2.989)		26	1,852	1.427 (0.874-2.330)	
III+IV	90	49	289	3.640 (2.416-5.486)		48	770	2.764 (1.823-4.190)	
Histological grade[e]					0.649				0.748
G1	55	21	990	1		18	2,116	1	
G2	177	64	754	1.218 (0.744-1.997)		60	1,685	1.181 (0.697-2.000)	
G3	121	48	828	1.249 (0.748-2.087)		43	1,622	1.233 (0.711-2.140)	
G4	12	2	NA	0.623 (0.146-2.659)		5	NA	1.693 (0.626-4.584)	
Serum AFP[f], ng/ml					0.788				0.832
≤400	213	77	912	1		62	2,456	1	
>400	64	21	1,509	0.936 (0.576-1.520)		22	2,486	1.055 (0.645-1.724)	
Radical resection[g]					0.011				0.006
R0	323	121	912	1		110	1,852	1	
R1+R2+RX	40	17	478	1.916 (1.149-3.193)		17	837	2.030 (1.213-3.395)	

Table SIV. Continued.

		RFS				OS			
Variables	Patients (n=370)	No. of events	MRT (days)	Crude HR (95% CI)	Log-rank P-value	No. of events	MST (days)	Crude HR (95% CI)	Log-rank P-value
Microvascular invasion[h]					0.028				0.154
No	206	64	1,279	1		60	2,131	1	
Yes	108	43	644	1.540 (1.045-2.268)		36	2,486	1.351 (0.892-2.047)	
Child-Pugh score[i]					0.242				0.18
A	216	83	990	1		59	2,542	1	
B+C	22	8	1,286	1.542 (0.742-3.204)		9	1,005	1.614 (0.796-3.270)	

[a] Information on BMI was unavailable in 36 patients. [b] Information on alcohol consumption was unavailable in 19 patients. [c] Information on Ishak fibrosis score was unavailable in 159 patients. [d] Information on tumor stage was unavailable in 24 patients; [e] Information on histological grade was unavailable in 5 patients. [f] Information on serum AFP was unavailable in 93 patients. [g] Information on radical resection was unavailable in 7 patients. [h] Information on microvascular invasion was unavailable in 56 patients. [i] Information on Child-Pugh score was unavailable in 132 patients. HCC, hepatocellular carcinoma; TCGA, The Cancer Genome Atlas; RFS, recurrence-free survival; OS, overall survival; HR, hazard ratio; 95% CI, 95% confidence interval; BCLC, Barcelona Clinic Liver Cancer; MRT, median recurrence time; MST, median survival time; BMI, body mass index; AFP, α-fetoprotein.