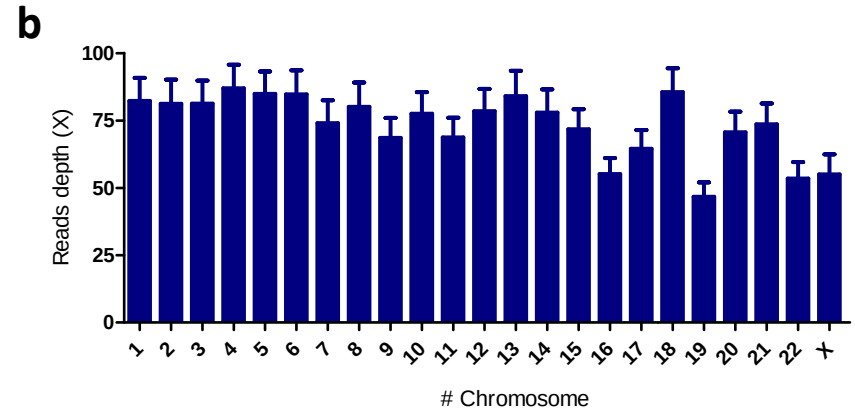
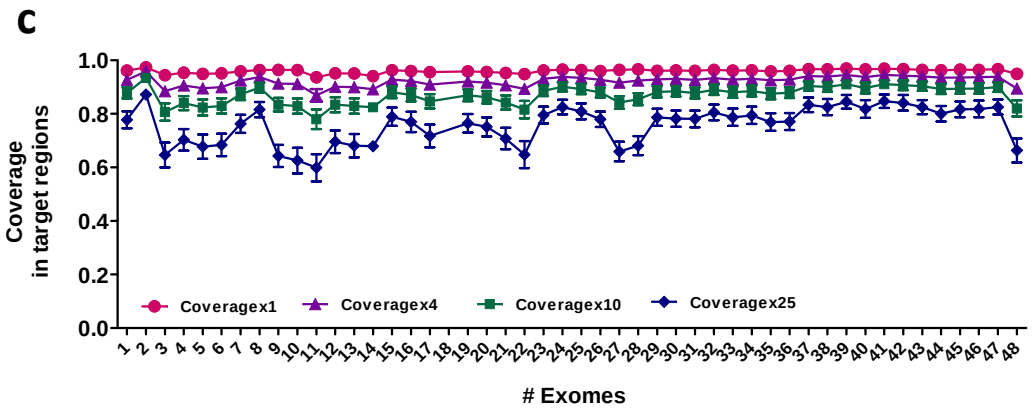
Author manuscript, published in "Nature Genetics 2012;44(6):694-8"
DOI : 10.1038/ng.2256

a

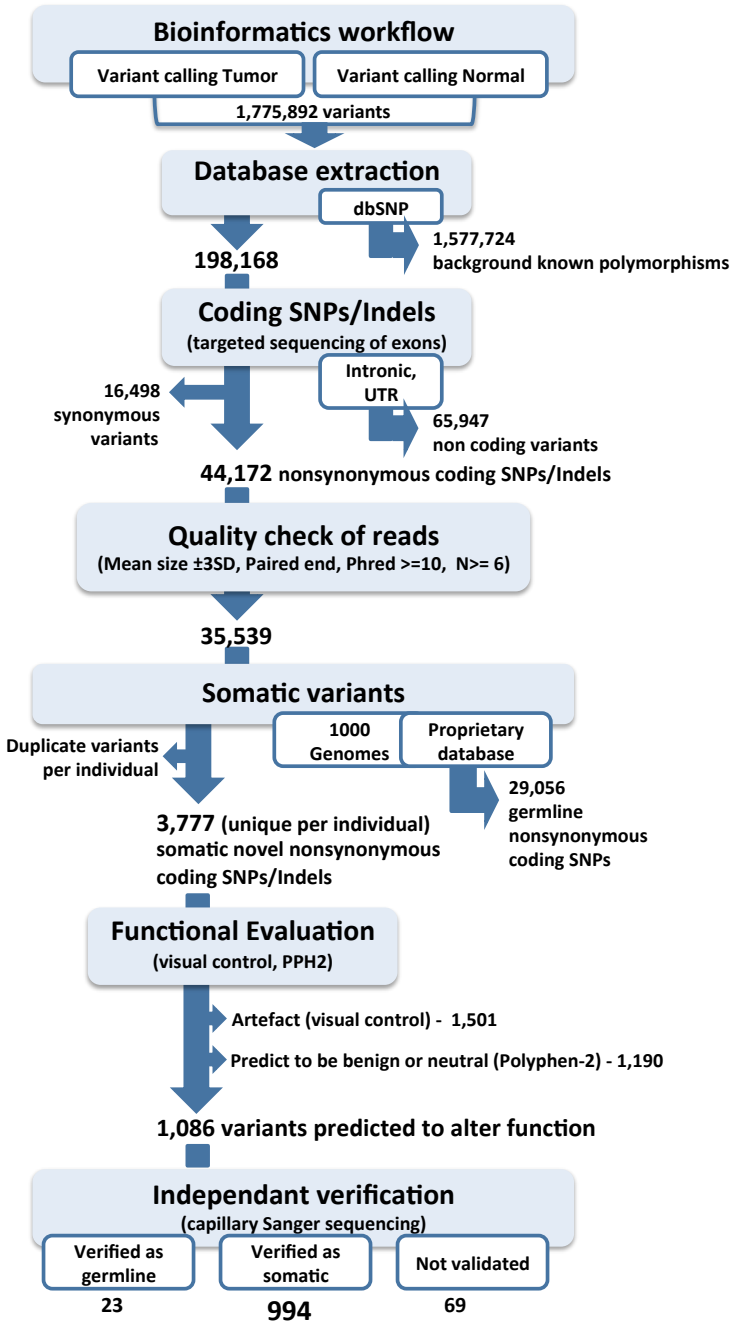
Final target bases	46.2 Mb
Target bases covered	43.3 Mb
Percent target bases covered	93.81%
Average depth	73.3
Median depth	70
Coverage at 25x	75.9%
Coverage at 10x	87.0%
Coverage at 4x	92.3%
Coverage at 1x	96.0%



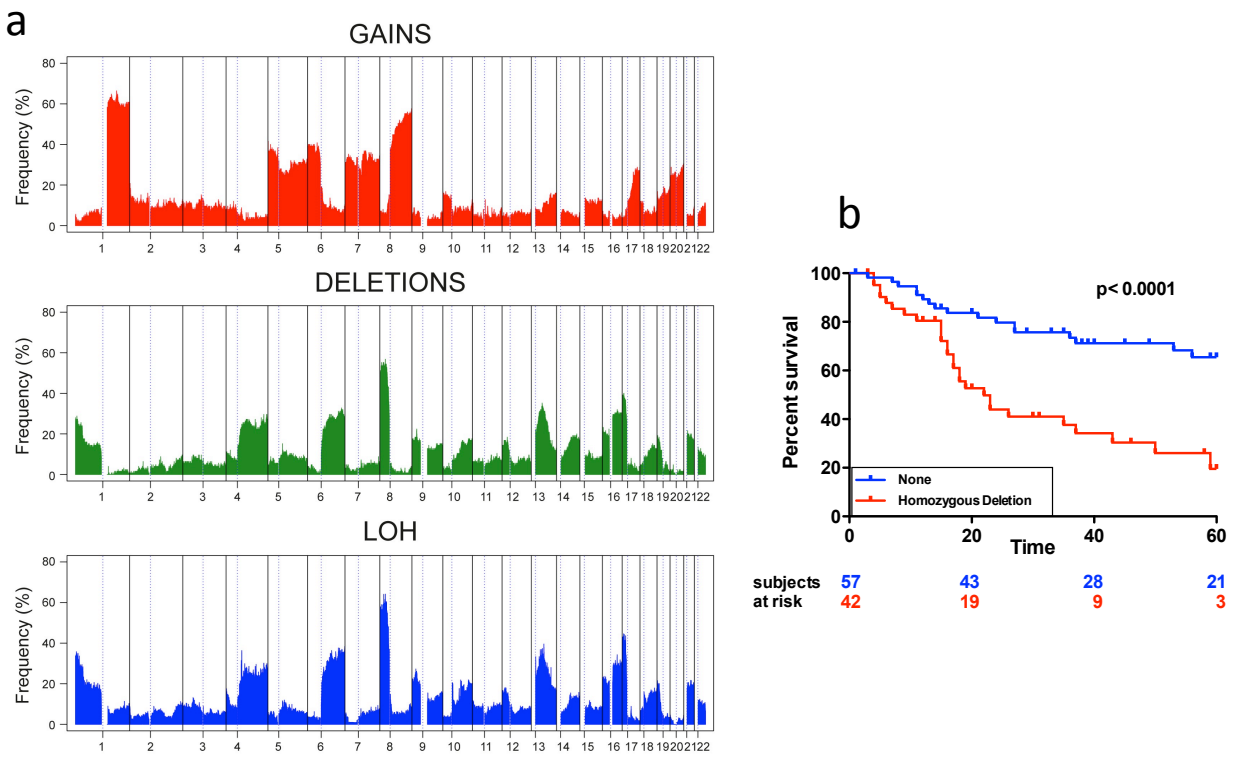


Supplementary Figure 1. **Statistics of mapping of sequencing reads**

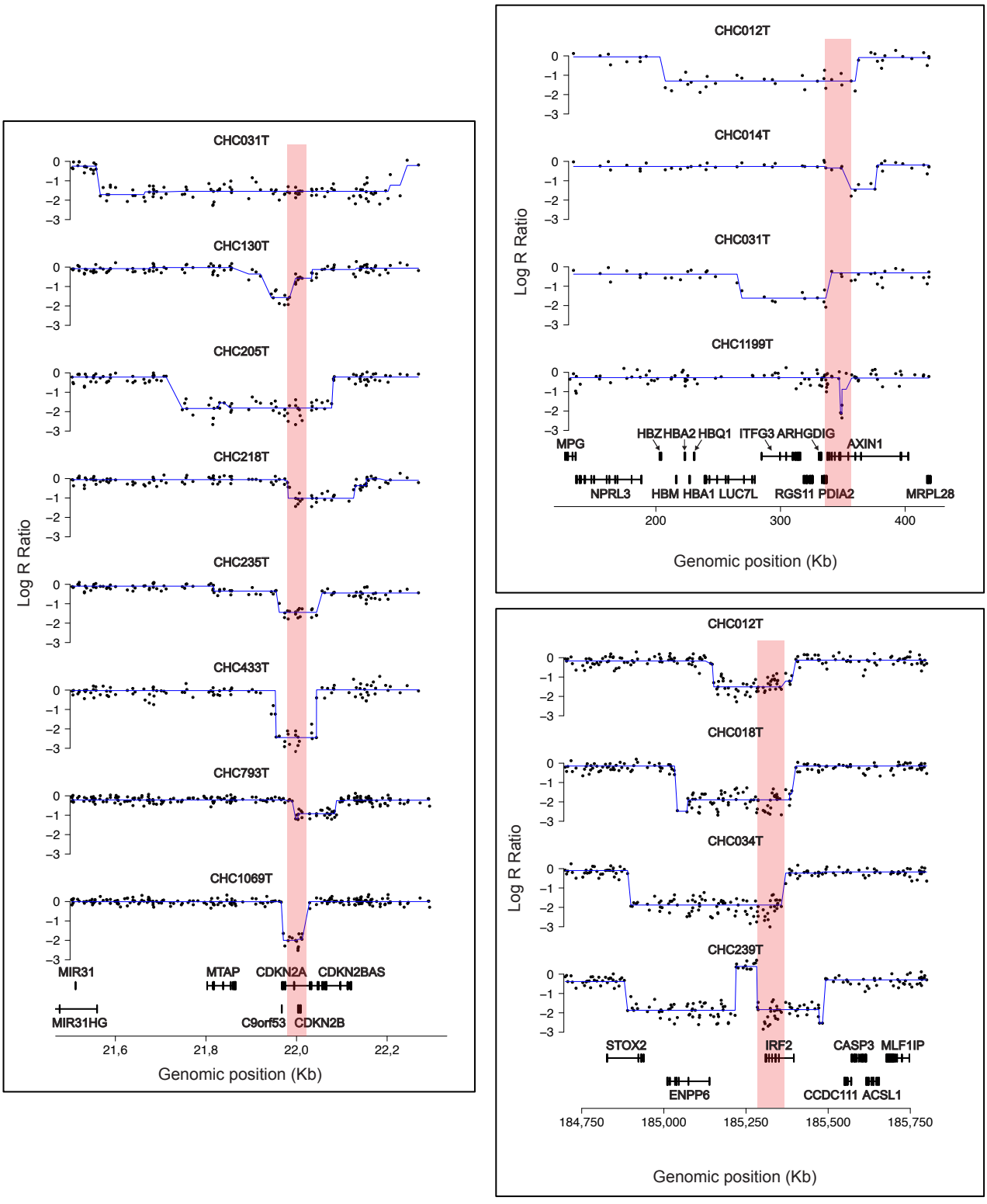
a, summary statistics for whole-exome sequence reads of 24 HCC with their non tumor liver tissues. **b,** mean depth (with 95% IC) of reads on each chromosome, **c,** cumulative fraction of coding bases covered in captured regions. A 1-fold, 4-fold, 10-fold and 25-fold coverage were considered (mean with 95% IC) per exome (numbered #1-48).



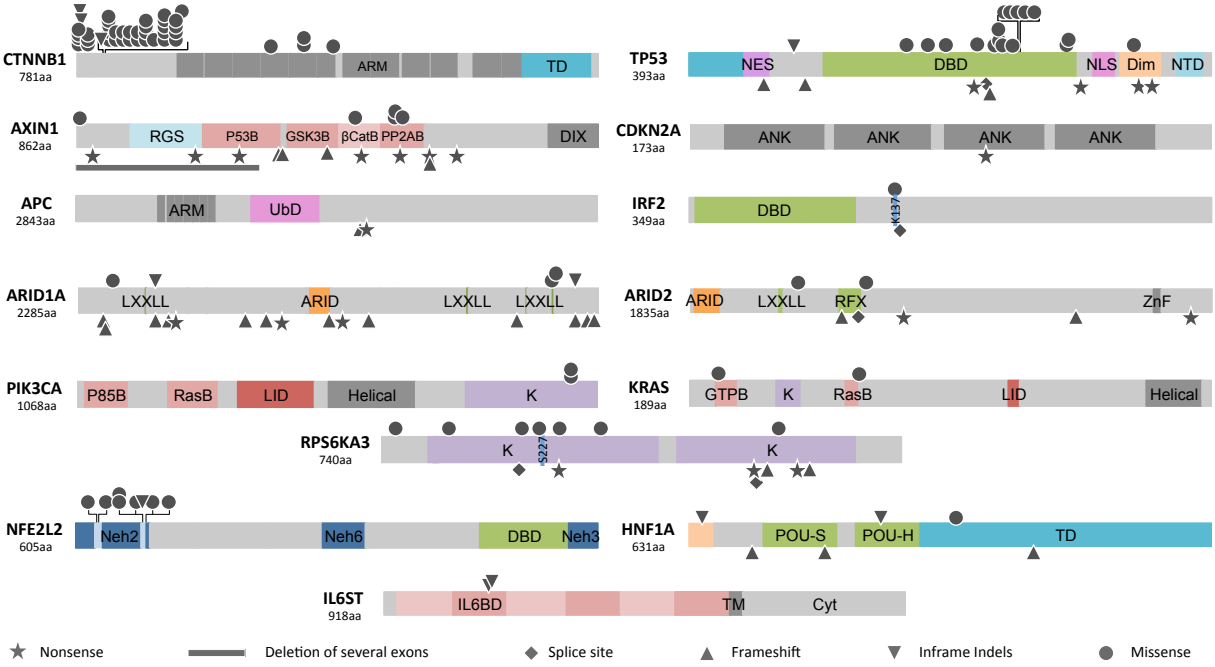
Supplementary Figure 2. Whole-exome sequencing analysis flowchart. Extraction of functionally somatic gene mutations for 24 HCC. Boxes refer to major bioinformatics steps; arrows indicate the number of variants obtained or removed from subsequent analysis. Variants were filtered for their coding localization, annotation in dbSNP31 or 1000 genomes, somatic and functionally impairment. The per-base and reads quality scores were used to filter false positive gene mutation events.



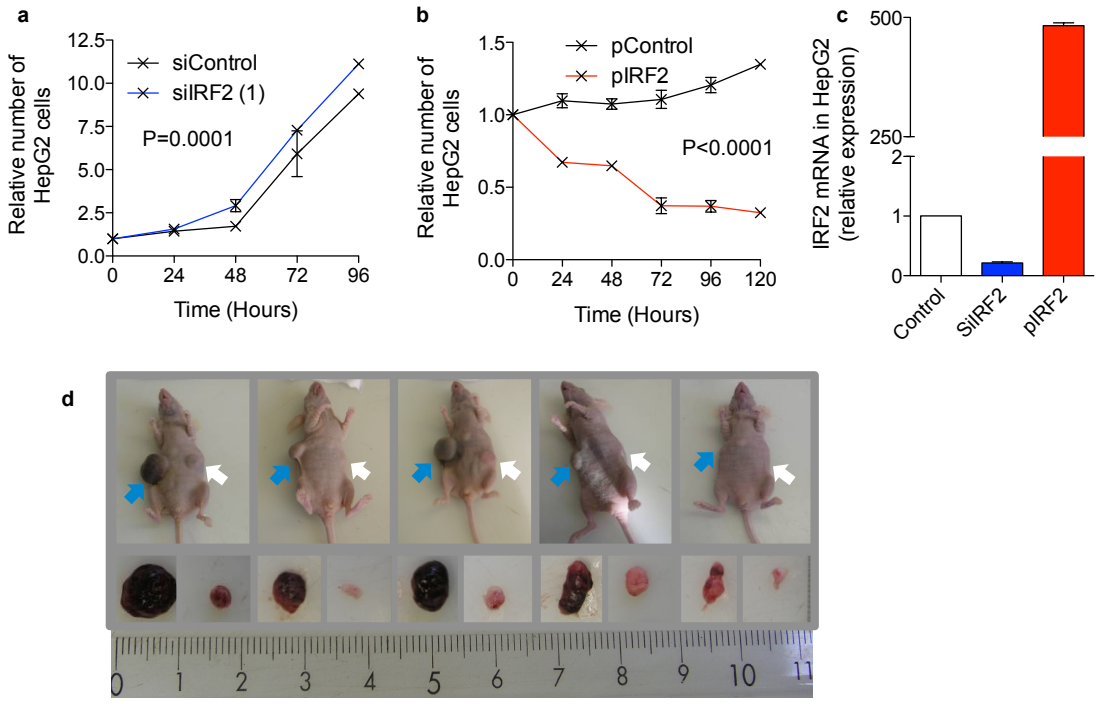
Supplementary Figure 3. Genome-wide copy number changes and recurrent homozygous deletions in HCC. **a**, Frequency of gains, deletions, and losses of heterozygosity (LOH) along the genome in a series of 125 HCC. **b**, Kaplan-Meier analysis comparing survival of cases presenting homozygous deletions (n=42) versus those without local losses (n=57). Univariate Cox P-value for risk index is included. Only patients with curative (R0) resection were included in survival analysis.



Supplementary Figure 4. Recurrent homozygous deletions at *CDKN2A/B*, *AXIN1* and *IRF2* loci. Raw log R ratios are represented as black dots, and smoothed log R ratios as blue lines. The minimal region of loss is indicated in red for each region.



Supplementary Figure 5. Somatic mutation spectra in 125 HCC. Inactivating and activating mutations are shown above and below the core protein, respectively. Functional domains are colored boxes. ANK: Ankyrin repeat, ARM: Armadillo repeat, βCatB: βCatenin binding Domain, Cyt: Cytosolic Domain, DBD: DNA Binding domain, Dim: Dimerization Domain, GSK3B: GSK3 Binding Domain, GTPB: GTP binding Domain, IL6BD: IL6 Binding Domain, K: Kinase domain, LID: Lipid interaction domain, Neh: Nrf2-ECH Homology Domain, NES: Nuclear Export Signal, NLS: Nuclear Localization Signal, NTD: Negative Transactivation Domain, P53B: P53 Binding Domain, P85B: P85 Binding Domain, PP2AB: PP2A Binding Domain, RasB: Ras Binding Domain, RGS: regulator of G-protein signalling, TD: Transactivation domain, TM: Transmembrane domain, UbD: Ubiquitinylated domain.



Supplementary Figure 6. IRF2 as a new tumor suppressor gene in HCC controlling p53 pathway

a, Effect of *in vitro* IRF2 silencing in HepG2 hepatobalstoma cell line: increased cell proliferation with IRF2 siRNA (SiIRF2) when compared to control siRNA (triplicates, mean±SD, regression analysis). **b**, IRF2 overexpression in HepG2 cell line by transfection of a plasmid containing the coding sequence of IRF2 (pIRF2) induced dramatic cell death when compared to HepG2 transfected with an empty plasmid (pControl; triplicates, mean±SD, regression analysis) **c.** Relative mRNA expression was quantified by qRT-PCR (*n*=3; mean ± SD). **d.** Xenograft model in CD1 nude mice injected in right flank with HepaRG stably transfected with ShIRF2(1) (blue arrow) and in left flank with HepaRG stably transfected with ShControl (white arrow). Respective subcutaneous tumors after 4 weeks of cell injection are displayed below.

Supplementary Table 1: Clinical, histological and molecular data of HCC

	24 HCC (Exome sequencing)	125 HCC (series of validation)
Age		
< 60 years	3 (12.5%)	46 (37%)
≥ 60 years	21 (87.5%)	79 (63%)
Gender		
Male	20 (83%)	100 (80%)
Female	4 (17%)	25 (20%)
Etiology (*)		
HCV	4 (17%)	24 (19%)
HBV	1 (4%)	35 (28%)
Alcohol	12 (50%)	43 (34%)
NASH	2 (8%)	5 (4%)
Hemochromatosis	0 (0%)	6 (5%)
Other	7 (29%) (*) including 2 cases with ≥ 2 risk factors	26 (21%) (*) including 14 cases with ≥ 2 risk factors
Tumor size (n=124)		
≤ 50 mm	12 (50%)	56 (45%)
> 50 mm	12 (50%)	68 (55%)
Tumor features		
Unique nodule (n=124)	18 (75%)	94 (76%)
Satellites nodules (n=124)	9 (38%)	59 (48%)
Vascular invasion (n=122)	11 (46%)	61 (50%)
Differentiation (n=120)		
Edmonson I-II	11 (48%)	60 (50%)
Edmonson III-IV	12 (52%)	60 (50%)
Non tumor liver (n=124)		
Metavir score F0-F1	9 (37%)	45 (36%)
Metavir score F2-F3	7 (29%)	33 (27%)
Metavir score F4	8 (33%)	46 (37%)
Apha Foeto Protein (n=108)		
≥ 24 ng/ml	7 (37%)	52 (48%)
Mutations		
TP53	3 (13%)	26 (21%)
CTNNB1	11 (46%)	41 (33%)
AXIN1	5 (21%)	19 (15%)
CDKN2A	2 (8%)	9 (7%)
KRAS	0 (0%)	2 (1.6%)
ARID2	2 (8%)	7 (5.6%)
Transcriptome Groups (n=123)		
G1	1 (4%)	15 (12%)
G2	0 (0%)	13 (11%)
G3	4 (17%)	19 (16%)
G4	8 (33%)	38 (30%)
G5	7 (29%)	25 (20%)
G6	4 (17%)	13 (11%)

Supplementary Table 2: Clinical, histological and molecular data of HCC

ID	Age (year)	Gender	Etiology	Tumor size (mm)	Microscopic Vascular Invasion	BCLC	Edmonson	METAVIR	AFP (ng/ml)	Transcriptome subgroups	Ploidy	FAA	PFS time	PFS status	OS time	OS status
CHC008T	73	F	HBV	20	no	0	I-II	F4	≥24	G4	2	0	1	1	7	1
CHC012T	35	M	HBV	80	yes	A		F4	≥24	G1	3	0.63	8	1	15	1
CHC013T	62	M	HCV	30	yes	A	I-II	F4	≥24	G5	2	0.16	6	1	15	1
CHC014T	29	M	HBV	130	yes	A	III-IV	F2-F3	≥24	G3	3	0.74	3	1	5	1
CHC018T	34	F	HBV	170	yes	A	III-IV	F2-F3	≥24	G1	3	0.34	14	1	35	1
CHC028T	63	M	HCV	30	yes	A	III-IV	F4	<24	G6	3	0.61	40	1	60	0
CHC031T	67	M	AL	16	no	0	I-II	F4	<24	G5	3	0.76	15	1	26	1
CHC032T	59	M	HBV	25	no	B	I-II	F4	≥24	-	2	0	NE	NE	NE	NE
CHC033T	38	M	HBV	250	yes	C	III-IV	F2-F3	≥24	-	2	0.32	NE	NE	NE	NE
CHC034T	55	M	HBV	170	yes	A	III-IV	F2-F3	≥24	G2	3	0.63	12	1	23	1
CHC037T	50	M	Other	120	no	A	I-II	F0-F1	<24	G4	2	0.47	60	0	60	0
CHC043T	55	M	HBV	50	no	A	III-IV	F2-F3	≥24	G3	4	0.82	58	0	58	0
CHC046T	61	F	HBV	65	yes	C	III-IV	F4	≥24	G3	3	0.74	12	0	12	0
CHC051T	68	F	HCV	60	no	A		F4	≥24	G6	2	0.13	32	1	53	1
CHC059T	40	M	AL	80	yes	C	III-IV	F0-F1	≥24	G6	2	0.05	16	1	16	1
CHC060T	68	M	AL	28	yes	C	III-IV	F4	<24	G1	2	0	21	1	27	1
CHC081T	75	F	HBV	90	no	A	I-II	F4	≥24	G4	2	0.11	NE	NE	NE	NE
CHC097T	56	M	Other	70	yes	B	I-II	F0-F1	<24	G5	2	0.16	13	1	37	1
CHC100T	68	M	HCV AL	20	yes	A	III-IV	F4		G2	4	0.42	NE	NE	NE	NE
CHC1035T	68	M	HBV AL	75	no	A	I-II	F2-F3	<24	G5	2	0.3	10	1	30	0
CHC1040T	72	M	AL	160	yes	A	III-IV	F2-F3	≥24	G4	2	0.3	33	1	35	0
CHC1041T	68	M	Other	10	no	0	I-II	F0-F1	<24	G6	2	0.2	35	0	35	0
CHC1044T	78	M	AL	16	yes	0	III-IV	F2-F3	≥24	G1	2	0.15	33	0	33	0
CHC1052T	75	M	AL	130	yes	A	III-IV	F2-F3	<24	G4	3	0.52	1	0	1	0
CHC1053T	73	M	AL	35	yes	A	III-IV	F4	≥24	G4	2	0.15	19	1	19	1
CHC1055T	67	M	AL	200	yes	B	III-IV	F2-F3	≥24	G3	2	0.15	6	1	6	1
CHC1060T	66	M	NASH	30	no	A	III-IV	F4		G4	2	0	29	0	29	0
CHC1061T	79	F	Other	150	yes	A	I-II	F0-F1	<24	G4	4	0.28	13	1	39	0
CHC1062T	65	M	HM	30	yes	A	I-II	F2-F3	≥24	G2	2	0	36	0	36	0
CHC1065T	77	M	Other	35	yes	C	I-II	F0-F1	<24	G4	2	0.12	22	1	40	0
CHC1069T	77	M	AL	50	yes	A	III-IV	F2-F3	<24	G5	2	0.28	3	0	3	0
CHC1146T	59	M	AL	170	yes	C	III-IV	F0-F1	≥24	G3	2	0.25	16	1	18	1
CHC1154T	43	M	HBV	130	yes	A	I-II	F2-F3	≥24	G6	3	0.45	60	0	60	0
CHC115T	59	M	NASH	70	yes	A	I-II	F0-F1	<24	G5	4	0.11	24	1	60	0
CHC1162T	59	M	AL	55		B	I-II	F4	<24	G4	2	0	60	0	60	0
CHC1185T	52	M	HBV	30	no	A	III-IV	F4	≥24	G1	2	0.18	60	0	60	0
CHC1190T	68	F	HCV AL	22	yes	A	I-II	F2-F3	≥24	G4	2	0	27	1	60	0
CHC1192T	40	M	HBV	70	yes	A	III-IV	F4	≥24	G2	4	0.48	9	1	18	1
CHC1196T	26	M	HBV	90	yes	A	III-IV	F2-F3	≥24	G1	2	0.13	3	1	11	1
CHC1199T	62	M	Other	140	yes	C	I-II	F0-F1	<24	G2	2	0.35	20	1	43	1
CHC1201T	72	M	AL	60	no	A	I-II	F4	<24	G4	3	0.45	30	1	60	0
CHC121T	66	M	AL	120	no	A	I-II	F0-F1	<24	G5	2	0.18	60	0	60	0
CHC123T	42	M	HBV			0		F0-F1		G4	2	0.34	4	1	4	1
CHC126T	68	F	HCV	70	no	A		F4	≥24	G3	3	0.61	60	0	60	0
CHC129T	61	F	Other	130	yes	A	I-II	F0-F1	≥24	G5	2	0.21	4	1	4	1
CHC130T	60	M	Other	180	no	A	I-II	F0-F1	<24	G5	2	0.29	20	1	31	0
CHC137T	71	M	HBV	35	no	A	III-IV	F2-F3	≥24	G5	3	0.61	60	0	60	0
CHC141T	67	F	Other	35	yes	A	III-IV	F0-F1	≥24	G1	4	0.24	60	0	60	0
CHC152T	64	M	HBV	30	no	C		F4	<24	G6	2	0.11	NE	NE	NE	NE
CHC154T	67	F	Other	90	no	A	I-II	F0-F1	<24	G4	2	0.11	16	1	49	0
CHC155T	62	M	AL	35	no	A	I-II	F4	<24	G4	2	0.03	16	1	20	0
CHC158T	65	M	HBV AL	25	no	A	I-II	F4	<24	G4	2	0.24	20	0	20	0
CHC164T	65	M	Other	100	no	B	I-II	F0-F1	<24	G5	2	0.32	36	1	36	1
CHC168T	67	M	AL	100	yes	A	I-II	F4	≥24	G6	2	0.24	3	1	3	1
CHC191T	71	M	AL	110	yes	C	I-II	F0-F1	<24	G4	2	0.13	11	1	11	1
CHC195T	71	M	AL	70	no	A	I-II	F0-F1	<24	G4	2	0.32	60	0	60	0
CHC196T	33	M	Other	100	no	A	I-II	F0-F1	<24	G4	2	0	60	0	60	0
CHC197T	73	M	AL	130	yes	B	III-IV	F2-F3	≥24	G6	2	0.39	36	1	60	0
CHC203T	45	M	AL	50	no	A	I-II	F4	≥24	G4	2	0.21	15	0	15	0
CHC205T	45	M	AL	100	no	A	III-IV	F0-F1	≥24	G3	3	0.61	2	1	9	1
CHC206T	63	M	HBV	40	no	B	III-IV	F4	<24	G4	2	0	NE	NE	NE	NE
CHC208T	79	M	HCV AL	45	yes	A	III-IV	F2-F3	≥24	G3	2	0.37	6	1	17	1
CHC210T	58	M	HCV	50	no	B	III-IV	F4		G4	2	0.24	NE	NE	NE	NE
CHC211T	68	M	AL	80	yes	C	I-II	F0-F1	<24	G4	2	0.21	12	1	12	1
CHC218T	69	M	Other	130	yes	C	III-IV	F0-F1	≥24	G4	2	0.26	NE	NE	NE	NE
CHC226T	42	M	HBV	190	yes	C	I-II	F2-F3		G3	2	0.42	NE	NE	NE	NE
CHC228T	48	M	Other	145	yes	C	III-IV	F0-F1	≥24	G1	3	0.37	4	1	14	1
CHC229T	64	F	HCV	55	yes	A	III-IV	F4	<24	G3	2	0.24	NE	NE	NE	NE
CHC230T	70	M	Other	160	no	A	I-II	F0-F1	<24	G5	2	0.24	60	0	60	0
CHC235T	66	F	HCV	30	no	A	I-II	F4	≥24	G1	2	0.42	46	0	46	0
CHC237T	26	F	HBV	125	no	B	III-IV	F0-F1	≥24	G1	2	0.24	11	0	11	0
CHC239T	21	F	HBV	100	yes	A	I-II	F2-F3	<24	G2	2	0.32	12	0	12	0
CHC241T	59	M	HBV	30	no	A	III-IV	F2-F3	<24	G4	2	0.29	60	0	60	0
CHC242T	69	M	Other	150	no	A	I-II	F0-F1	<24	G6	2	0.13	49	1	59	1
CHC245T	62	M	HBV	3	no	0	I-II	F4	<24	G2	2	0.34	9	1	13	1
CHC250T	34	M	HBV HCV	70	no	C	I-II	F4	≥24	G1	2	0.32	NE	NE	NE	NE

Supplementary Table 2: Clinical, histological and molecular data of HCC

ID	Age (year)	Gender	Etiology	Tumor size (mm)	Microscopic Vascular Invasion	BCLC	Edmonson	METAVIR	AFP (ng/ml)	Transcriptome subgroups	Ploidy	FAA	PFS time	PFS status	OS time	OS status
CHC252T	57	M	HBV HCV	17	no	0	I-II	F2-F3	≥24	G1	3	0.55	33	1	60	0
CHC253T	66	M	Other	80	yes	C	III-IV	F4	<24	G3	2	0.03	NE	NE	NE	NE
CHC254T	62	M	HBV HCV	80	yes	C	III-IV	F4	<24	G3	4	0.53	8	1	14	0
CHC258T	56	M	Other	100	no	A	I-II	F0-F1		G5	2	0.21	60	0	60	0
CHC301T	77	M	NASH	45	no	B	I-II	F2-F3	<24	G3	2	0.21	44	1	50	1
CHC302T	72	M	HCV	45	no	A	I-II	F2-F3		G5	2	0.13	60	0	60	0
CHC303T	73	M	AL	90	yes	A	III-IV	F4	≥24	G5	2	0.18	NE	NE	NE	NE
CHC304T	77	M	AL	180	yes	C	III-IV	F0-F1	≥24	G3	3	0.71	6	1	22	1
CHC306T	67	M	HCV	20	no	0	I-II	F4		G4	2	0.13	NE	NE	NE	NE
CHC307T	53	M	AL	30	yes	A	III-IV	F4		G4	2	0.16	NE	NE	NE	NE
CHC309T	69	F	HCV	20	yes	0	III-IV	F2-F3		G2	2	0.18	NE	NE	NE	NE
CHC313T	43	F	HCV	130	yes	A	III-IV	F2-F3	≥24	G4	2	0.21	4	1	11	1
CHC314T	71	M	HCV AL	45	no	A	I-II	F2-F3	<24	G4	2	0.21	59	0	59	0
CHC317T	68	F	HCV	15	no	A	III-IV	F4		G5	2	0.11	NE	NE	NE	NE
CHC320T	64	M	HCV AL	35	no	B	III-IV	F4		G6	2	0.02	NE	NE	NE	NE
CHC322T	73	M	AL	40	no	A	III-IV	F4	<24	G4	3	0.58	21	1	21	1
CHC326T	48	M	HBV	18	no	A	I-II	F4		G4	2	0.03	NE	NE	NE	NE
CHC327T	62	M	HCV	25	no	A	I-II	F4		G1	2	0.13	NE	NE	NE	NE
CHC333T	72	M	AL	42	no	A	I-II	F2-F3	<24	G5	2	0.29	NE	NE	NE	NE
CHC335T	68	M	HBV	160	yes	A	I-II	F2-F3	≥24	G6	2	0.05	59	0	59	0
CHC339T	26	F	HBV	100	yes	C	I-II	F2-F3	≥24	G2	3	0.55	34	1	56	1
CHC361T	67	F	Other	60	no	A	I-II	F0-F1	<24	G5	2	0.03	60	0	60	0
CHC398T	50	M	HBV	40	no	0	I-II			G2	2	0.21	NE	NE	NE	NE
CHC399T	67	M	HM	30	no	A	I-II	F2-F3	<24	G6	2	0.18	26	1	37	0
CHC402T	27	M	HBV HCV	65	no	B	I-II	F4	≥24	G2	2	0.34	11	1	16	1
CHC405T	77	M	HM	43	no	A	I-II	F0-F1	<24	G4	2	0.05	38	0	38	0
CHC429T	61	F	Other	45	yes	A	III-IV	F0-F1	≥24	G5	2	0.08	23	1	60	0
CHC430T	50	M	HCV	60	yes	B	III-IV	F4	<24	G5	2	0.05	8	1	8	1
CHC433T	69	M	AL	180	yes	A	I-II	F0-F1	<24	G5	2	0.34	11	1	15	1
CHC434T	71	F	Other	80	no	A	III-IV	F0-F1	≥24	G1	4	0.5	26	1	60	0
CHC437T	59	M	AL	50	no	A	I-II	F4		G5	2	0.18	13	1	24	1
CHC438T	75	M	Other	185	no	A	III-IV	F0-F1	<24	G2	2	0.32	NE	NE	NE	NE
CHC441T	77	M	HM	40	no	A	III-IV	F0-F1		G3	2	0.18	6	1	7	1
CHC445T	55	M	HCV AL	14	no	0	I-II	F4	≥24	G4	2	0.03	13	0	13	0
CHC465T	42	F	Other	100		A	I-II	F0-F1	<24	G4	2	0.08	60	0	60	0
CHC469T	32	F	Other	135	yes	C	III-IV	F0-F1	<24	G6	2	0.34	12	1	23	1
CHC609T	60	M	HBV AL	50	yes	B	III-IV	F2-F3	<24	G5	2	0.45	18	1	50	0
CHC614T	60	M	NASH	30	yes	A	III-IV	F2-F3	<24	G5	2	0.1	12	0	12	0
CHC715T	46	M	NASH AL	40	yes	B	III-IV	F0-F1	<24	G4	2	0.13	NE	NE	NE	NE
CHC725T	59	M	HBV	27	no	A	III-IV	F4	<24	G2	2	0.18	NE	NE	NE	NE
CHC793T	61	M	HM	80	yes	A	III-IV	F0-F1	≥24	G3	2	0.35	20	1	37	1
CHC794T	72	M	HM	160	yes	C	III-IV	F0-F1	≥24	G3	3	0.53	1	1	5	1
CHC798T	72	M	AL	95	no	A	I-II	F0-F1	<24	G4	2	0.18	16	0	16	0
CHC882T	54	M	AL	40	no	A	III-IV	F0-F1	<24	G3	2	0.21	NE	NE	NE	NE
CHC891T	72	F	Other	45	yes	A	III-IV	F4	≥24	G1	2	0.25	7	1	16	1
CHC909T	69	M	Other	210	yes	C	III-IV	F0-F1	≥24	G3	2	0.32	37	0	37	0
CHC918T	82	M	AL	95	no	A	I-II	F0-F1	<24	G4	2	0.13	45	0	45	0
CHC961T	57	M	AL	190	yes	B	III-IV	F0-F1	<24	G5	2	0.26	7	1	17	1
CHC983T	53	M	AL	50	no	B	III-IV	F4	<24	G4	2	0.05	6	1	27	1

AL= Alcohol intake; HM= Hemochromatosis

NE= patients non evaluable for survival (including transplantation, non curative resection)

Supplementary Table 3. List of all somatic mutations identified in the exome sequencing of 24 HCC

HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic position hg19)	Amino Acid	Mutation Type
CHC433T	ENSG00000168036	CTNNB1	3	g.41266098A>G	p.Asp32Gly	missense
CHC1041T	ENSG00000168036	CTNNB1	3	g.41266098A>T	p.Asp32Val	missense
CHC051T	ENSG00000168036	CTNNB1	3	g.41266100T>C	p.Ser33Pro	missense
CHC429T	ENSG00000168036	CTNNB1	3	g.41266101C>G	p.Ser33Cys	missense
CHC301T	ENSG00000168036	CTNNB1	3	g.41266107T>G	p.Ile35Ser	missense
CHC320T	ENSG00000168036	CTNNB1	3	g.41266113C>G	p.Ser37Cys	missense
CHC614T	ENSG00000168036	CTNNB1	3	g.41266125C>A	p.Thr41Asn	missense
CHC1052T	ENSG00000168036	CTNNB1	3	g.41266128_41266129insCAGCTC	p.Thr42_Ala43insSerSer	insertion
CHC121T	ENSG00000168036	CTNNB1	3	g.41266136T>G	p.Ser45Ala	missense
CHC302T	ENSG00000168036	CTNNB1	3	g.41266137C>A	p.Ser45Tyr	missense
CHC197T	ENSG00000168036	CTNNB1	3	g.41266137C>T	p.Ser45Phe	missense
CHC434T	ENSG00000103126	AXIN1	16	g.347772G>T	p.Tyr578X	nonsense
CHC1065T	ENSG00000103126	AXIN1	16	g.354326_354327insA	p.Glu411ValfsX13	insertion
CHC1053T	ENSG00000103126	AXIN1	16	g.354381_354406del	p.Glu384AspfsX31	deletion
CHC306T	ENSG00000103126	AXIN1	16	g.364602del	p.Asp320GlufsX94	deletion
CHC306T	ENSG00000103126	AXIN1	16	g.396233C>A	p.Gly265X	nonsense
CHC1053T	ENSG00000177189	RPS6KA3	X	g.20181154A>C	p.Leu590X	nonsense
CHC258T	ENSG00000177189	RPS6KA3	X	g.20194611C>A	p.Gly314X	nonsense
CHC1053T	ENSG00000177189	RPS6KA3	X	g.20205972C>T	p.Asp250Asn	missense
CHC434T	ENSG00000177189	RPS6KA3	X	g.20206044A>T	p.Tyr226Asn	missense
CHC429T	ENSG00000177189	RPS6KA3	X	g.20222175T>C	p.Tyr97Cys	missense
CHC155T	ENSG00000117713	ARID1A	1	g.27056173_27056174insT	p.Met390IlefsX10	insertion
CHC205T	ENSG00000117713	ARID1A	1	g.27099938_27099962del	p.Gly1274GlufsX7	deletion
CHC205T	ENSG00000117713	ARID1A	1	g.27099964T>G	p.Tyr1281X	nonsense
CHC320T	ENSG00000117713	ARID1A	1	g.27106640T>A	p.Val2084Asp	missense
CHC121T	ENSG00000164796	CSMD3	8	g.113318267C>A	p.Trp2680Cys	missense
CHC121T	ENSG00000164796	CSMD3	8	g.113318310G>A	p.Ser2666Phe	missense
CHC051T	ENSG00000164796	CSMD3	8	g.113364712T>G	p.Lys2063Thr	missense
CHC307T	ENSG00000164796	CSMD3	8	g.114031312del	p.Phe338LeufsX11	deletion
CHC1035T	ENSG00000163638	ADAMTS9	3	g.64527575G>T	p.Ser1712Arg	missense
CHC301T	ENSG00000163638	ADAMTS9	3	g.64627650C>A	p.Cys577Phe	missense
CHC301T	ENSG00000163638	ADAMTS9	3	g.64640135C>A	splicing	intron
CHC1065T	ENSG00000163631	ALB	4	g.74274500_74274501del	p.Asn154X	deletion
CHC614T	ENSG00000163631	ALB	4	g.74277791_74277801del	p.Val265MetfsX8	deletion
CHC258T	ENSG00000163631	ALB	4	g.74284018_74284020del	p.Lys549del	deletion
CHC205T	ENSG00000084674	APOB	2	g.21239482_21239483insATAA	p.Asn1054IlefsX11	insertion
CHC302T	ENSG00000084674	APOB	2	g.21251397A>G	p.Leu544Pro	missense
CHC1041T	ENSG00000084674	APOB	2	g.21252826del	p.Glu472AsnfsX16	deletion
CHC307T	ENSG00000183117	CSMD1	8	g.3205676A>T	p.Cys1104X	nonsense
CHC155T	ENSG00000165323	FAT3	11	g.92085687G>T	p.Asp137Tyr	missense
CHC301T	ENSG00000165323	FAT3	11	g.92086194G>A	p.Gly306Arg	missense
CHC155T	ENSG00000165323	FAT3	11	g.92620270G>T	p.Asp4348Tyr	missense
CHC614T	ENSG00000116044	NFE2L2	2	g.178098800T>C	p.Glu82Gly	missense
CHC1041T	ENSG00000116044	NFE2L2	2	g.178098807T>G	p.Thr80Pro	missense
CHC205T	ENSG00000116044	NFE2L2	2	g.178098959T>C	p.Asp29Gly	missense
CHC433T	ENSG00000156709	AIFM1	X	g.129267388T>A	p.Arg450Trp	missense
CHC429T	ENSG00000156709	AIFM1	X	g.129271128A>G	p.Phe334Leu	missense
CHC429T	ENSG00000163286	ALPPL2	2	g.233273095G>A	p.Trp256X	nonsense
CHC429T	ENSG00000189079	ARID2	12	g.46244040G>T	p.Glu712X	nonsense
CHC301T	ENSG00000138175	ARL3	10	g.104436683C>A	p.Val173Phe	missense
CHC121T	ENSG00000198960	ARMCX6	X	g.100871207C>A	p.Gly135Val	missense
CHC121T	ENSG00000198960	ARMCX6	X	g.100871208C>A	p.Gly135X	nonsense
CHC433T	ENSG00000112249	ASCC3	6	g.101110274T>C	p.Thr809Ala	missense
CHC433T	ENSG00000118322	ATP10B	5	g.160047869C>A	p.Ser634Ile	missense
CHC301T	ENSG00000118322	ATP10B	5	g.160061403G>A	p.Arg447Cys	missense
CHC614T	ENSG00000105726	ATP13A1	19	g.19758027A>G	p.Tyr1006His	missense
CHC155T	ENSG00000105726	ATP13A1	19	g.19758063T>C	p.Asn994Asp	missense
CHC433T	ENSG00000187527	ATP13A5	3	g.193029609G>A	p.Pro814Leu	missense
CHC1035T	ENSG00000187527	ATP13A5	3	g.193036884G>C	p.Phe643Leu	missense
CHC429T	ENSG00000197299	BLM	15	g.91290711C>T	p.Pro30Leu	missense
CHC302T	ENSG00000197299	BLM	15	g.91304159A>G	p.Tyr519Cys	missense
CHC322T	ENSG00000182326	C1S	12	g.7173239dup	p.Trp283LeufsX14	duplication
CHC301T	ENSG00000182326	C1S	12	g.7169912G>A	p.Gly47Arg	missense
CHC429T	ENSG00000153132	CLGN	4	g.141317095C>T	p.Ala343Thr	missense
CHC302T	ENSG00000153132	CLGN	4	g.141334123T>A	p.Glu37Val	missense
CHC302T	ENSG00000176566	DCAF4L2	8	g.88885884C>A	p.Gly106Cys	missense
CHC1035T	ENSG00000176566	DCAF4L2	8	g.88886169C>A	p.Glu11X	nonsense
CHC322T	ENSG00000198947	DMD	X	g.31514964G>A	p.Arg2830Trp	missense
CHC301T	ENSG00000198947	DMD	X	g.32834622C>G	p.Asp165His	missense
CHC155T	ENSG00000124721	DNAH8	6	g.38793962C>A	p.Ala1076Asp	missense
CHC434T	ENSG00000124721	DNAH8	6	g.38795966_38795975del	p.Tyr1147X	deletion
CHC1055T	ENSG00000130158	DOCK6	19	g.11348904C>T	p.Val574Met	missense
CHC302T	ENSG00000130158	DOCK6	19	g.11354495C>A	p.Glu363X	nonsense
CHC320T	ENSG00000171560	FGA	4	g.155505794_155505795del	p.Gly695PhefsX6	deletion
CHC302T	ENSG00000171560	FGA	4	g.155510662C>A	p.Gly36Val	missense
CHC1055T		FIGNL2	12	g.52216187G>A	p.Thr4Ile	missense
CHC1053T	ENSG00000110422	HIPK3	11	g.33309053T>G	p.Tyr365Asp	missense
CHC320T	ENSG00000110422	HIPK3	11	g.33373152A>G	splicing	intron
CHC1061T	ENSG00000135100	HNF1A	12	g.121426648_121426651del	p.Arg114TrpfsX40	deletion
CHC155T	ENSG00000135100	HNF1A	12	g.121437143C>T	p.Thr525Ile	missense
CHC1061T	ENSG00000086758	HUWE1	X	g.53581856G>C	p.Tyr2744X	nonsense
CHC429T	ENSG00000086758	HUWE1	X	g.53644075G>C	p.Pro605Ala	missense
CHC429T	ENSG00000102313	ITIH5L	X	g.54776357C>A	p.Gly1305Cys	missense
CHC433T	ENSG00000102313	ITIH5L	X	g.54815056T>A	p.Arg215Trp	missense
CHC301T	ENSG00000198399	ITSN2	2	g.24477267_24477268insA	p.Lys974AsnfsX33	insertion
CHC1041T	ENSG00000198399	ITSN2	2	g.24533166A>C	p.Leu214Val	missense
CHC1055T	ENSG00000138688	KIAA1109	4	g.123140664G>T	p.Arg806Leu	missense
CHC1061T	ENSG00000138688	KIAA1109	4	g.123188092G>C	p.Arg2491Thr	missense
CHC320T	ENSG00000122778	KIAA1549	7	g.138524987G>T	p.Ala1780Asp	missense
CHC1052T	ENSG00000122778	KIAA1549	7	g.138566137 C>T	p.Gly1359Glu	missense
CHC614T	ENSG00000161850	KRT82	12	g.52797639G>T	p.Gln156Lys	missense
CHC429T	ENSG00000135443	KRT85	12	g.52760844C>T	p.Ala116Thr	missense
CHC1052T	ENSG00000161813	LARP4	12	g.50869451C>G	p.Ser660Cys	missense
CHC433T	ENSG00000168702	LRP1B	2	g.141200113C>G	p.Glu3458Asp	missense
CHC433T	ENSG00000151276	MAGI1	3	g.65367726C>A	p.Val843Leu	missense
CHC1052T	ENSG00000166603	MC4R	18	g.58038652T>G	p.Lys311Gln	missense

Supplementary Table 3. List of all somatic mutations identified in the exome sequencing of 24 HCC

HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic position hg19)	Amino Acid	Mutation Type
CHC197T	ENSG00000166603	MC4R	18	g.58039311A>T	p.Met91Lys	missense
CHC121T	ENSG00000175471	MCTP1	5	g.94275805C>T	p.Gly386Arg	missense
CHC155T	ENSG00000175471	MCTP1	5	g.94353071C>G	p.Gly280Arg	missense
CHC1052T	ENSG00000168404	MLKL	16	g.74708973del	p.Lys422AsnfsX5	deletion
CHC1052T	ENSG00000168404	MLKL	16	g.74708974T>A	p.Lys422Met	missense
CHC1065T	ENSG00000166670	MMP10	11	g.102645969A>G	p.Leu339Ser	missense
CHC121T	ENSG00000166670	MMP10	11	g.102650238del	p.Tyr115SerfsX4	deletion
CHC155T	ENSG00000181143	MUC16	19	g.9008346C>T	splicing	intron
CHC322T	ENSG00000181143	MUC16	19	g.9090101del	p.Leu572X	deletion
CHC429T	ENSG00000154654	NCAM2	21	g.22656588G>A	p.Val69Met	missense
CHC301T	ENSG00000154654	NCAM2	21	g.22881300A>C	p.Thr736Pro	missense
CHC1061T	ENSG00000100968	NFATC4	14	g.24841806del	p.Lys516SerfsX3	deletion
CHC155T	ENSG00000100968	NFATC4	14	g.24843538G>A	p.Arg643His	missense
CHC1061T	ENSG00000155561	NUP205	7	g.135279433C>G	p.Pro657Ala	missense
CHC429T	ENSG00000155561	NUP205	7	g.135287699A>G	p.Asn887Asp	missense
CHC155T	ENSG00000186117	OR5L1	11	g.55579487C>T	p.Pro182Leu	missense
CHC1052T	ENSG00000186117	OR5L1	11	g.55579674C>A	p.His244Gln	missense
CHC1052T	ENSG00000125879	OTOR	20	g.16729554C>T	p.Pro53Leu	missense
CHC433T	ENSG00000125879	OTOR	20	g.16729567C>G	p.Phe57Leu	missense
CHC434T	ENSG00000116117	PARD3B	2	g.205983655C>A	p.Leu231Ile	missense
CHC301T	ENSG00000116117	PARD3B	2	g.205989162G>T	p.Arg426Leu	missense
CHC429T	ENSG00000102290	PCDH11X	X	g.91456373G>A	splicing	intron
CHC429T	ENSG00000102290	PCDH11X	X	g.91873287C>A	p.Thr1131Asn	missense
CHC121T	ENSG00000197991	PCDH20	13	g.61986389C>A	p.Gly615Trp	missense
CHC614T	ENSG00000197991	PCDH20	13	g.61989221G>T	p.Pro24Gln	missense
CHC429T	ENSG00000187372	PCDHB13	5	g.140594857G>T	p.Glu388X	nonsense
CHC155T	ENSG00000187372	PCDHB13	5	g.140595883G>T	p.Gly730Cys	missense
CHC1052T	ENSG00000099139	PCSK5	9	g.78794565C>A	p.His652Asn	missense
CHC1041T	ENSG00000099139	PCSK5	9	g.78953327T>C	p.Cys1617Arg	missense
CHC1041T	ENSG00000174840	PDE12	3	g.57542299C>T	p.Arg65Cys	missense
CHC433T	ENSG00000174840	PDE12	3	g.57545728A>T	p.Lys609Asn	missense
CHC1035T	ENSG00000134853	PDGFRA	4	g.55152023C>A	p.Leu819Met	missense
CHC205T	ENSG00000134853	PDGFRA	4	g.55156639_55156647del	p.Ala1014_Ser1016del	deletion
CHC051T	ENSG00000130024	PHF10	6	g.170115879_170115880insA	p.Lys206AsnfsX6	insertion
CHC1041T	ENSG00000105851	PIK3CG	7	g.106508490G>A	p.Val162Ile	missense
CHC434T	ENSG00000105851	PIK3CG	7	g.106520043C>A	p.Ser824X	nonsense
CHC301T	ENSG00000101333	PLCB4	20	g.9370557T>C	p.Phe397Ser	missense
CHC429T	ENSG00000101333	PLCB4	20	g.9424651A>T	p.Arg918Trp	missense
CHC197T	ENSG00000046889	PREX2	8	g.68965367G>C	p.Gly327Arg	missense
CHC433T	ENSG00000046889	PREX2	8	g.69104724C>T	p.Ala1523Val	missense
CHC429T	ENSG00000101292	PROKR2	20	g.5283292del	p.Ile184LeufsX56	deletion
CHC205T	ENSG00000101292	PROKR2	20	g.5294732A>G	p.Leu95Pro	missense
CHC434T	ENSG00000153707	PTPRD	9	g.8521544G>A	p.Arg232Cys	missense
CHC434T	ENSG00000134597	RBMX2	X	g.129543262C>T	p.Arg69Trp	missense
CHC1041T	ENSG00000134597	RBMX2	X	g.129546368A>G	p.Lys172Arg	missense
CHC1061T	ENSG00000079841	RIMS1	6	g.72967838G>T	p.Arg927Ser	missense
CHC1041T	ENSG00000079841	RIMS1	6	g.73100381del	p.Arg1483SerfsX21	deletion
CHC434T	ENSG00000241343	RPL36A	X	g.100646036T>C	splicing	intron
CHC197T	ENSG00000241343	RPL36A	X	g.100646511dup	p.Thr60AspfsX19	duplication
CHC301T	ENSG00000198626	RYR2	1	g.237811777G>A	p.Gly2459Glu	missense
CHC1035T	ENSG00000198626	RYR2	1	g.237936853G>T	p.Gly3894Trp	missense
CHC301T	ENSG00000156398	SFXN2	10	g.104491503T>G	p.Val206Gly	missense
CHC614T	ENSG00000127616	SMARCA4	19	g.11141554C>A	p.Asp1177Glu	missense
CHC306T	ENSG00000163554	SPTA1	1	g.158624466G>C	p.Arg991Gly	missense
CHC155T	ENSG00000163554	SPTA1	1	g.158636156T>G	p.Asn724His	missense
CHC1061T	ENSG00000133138	TBC1D8B	X	g.106066520_106066521insA	p.Glu218ArgfsX21	insertion
CHC306T	ENSG00000133138	TBC1D8B	X	g.106069360C>T	p.Pro310Ser	missense
CHC302T	ENSG00000198586	TLK1	2	g.171863026T>G	p.Asn576His	missense
CHC302T	ENSG00000198586	TLK1	2	g.171863367T>C	p.Glu514Gly	missense
CHC051T	ENSG00000158882	TOMM40L	1	g.161197755A>C	p.Asn154His	missense
CHC1052T	ENSG00000158882	TOMM40L	1	g.161197758_161197762del	p.Leu157TrpfsX69	deletion
CHC1061T	ENSG00000141510	TP53	17	g.7574017C>A	p.Arg337Leu	missense
CHC1055T	ENSG00000141510	TP53	17	g.7579520_7579521ins17	p.Glu56AlafsX73	insertion
CHC205T	ENSG00000042781	USH2A	1	g.216073468C>T	p.Gly2515Arg	missense
CHC614T	ENSG00000042781	USH2A	1	g.216595640C>A	p.Leu13Phe	missense
CHC433T	ENSG00000126870	WDR60	7	g.158679710A>T	splicing	intron
CHC1052T	ENSG00000126870	WDR60	7	g.158718881G>T	p.Gly754Val	missense
CHC320T	ENSG00000140836	ZFHX3	16	g.72992468G>C	p.Ser526X	nonsense
CHC322T	ENSG00000183579	ZNRF3	22	g.29444461T>A	p.Cys233Ser	missense
CHC1041T	ENSG00000183579	ZNRF3	22	g.29445379G>T	p.Glu304X	nonsense
CHC1052T	ENSG00000166535	A2ML1	12	g.8990935G>A	p.Asp287Asn	missense
CHC1041T	ENSG00000167972	ABCA3	16	g.2369582C>G	p.Lys291Asn	missense
CHC1052T	ENSG00000140798	ABCC12	16	g.48172207T>A	p.Glu304Val	missense
CHC433T	ENSG00000117528	ABCD3	1	g.94982631A>T	p.Arg642Ser	missense
CHC253T	ENSG00000138075	ABCG5	2	g.44052030_44052032del	p.Tyr301del	deletion
CHC205T	ENSG00000100997	ABHD12	20	g.25304040T>G	p.Lys115Gln	missense
CHC205T	ENSG00000011198	ABHD5	3	g.43743764G>A	p.Trp64X	nonsense
CHC205T	ENSG00000138443	ABI2	2	g.204231700T>G	p.Leu73Arg	missense
CHC433T	ENSG00000072778	ACADVL	17	g.7128403C>T	p.Pro652Leu	missense
CHC429T	ENSG00000157766	ACAN	15	g.89398140C>A	p.Pro775His	missense
CHC306T	ENSG00000111058	ACSS3	12	g.81647408C>G	p.Arg652Gly	missense
CHC429T	ENSG00000117148	ACTL8	1	g.18022124T>C	p.Ser12Pro	missense
CHC1061T	ENSG00000123612	ACVR1C	2	g.158412680C>A	p.Glu157X	nonsense
CHC197T	ENSG00000073670	ADAM11	17	g.42852104A>G	p.Met403Val	missense
CHC433T	ENSG00000148848	ADAM12	10	g.127724804G>A	p.Arg817X	nonsense
CHC1035T	ENSG00000008277	ADAM22	7	g.87763647G>T	p.Gly361Trp	missense
CHC433T	ENSG00000114948	ADAM23	2	g.207345992G>A	p.Ala157Thr	missense
CHC155T	ENSG00000151388	ADAMTS12	5	g.33684073G>A	p.Ser241Phe	missense
CHC301T	ENSG00000173157	ADAMTS20	12	g.43862407G>A	p.His407Tyr	missense
CHC121T	ENSG00000178031	ADAMTSL1	9	g.18574050A>G	p.Asp87Gly	missense
CHC155T	ENSG00000078549	ADCYAP1R1	7	g.31125052T>C	p.Ser222Pro	missense
CHC429T	ENSG00000198099	ADH4	4	g.100057768T>C	p.Tyr144Cys	missense
CHC434T	ENSG00000173020	ADRBK1	11	g.67046728_67046730del	p.Val83del	deletion
CHC320T	ENSG00000169129	AFAP1L2	10	g.116073668C>A	p.Gly252Cys	missense
CHC320T	ENSG00000172493	AFF1	4	g.88035557_88035582del	p.Trp525CysfsX19	deletion
CHC434T	ENSG00000155966	AFF2	X	g.148037388C>A	p.Pro605Thr	missense

Supplementary Table 3. List of all somatic mutations identified in the exome sequencing of 24 HCC

HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic position hg19)	Amino Acid	Mutation Type
CHC1052T	ENSG00000133612	AGAP3	7	g.150839673G>T	p.Trp742Leu	missense
CHC121T	ENSG00000166748	AGBL1	15	g.86791013G>T	p.Gly167Val	missense
CHC1053T	ENSG00000173744	AGFG1	2	g.228389633_228389634insT	indels	insertion
CHC1041T	ENSG00000164252	AGGF1	5	g.76326802G>T	splicing	intron
CHC433T	ENSG00000153207	AHCTF1	1	g.247070852C>A	splicing	intron
CHC051T	ENSG00000106305	AIMP2	7	g.6057645T>G	p.Tyr181X	nonsense
CHC306T	ENSG00000129221	AIPL1	17	g.6330331T>A	p.Asn171Ile	missense
CHC302T	ENSG00000108599	AKAP10	17	g.19812566_19812583del	p.Glu632_Lys637del	deletion
CHC1061T	ENSG00000023330	ALAS1	3	g.52240628G>T	p.Met342Ile	missense
CHC155T	ENSG00000136872	ALDOB	9	g.104184093_104184113del	p.Phe358X	deletion
CHC302T	ENSG00000091542	ALKBH5	17	g.18111543C>G	p.Leu340Val	missense
CHC1053T	ENSG00000178038	ALS2CL	3	g.46730893T>C	p.Glu13Gly	missense
CHC434T	ENSG00000243480	AMY2A	1	g.104160220G>A	p.Gly53Glu	missense
CHC1055T	ENSG00000145362	ANK2	4	g.114290867G>A	p.Ser3839Asn	missense
CHC322T	ENSG00000151150	ANK3	10	g.61830119C>A	p.Gly3507Val	missense
CHC301T	ENSG00000151687	ANKAR	2	g.190608051del	p.Asn1287LysfsX7	deletion
CHC301T	ENSG00000166839	ANKDD1A	15	g.65242180G>C	p.Arg490Ser	missense
CHC320T	ENSG00000185722	ANKFY1	17	g.4071195C>T	p.Gly1131Arg	missense
CHC302T	ENSG00000170209	ANKK1	11	g.113264433C>T	p.Pro139Leu	missense
CHC433T	ENSG00000168876	ANKRD49	11	g.2075dup	p.Ile37AsnfsX14	duplication
CHC302T	ENSG00000166825	ANPEP	15	g.90349277T>G	p.Ser180Arg	missense
CHC301T	ENSG00000104537	ANXA13	8	g.124748094_124748103del	p.Leu11AlafsX51	deletion
CHC1065T	ENSG00000034053	APBA2	15	g.29398928G>A	p.Arg608His	missense
CHC205T	ENSG00000134982	APC	5	g.152789_152790insT	p.Glu1573X	insertion
CHC301T	ENSG00000169621	APLF	2	g.68729883T>G	p.Phe63Leu	missense
CHC1053T	ENSG00000157500	APPL1	3	g.57294005G>A	p.Arg539His	missense
CHC302T	ENSG00000198931	APRT	16	g.88876116T>C	p.Gln178Arg	missense
CHC051T	ENSG00000078061	ARAF	X	g.47424300T>A	splicing	intron
CHC1053T	ENSG00000047365	ARAP2	4	g.36179625C>A	p.Glu561X	nonsense
CHC614T	ENSG00000132254	ARFIP2	11	g.6499281C>G	p.Glu229Gln	missense
CHC302T	ENSG00000071205	ARHGAP10	4	g.148887833T>A	p.Val520Asp	missense
CHC1055T	ENSG00000075884	ARHGAP15	2	g.143913066A>T	p.Lys3X	nonsense
CHC434T	ENSG00000074964	ARHGEF10L	1	g.18021773C>T	p.Thr1102Ile	missense
CHC307T	ENSG00000129675	ARHGEF6	X	g.135764990C>T	p.Arg469Gln	missense
CHC1035T	ENSG00000140691	ARMC5	16	g.31477529A>T	p.Gln709His	missense
CHC614T	ENSG00000105676	ARMC6	19	g.19168330_19168331del	p.Ala467ProfsX3	deletion
CHC320T	ENSG00000241685	ARPC1A	7	g.98942059T>A	p.Ser105Thr	missense
CHC433T	ENSG00000130429	ARPC1B	7	g.98984368G>C	p.Trp42Ser	missense
CHC121T	ENSG00000141480	ARRB2	17	g.4623914A>G	p.Asn372Ser	missense
CHC205T	ENSG00000197070	ARRDC1	9	g.140508854A>G	p.Gln241Arg	missense
CHC258T	ENSG00000111339	ART4	12	g.14993469C>T	p.Val255Ile	missense
CHC121T	ENSG00000161664	ASB16	17	g.42248221T>C	p.Trp22Arg	missense
CHC197T	ENSG00000138303	ASCC1	10	g.73956664G>A	p.Pro160Ser	missense
CHC302T	ENSG00000066279	ASPM	1	g.197073328_197073334del	p.Ile1683CysfsX7	deletion
CHC434T	ENSG00000171681	ATF7IP	12	g.14577104dup	p.Ala86SerfsX13	duplication
CHC1041T	ENSG00000145246	ATP10D	4	g.47578814T>C	p.Tyr1131His	missense
CHC1053T	ENSG00000058063	ATP11B	3	g.182576989C>G	p.Leu348Val	missense
CHC121T	ENSG00000105409	ATP1A3	19	g.42474375A>C	p.Val835Gly	missense
CHC197T	ENSG00000175054	ATR	3	g.142254963T>C	p.Gln1269Arg	missense
CHC433T	ENSG00000107518	ATRNL1	10	g.117045852C>A	p.Thr787Lys	missense
CHC1035T	ENSG00000167080	B4GALNT2	17	g.47241521C>T	p.Leu340Phe	missense
CHC306T	ENSG00000182272	B4GALNT4	11	g.379985G>T	p.Val870Leu	missense
CHC1035T	ENSG00000151929	BAG3	10	g.121436548del	p.Glu495AsnfsX71	deletion
CHC434T	ENSG00000156735	BAG4	8	g.38068002_38068004del	p.Gly456del	deletion
CHC433T	ENSG00000121753	BAI2	1	g.32207570T>A	splicing	intron
CHC155T	ENSG00000153064	BANK1	4	g.102951260T>A	p.Phe580Ile	missense
CHC1052T	ENSG00000138376	BARD1	2	g.215595141T>A	p.Glu665Asp	missense
CHC1052T	ENSG00000168062	BATF2	11	g.64764386T>G	p.Met1?	missense
CHC320T	ENSG00000099968	BCL2L13	22	g.18171818C>T	p.Ser99Leu	missense
CHC1055T	ENSG00000188761	BCL2L15	1	g.114423749C>T	p.Ser163Asn	missense
CHC429T	ENSG00000085185	BCORL1	X	g.129185928T>C	p.Met1597Thr	missense
CHC1061T	ENSG00000177324	BEND2	X	g.18189238C>T	p.Ala690Thr	missense
CHC306T	ENSG00000110330	BIRC2	11	g.102248780A>G	p.Met575Val	missense
CHC614T	ENSG00000164713	BRI3	7	g.97920464T>A	p.Phe96Tyr	missense
CHC1052T	ENSG00000136492	BRIP1	17	g.59853896G>A	p.Pro655Ser	missense
CHC301T	ENSG00000185658	BRWD1	21	g.40571534T>C	p.Tyr1603Cys	missense
CHC429T	ENSG00000156970	BUB1B	15	g.40462740A>G	p.Tyr81Cys	missense
CHC433T	ENSG00000005379	BZRAP1	17	g.56381753C>A	p.Arg1851Met	missense
CHC1053T	ENSG00000125730	C3	19	g.6677998C>A	p.Glu1629Asp	missense
CHC433T	ENSG00000039537	C6	5	g.41195946C>A	p.Val179Ile	missense
CHC1061T	ENSG00000021852	C8B	1	g.57399085G>A	p.Ala492Val	missense
CHC1052T	ENSG00000074410	CA12	15	g.63631039C>T	p.Val285Ile	missense
CHC433T	ENSG00000100346	CACNA1I	22	g.40060921C>A	p.Pro1282Thr	missense
CHC258T	ENSG00000151062	CACNA2D4	12	g.1994175T>A	p.Glu379Val	missense
CHC320T	ENSG00000067191	CACNB1	17	g.37342283G>A	p.Gln235X	nonsense
CHC301T	ENSG00000185933	CALHM1	10	g.105215429G>A	p.Gln211X	nonsense
CHC429T	ENSG00000110931	CAMKK2	12	g.121701718C>A	p.Arg217Leu	missense
CHC155T	ENSG00000118200	CAMSAP1L1	1	g.200818972del	p.Asp1025GlufsX6	deletion
CHC433T	ENSG00000132357	CARD6	5	g.40852644G>T	p.Ala404Ser	missense
CHC1041T	ENSG00000118307	CASC1	12	g.25264860A>G	p.Met542Thr	missense
CHC322T	ENSG00000147044	CASK	X	g.41383287C>T	p.Ala836Thr	missense
CHC1065T	ENSG00000118412	CASP8AP2	6	g.90630324del	p.Phe725LeufsX24	deletion
CHC051T	ENSG00000175294	CATSPER1	11	g.65788574T>G	p.Thr592Pro	missense
CHC429T	ENSG00000133962	CATSPERB	14	g.92171042G>A	p.Pro157Leu	missense
CHC433T	ENSG00000163001	CCDC104	2	g.55771377G>T	p.Glu267X	nonsense
CHC1035T	ENSG00000181378	CCDC108	2	g.219888039G>A	p.Arg904Cys	missense
CHC258T	ENSG00000180347	CCDC129	7	g.31622786C>A	p.Asp403Glu	missense
CHC1041T	ENSG00000244607	CCDC13	3	g.42798632del	p.Lys99SerfsX3	deletion
CHC1035T	ENSG00000162592	CCDC27	1	g.3670785C>A	p.Ala141Asp	missense
CHC614T	ENSG00000135127	CCDC64	12	g.120530841A>G	p.Asp533Gly	missense
CHC1041T	ENSG00000120647	CCDC77	12	g.542363_542364insGGGAGA	p.Gly233_Glu234insArgGly	insertion
CHC1052T	ENSG00000110104	CCDC86	11	g.60609901T>C	p.Ser102Pro	missense
CHC320T	ENSG00000185972	CCIN	9	g.36169747A>G	p.Asp83Gly	missense
CHC121T	ENSG00000167236	CCL23	17	g.34344913G>T	p.Leu8Ile	missense
CHC258T	ENSG00000121807	CCR2	3	g.46399680G>T	p.Cys221Phe	missense
CHC1061T	ENSG00000198445	CCT8L2	22	g.17072407C>G	p.Gly345Ala	missense

Supplementary Table 3. List of all somatic mutations identified in the exome sequencing of 24 HCC

HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic position hg19)	Amino Acid	Mutation Type
CHC155T	ENSG00000156535	CD109	6	g.74502461T>G	p.Tyr938X	nonsense
CHC1061T	ENSG00000134061	CD180	5	g.66479290T>C	p.Asn461Asp	missense
CHC429T	ENSG00000174807	CD248	11	g.66083264G>A	p.Pro412Leu	missense
CHC614T	ENSG00000153283	CD96	3	g.111356926A>T	p.Asp479Val	missense
CHC1053T	ENSG00000130177	CDC16	13	g.115012466A>G	p.Arg320Gly	missense
CHC051T	ENSG00000198752	CDC42BPB	14	g.103405957T>G	p.Asp1606Ala	missense
CHC1065T	ENSG00000140945	CDH13	16	g.82892035C>G	p.Ile38Met	missense
CHC051T	ENSG00000179242	CDH4	20	g.60427891G>A	p.Asp272Asn	missense
CHC429T	ENSG00000150394	CDH8	16	g.61855012 A>G	p.Tyr281His	missense
CHC1061T	ENSG00000163624	CDS1	4	g.85530581G>T	splicing	intron
CHC322T	ENSG00000093072	CECR1	22	g.17690270T>A	p.Asn100Tyr	missense
CHC320T	ENSG00000069998	CECR5	22	g.17622117A>T	p.Leu193His	missense
CHC1053T	ENSG00000198707	CEP290	12	g.88483000A>C	p.Leu1280Val	missense
CHC121T	ENSG00000172831	CES2	16	g.66974180A>G	p.Asp224Gly	missense
CHC429T	ENSG00000172824	CES4A	16	g.67035302G>A	p.Gly210Arg	missense
CHC258T	ENSG00000134389	CFHR5	1	g.196953165G>A	p.Val110Ile	missense
CHC155T	ENSG00000170004	CHD3	17	g.7812076C>G	p.Pro1834Ala	missense
CHC258T	ENSG00000111642	CHD4	12	g.6701868C>T	p.Arg923Lys	missense
CHC302T	ENSG00000188419	CHM	X	g.85236743G>A	p.Gln63X	nonsense
CHC1061T	ENSG00000110172	CHORDC1	11	g.89948386A>T	p.Cys43Ser	missense
CHC1065T	ENSG00000124302	CHST8	19	g.34263921G>T	p.Asp410Tyr	missense
CHC301T	ENSG00000127586	CHTF18	16	g.846056A>G	p.Gln812Arg	missense
CHC307T	ENSG00000148337	CIZ1	9	g.130943033C>T	p.Glu217Lys	missense
CHC121T	ENSG00000016602	CLCA4	1	g.87045737G>T	p.Lys823Asn	missense
CHC301T	ENSG00000013297	CLDN11	3	g.170140971G>A	p.Ala83Thr	missense
CHC306T	ENSG00000130779	CLIP1	12	g.122837329C>T	p.Val438Ile	missense
CHC322T	ENSG00000079101	CLUL1	18	g.633333C>T	p.Pro298Ser	missense
CHC1061T	ENSG00000070729	CNGB1	16	g.57991268G>T	p.Pro284His	missense
CHC155T	ENSG00000118432	CNR1	6	g.88854357C>G	p.Asp213His	missense
CHC1041T	ENSG00000082438	COBLL1	2	g.165584689_165584695del	p.Val149LeufsX10	deletion
CHC121T	ENSG00000204248	COL11A2	6	g.33156861C>A	p.Gly113Cys	missense
CHC121T	ENSG00000111799	COL12A1	6	g.75827230C>A	p.Val2463Phe	missense
CHC1035T	ENSG00000108821	COL1A1	17	g.48266608C>T	p.Gly953Val	missense
CHC155T	ENSG00000171502	COL24A1	1	g.86524808C>A	p.Arg601Met	missense
CHC322T	ENSG00000134871	COL4A2	13	g.111086756_111086757del	p.Gly232ThrfsX7	deletion
CHC433T	ENSG00000130635	COL5A1	9	g.137648663A>T	p.Lys627Met	missense
CHC302T	ENSG00000173163	COMMD1	2	g.62362984_62363004del	p.Leu161_Lys167del	deletion
CHC433T	ENSG00000111652	COPS7A	12	g.6840174G>T	p.Gly266Val	missense
CHC614T	ENSG00000166260	COX11	17	g.53040247_53040248dup	p.Pro227IlefsX6	insertion
CHC1065T	ENSG00000080618	CPB2	13	g.46632373G>C	p.Gln314Glu	missense
CHC429T	ENSG00000214575	CPEB1	15	g.83226697C>T	p.Gly140Glu	missense
CHC433T	ENSG00000196353	CPNE4	3	g.131274372C>A	p.Gly362Val	missense
CHC320T	ENSG00000124772	CPNE5	6	g.36716015T>A	p.Asp334Val	missense
CHC121T	ENSG00000100884	CPNE6	14	g.24546576G>A	p.Val505Met	missense
CHC121T	ENSG00000150938	CRIM1	2	g.36764602C>A	p.Gln846Lys	missense
CHC197T	ENSG00000213923	CSNK1E	22	g.38694910G>T	p.Arg256Ser	missense
CHC121T	ENSG00000173546	CSPG4	15	g.75970125C>A	p.Asp1685Tyr	missense
CHC1052T	ENSG00000198561	CTNND1	11	g.57571197G>A	p.Glu509Lys	missense
CHC434T	ENSG00000169862	CTNND2	5	g.10973648C>T	p.Asp1199Asn	missense
CHC1035T	ENSG00000107611	CUBN	10	g.16957911G>T	p.His2373Gln	missense
CHC433T	ENSG00000055130	CUL1	7	g.148481130A>T	p.Glu420Val	missense
CHC197T	ENSG00000163510	CWC22	2	g.180815577T>C	p.Thr632Ala	missense
CHC322T	ENSG00000095485	CWF19L1	10	g.102016204C>T	p.Gly107Arg	missense
CHC051T	ENSG00000138755	CXCL9	4	g.76926006C>A	p.Asp78Tyr	missense
CHC433T	ENSG00000167740	CYB5D2	17	g.4058127del	p.Gly184AlafsX13	deletion
CHC306T	ENSG00000071967	CYBRD1	2	g.172409907C>T	p.Arg152X	nonsense
CHC121T	ENSG00000130649	CYP2E1	10	g.135347282T>A	p.Leu283X	nonsense
CHC197T	ENSG00000197446	CYP2F1	19	g.41628015T>C	p.Cys267Arg	missense
CHC197T	ENSG00000134780	DAGLA	11	g.61490434T>C	splicing	intron
CHC121T	ENSG00000196730	DAPK1	9	g.90321432A>G	p.Gln1149Arg	missense
CHC302T	ENSG00000070190	DAPP1	4	g.100756805C>A	p.His43Asn	missense
CHC301T	ENSG00000078725	DBC1	9	g.121976292C>T	p.Cys276Tyr	missense
CHC205T	ENSG00000170959	DCDC5	11	g.30902810T>A	p.Arg814X	nonsense
CHC205T	ENSG00000166341	DCHS1	11	g.6654847G>A	p.Arg751Trp	missense
CHC306T	ENSG00000118655	DCLRE1B	1	g.114453990G>T	p.Arg259Leu	missense
CHC205T	ENSG00000080166	DCT	13	g.95114433A>G	p.Tyr292His	missense
CHC121T	ENSG00000170967	DDI1	11	g.103908358C>A	p.Gln270Lys	missense
CHC429T	ENSG00000165359	DDX26B	X	g.134715453G>T	p.Arg826Ser	missense
CHC320T	ENSG00000067048	DDX3Y	Y	g.15028344T>C	p.Val494Ala	missense
CHC1041T	ENSG00000107625	DDX50	10	g.70673842_70673843insT	p.Ser326PhefsX21	insertion
CHC434T	ENSG00000176782	DEFB104A	8	g.7698598C>T	p.Thr34Ile	missense
CHC1061T	ENSG00000119522	DENND1A	9	g.126144679C>T	p.Glu688Lys	missense
CHC1065T	ENSG00000137145	DENND4C	9	g.19300207C>G	p.Leu161Val	missense
CHC1052T	ENSG00000095397	DFNB31	9	g.117266498G>A	p.Ser195Phe	missense
CHC306T	ENSG00000136267	DGKB	7	g.14378298A>C	p.Leu656Arg	missense
CHC429T	ENSG00000116133	DHCR24	1	g.55341714G>C	p.Arg132Gly	missense
CHC121T	ENSG00000181192	DHTKD1	10	g.12126663G>T	p.Trp145Cys	missense
CHC433T	ENSG00000139734	DIAPH3	13	g.60435576A>T	p.Val901Glu	missense
CHC155T	ENSG00000006377	DLX6	7	g.96639195G>T	p.Gly240Cys	missense
CHC301T	ENSG00000197653	DNAH10	12	g.124305236dup	p.Glu1253ArgfsX20	duplication
CHC320T	ENSG00000183914	DNAH2	17	g.7660536G>A	p.Val678Ile	missense
CHC306T	ENSG00000158486	DNAH3	16	g.20996748C>T	p.Gly2439Glu	missense
CHC155T	ENSG00000039139	DNAH5	5	g.13811834T>A	p.Leu2443Phe	missense
CHC1035T	ENSG00000118997	DNAH7	2	g.196651884C>A	p.Lys3576Asn	missense
CHC433T	ENSG00000118997	DNAH7	2	g.196723366_196723367insAG	p.Glu2633AspfsX4	insertion
CHC121T	ENSG00000007174	DNAH9	17	g.11726297C>A	p.Cys3064X	nonsense
CHC155T	ENSG00000171595	DNAI2	17	g.72278000G>T	p.Gly15Val	missense
CHC1065T	ENSG00000178401	DNAJC22	12	g.49742950_49742953del	p.Ser100ProfsX16	deletion
CHC433T	ENSG00000187957	DNER	2	g.230253046A>T	p.Leu597Gln	missense
CHC429T	ENSG00000088538	DOCK3	3	g.51395492G>A	p.Arg1623Gln	missense
CHC434T	ENSG00000115325	DOK1	2	g.74784185G>A	p.Gly464Arg	missense
CHC429T	ENSG00000159147	DONSON	21	g.34955900A>C	p.Tyr286X	nonsense
CHC051T	ENSG00000175497	DPP10	2	g.116598368T>C	p.Leu746Pro	missense
CHC301T	ENSG00000113657	DPYSL3	5	g.146795328A>G	p.Ile255Thr	missense
CHC1053T	ENSG00000175065	DSG4	18	g.28993333G>C	p.Glu985Asp	missense
CHC205T	ENSG00000096696	DSP	6	g.7580297_7580301del	p.Glu1292ArgfsX11	deletion

Supplementary Table 3. List of all somatic mutations identified in the exome sequencing of 24 HCC

HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic position hg19)	Amino Acid	Mutation Type
CHC429T	ENSG00000135144	DTX1	12	g.113532598G>A	p.Cys411Tyr	missense
CHC121T	ENSG00000120129	DUSP1	5	g.172195846G>T	p.Phe341Leu	missense
CHC429T	ENSG00000187240	DYNC2H1	11	g.103270517_103270518insA	p.Ala4102AspfsX63	insertion
CHC121T	ENSG00000106823	ECM2	9	g.95256390G>C	p.Ser636X	nonsense
CHC433T	ENSG00000134109	EDEM1	3	g.5241287A>T	p.Asn198Ile	missense
CHC1052T	ENSG00000130038	EFCAB4B	12	g.3763565G>T	p.Leu287Met	missense
CHC205T	ENSG00000126070	EIF2C3	1	g.36475119C>A	p.Thr358Lys	missense
CHC051T	ENSG00000104131	EIF3J	15	g.44843655del	p.Ile77X	deletion
CHC320T	ENSG00000162374	ELAVL4	1	g.50661248T>A	p.Val192Glu	missense
CHC302T	ENSG00000102034	ELF4	X	g.129205085C>A	p.Val247Leu	missense
CHC197T	ENSG00000110675	ELMOD1	11	g.107506390C>A	p.Leu107Met	missense
CHC121T	ENSG00000132205	EMILIN2	18	g.2892076A>G	p.Arg651Gly	missense
CHC1055T	ENSG00000100393	EP300	22	g.41525894T>G	p.Val390Gly	missense
CHC434T	ENSG00000116016	EPAS1	2	g.46597022A>T	p.Glu279Val	missense
CHC306T	ENSG00000119888	EPCAM	2	g.47600959G>A	p.Cys66Tyr	missense
CHC121T	ENSG00000044524	EPHA3	3	g.89448579del	p.Ala515LeufsX30	deletion
CHC1052T	ENSG00000116106	EPHA4	2	g.222428753C>T	p.Gly174Glu	missense
CHC051T	ENSG00000145242	EPHA5	4	g.66233102C>A	p.Glu633X	nonsense
CHC301T	ENSG00000080224	EPHA6	3	g.96706224C>G	p.Tyr167X	nonsense
CHC429T	ENSG00000178567	EPM2AIP1	3	g.37033992C>T	p.Val193Ile	missense
CHC1035T	ENSG00000121053	EPX	17	g.56274527C>A	p.Asp343Glu	missense
CHC121T	ENSG00000178607	ERN1	17	g.62121362G>A	p.Pro974Ser	missense
CHC1052T	ENSG00000196482	ESRRG	1	g.216692704del	p.Ile308PhefsX2	deletion
CHC051T	ENSG00000126860	EVI2A	17	g.29645740A>G	p.Ser98Pro	missense
CHC121T	ENSG00000116903	EXOC8	1	g.231473409A>T	p.Val28Glu	missense
CHC433T	ENSG00000110723	EXPH5	11	g.108382711A>C	p.Leu1175Val	missense
CHC051T	ENSG00000106462	EZH2	7	g.148507430T>C	p.Asn675Ser	missense
CHC429T	ENSG00000143278	F13B	1	g.197021884C>T	p.Gly479Arg	missense
CHC433T	ENSG00000177096	FAM109B	22	g.42473985T>A	p.Trp230Arg	missense
CHC301T	ENSG00000135842	FAM129A	1	g.184801036C>T	p.Arg221Gln	missense
CHC197T	ENSG00000167483	FAM129C	19	g.17653000G>A	p.Arg440His	missense
CHC301T	ENSG00000141699	FAM134C	17	g.40734153G>A	p.Ser360Phe	missense
CHC121T	ENSG00000051009	FAM160A2	11	g.6239185G>A	p.Pro558Leu	missense
CHC197T	ENSG00000184305	FAM190A	4	g.91230195G>T	p.Ala254Ser	missense
CHC1052T	ENSG00000174016	FAM46D	X	g.79698174G>T	p.Val46Phe	missense
CHC051T	ENSG00000223611	FAM48B2	X	g.24331429C>A	p.Asp2Tyr	missense
CHC1052T	ENSG00000197872	FAM49A	2	g.16740786A>C	p.Ile260Ser	missense
CHC429T	ENSG00000128923	FAM63B	15	g.59114015G>T	p.Glu408X	nonsense
CHC434T	ENSG00000042062	FAM65C	20	g.49211912C>A	p.Glu678X	nonsense
CHC1052T	ENSG00000187790	FANCM	14	g.45645104A>T	p.Leu1049Phe	missense
CHC306T	ENSG00000064763	FAR2	12	g.29450121T>C	p.Ile178Thr	missense
CHC433T	ENSG00000124279	FASTKD3	5	g.7867364T>C	p.Asn278Ser	missense
CHC301T	ENSG00000086570	FAT2	5	g.150934191G>T	p.Ser1226Tyr	missense
CHC121T	ENSG00000196159	FAT4	4	g.126373142_126373143insA	p.Leu3658ThrfsX10	insertion
CHC1065T	ENSG00000138829	FBN2	5	g.127670451C>A	p.Gln1353His	missense
CHC320T	ENSG00000145780	FEM1C	5	g.114860919C>A	p.Asp314Tyr	missense
CHC433T	ENSG00000171564	FGB	4	g.155490729T>C	p.Leu341Ser	missense
CHC614T	ENSG00000137440	FGFBP1	4	g.15937894C>A	p.Arg121Leu	missense
CHC429T	ENSG00000137460	FHDC1	4	g.153897444A>G	p.Lys1001Glu	missense
CHC1055T	ENSG00000134775	FHOD3	18	g.34192058G>T	p.Glu319Asp	missense
CHC301T	ENSG00000118407	FILIP1	6	g.76023200C>T	p.Ser783Asn	missense
CHC614T	ENSG00000136068	FLNB	3	g.58120403del	p.Gly1557AlafsX31	deletion
CHC433T	ENSG00000037280	FLT4	5	g.180047310T>A	splicing	intron
CHC301T	ENSG00000157827	FMNL2	2	g.153435429C>T	p.Pro245Ser	missense
CHC197T	ENSG00000164694	FNDC1	6	g.159653367C>T	p.Pro608Leu	missense
CHC302T	ENSG00000138759	FRAS1	4	g.79328946G>A	p.Trp1420X	nonsense
CHC1055T	ENSG00000172159	FRMD3	9	g.85928629C>A	p.Leu210Phe	missense
CHC302T	ENSG00000156869	FRRS1	1	g.100174614G>C	p.Ser574X	nonsense
CHC121T	ENSG00000106328	FSCN3	7	g.127235893C>A	p.Ala226Glu	missense
CHC433T	ENSG00000140564	FURIN	15	g.91425068del	p.Gly782AlafsX31	deletion
CHC429T	ENSG00000082074	FYB	5	g.39202156C>T	p.Glu303Lys	missense
CHC320T	ENSG00000105325	FZR1	19	g.3533382C>G	p.Arg445Gly	missense
CHC302T	ENSG00000143458	GABPB2	1	g.151090437del	p.Gly351AlafsX26	deletion
CHC433T	ENSG00000145863	GABRA6	5	g.161113327G>A	p.Asp44Asn	missense
CHC320T	ENSG00000145864	GABRB2	5	g.160886741C>A	p.Trp116Leu	missense
CHC302T	ENSG00000163285	GABRG1	4	g.46066503T>A	p.Asn194Tyr	missense
CHC306T	ENSG00000117308	GALE	1	g.24122689C>T	p.Ala314Thr	missense
CHC429T	ENSG00000156958	GALK2	15	g.49528110A>G	p.Tyr110Cys	missense
CHC301T	ENSG00000174473	GALNTL6	4	g.173803975G>T	p.Asp320Tyr	missense
CHC1041T	ENSG00000128310	GALR3	22	g.38219640T>C	p.Val76Ala	missense
CHC1061T	ENSG00000213930	GALT	9	g.34646773C>A	p.Phe24Leu	missense
CHC051T	ENSG00000183087	GAS6	13	g.114535391C>A	p.Asp342Tyr	missense
CHC306T	ENSG00000084734	GCKR	2	g.27724006C>T	p.Pro185Leu	missense
CHC433T	ENSG00000089154	GCN1L1	12	g.120589084C>T	p.Ala1392Thr	missense
CHC1035T	ENSG00000178295	GEN1	2	g.17961923G>A	p.Asp482Asn	missense
CHC433T	ENSG00000125447	GGA3	17	g.73238979A>G	p.Leu181Pro	missense
CHC433T	ENSG00000137563	GGH	8	g.63942752_63942753del	p.Tyr83X	deletion
CHC1061T	ENSG00000152661	GJA1	6	g.121768961C>T	p.Ala323Val	missense
CHC301T	ENSG00000197045	GMFB	14	g.54950479A>G	p.Ser4Pro	missense
CHC1035T	ENSG00000130755	GMFG	19	g.39820183C>G	splicing	intron
CHC155T	ENSG00000114353	GNAI2	3	g.50290615T>C	p.Tyr155His	missense
CHC1041T	ENSG00000100522	GNPNAT1	14	g.53248574_53248608del	p.Lys80SerfsX17	deletion
CHC197T	ENSG00000135677	GNS	12	g.65130840_65130847del	p.Glu345AspfsX26	deletion
CHC197T	ENSG00000144674	GOLGA4	3	g.37367712del	p.Trp1467X	deletion
CHC205T	ENSG00000066455	GOLGA5	14	g.93263954del	p.Pro58LeufsX21	deletion
CHC197T	ENSG00000173230	GOLGB1	3	g.121413124T>G	p.Leu2077Phe	missense
CHC1035T	ENSG00000135052	GOLM1	9	g.88642739G>T	p.Thr400Lys	missense
CHC322T	ENSG00000120370	GORAB	1	g.170521158del	p.Lys247SerfsX15	deletion
CHC434T	ENSG00000186566	GPATCH8	17	g.42475011_42475025del	p.Ala1474_Ala1478del	deletion
CHC197T	ENSG00000136235	GPNMB	7	g.23309730C>A	p.Asn467Lys	missense
CHC434T	ENSG00000153292	GPR110	6	g.46995471_46995472insA	p.Lys32AsnfsX7	insertion
CHC1035T	ENSG00000164393	GPR111	6	g.47649967G>T	p.Val490Phe	missense
CHC429T	ENSG00000144820	GPR128	3	g.100328802C>G	p.Ile34Met	missense
CHC1035T	ENSG00000181619	GPR135	14	g.59930761G>A	p.Ser395Leu	missense
CHC433T	ENSG00000187037	GPR141	7	g.37780260A>G	p.Lys89Glu	missense
CHC1035T	ENSG00000164199	GPR98	5	g.90015949G>T	p.Ala3178Ser	missense

Supplementary Table 3. List of all somatic mutations identified in the exome sequencing of 24 HCC

HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic position hg19)	Amino Acid	Mutation Type
CHC1065T	ENSG00000173612	GPRC6A	6	g.117113552G>T	p.Thr845Lys	missense
CHC429T	ENSG00000169258	GPRIN1	5	g.176025011G>T	p.Leu609Met	missense
CHC155T	ENSG00000121957	GPSM2	1	g.109466721G>C	p.Ser567Thr	missense
CHC322T	ENSG00000083307	GRHL2	8	g.102631864A>C	p.Asn399Thr	missense
CHC433T	ENSG00000155511	GRIA1	5	g.153085558T>A	p.Phe585Tyr	missense
CHC1035T	ENSG00000120251	GRIA2	4	g.158242707C>A	p.Leu280Met	missense
CHC205T	ENSG00000105737	GRIK5	19	g.42546751C>G	p.Glu476Gln	missense
CHC155T	ENSG00000150086	GRIN2B	12	g.13716331A>G	p.Tyr1281His	missense
CHC434T	ENSG00000077235	GTF3C1	16	g.27497443G>A	p.Arg1245Cys	missense
CHC258T	ENSG00000152402	GUCY1A2	11	g.106810383T>C	p.Met337Val	missense
CHC429T	ENSG00000164116	GUCY1A3	4	g.156638372_156638373insA	p.His545GlnfsX17	insertion
CHC155T	ENSG00000145681	HAPLN1	5	g.82940219G>T	p.Ser246Arg	missense
CHC051T	ENSG00000128708	HAT1	2	g.172823364T>G	p.Ser239Arg	missense
CHC205T	ENSG00000048052	HDAC9	7	g.19015534T>A	p.Leu1043Gln	missense
CHC433T	ENSG00000165259	HDX	X	g.83599258C>A	p.Glu554X	nonsense
CHC320T	ENSG00000171495	HEATR7B2	5	g.41018834A>G	p.Trp878Arg	missense
CHC433T	ENSG00000198265	HELZ	17	g.65141916_65141918del	p.Thr904del	deletion
CHC433T	ENSG00000103657	HERC1	15	g.63916477T>G	p.Gln4442Pro	missense
CHC1061T	ENSG00000138646	HERC5	4	g.89384746G>A	p.Gly251Asp	missense
CHC1035T	ENSG00000010704	HFE	6	g.26091742G>T	p.Ala181Ser	missense
CHC614T	ENSG00000019991	HGF	7	g.81332001G>A	p.Arg695Cys	missense
CHC320T	ENSG00000164161	HHIP	4	g.145568017G>A	p.Gly64Arg	missense
CHC614T	ENSG00000197846	HIST1H2BF	6	g.26199992A>G	p.Asp69Gly	missense
CHC155T	ENSG00000143341	HMCN1	1	g.186034381C>A	p.Pro2509Thr	missense
CHC433T	ENSG00000108753	HNF1B	17	g.36070533_36070555del	p.Ser388ProfsX4	deletion
CHC1061T	ENSG00000092199	HNRNPC	14	g.21702304del	p.Arg17ValfsX51	deletion
CHC322T	ENSG00000170689	HOXB9	17	g.46700371C>T	p.Arg215Lys	missense
CHC197T	ENSG00000107521	HPS1	10	g.100183582A>G	p.Leu487Pro	missense
CHC1052T	ENSG00000002587	HS3ST1	4	g.11401185_11401193del	p.Leu146_Asp148del	deletion
CHC1061T	ENSG00000122254	HS3ST2	16	g.22926390T>C	p.Val204Ala	missense
CHC614T	ENSG00000176387	HSD11B2	16	g.67470705C>G	p.Tyr339X	nonsense
CHC1061T	ENSG00000142798	HSPG2	1	g.22179298G>A	p.Gln2207X	nonsense
CHC614T	ENSG00000136273	HUS1	7	g.48016433A>C	p.Leu120X	nonsense
CHC614T	ENSG00000214042	IFNA7	9	g.21201716A>T	p.Ile150Asn	missense
CHC1052T	ENSG00000161405	IKZF3	17	g.37922201G>A	p.Arg458Cys	missense
CHC429T	ENSG00000115598	IL1RL2	2	g.102828617C>T	p.Ser236Leu	missense
CHC429T	ENSG00000162594	IL23R	1	g.67724232A>G	p.Ile437Met	missense
CHC306T	ENSG00000175189	INHBC	12	g.57843732A>G	p.Tyr329Cys	missense
CHC302T	ENSG00000204084	INPP5B	1	g.38397690A>T	p.Trp143Arg	missense
CHC051T	ENSG00000164066	INTU	4	g.128637514_128637515del	p.Tyr918CysfsX5	deletion
CHC1065T	ENSG00000176095	IP6K1	3	g.49770340A>G	p.Leu167Pro	missense
CHC1041T	ENSG00000159387	IRX6	16	g.55360333C>A	p.Ala44Glu	missense
CHC121T	ENSG00000213949	ITGA1	5	g.52177831G>A	p.Ala251Thr	missense
CHC429T	ENSG00000156886	ITGAD	16	g.31429802T>G	p.Ser899Arg	missense
CHC1035T	ENSG00000123104	ITPR2	12	g.26748469C>T	p.Glu1437Lys	missense
CHC614T	ENSG00000148841	ITPRIP	10	g.106075076A>G	p.Val245Ala	missense
CHC433T	ENSG00000161999	JMJD8	16	g.733021dup	p.Leu237ProfsX23	duplication
CHC1065T	ENSG00000011201	KAL1	X	g.8522077G>A	p.Arg424X	nonsense
CHC1061T	ENSG00000120696	KBTBD7	13	g.41766431C>A	p.Glu655X	nonsense
CHC433T	ENSG00000158445	KCNB1	20	g.47989865T>C	p.Ile744Met	missense
CHC433T	ENSG00000182674	KCNB2	8	g.73848291C>A	p.Ala234Glu	missense
CHC301T	ENSG00000116396	KCNC4	1	g.110765914C>G	p.Ser336Cys	missense
CHC1052T	ENSG00000026559	KCNG1	20	g.49626445G>A	p.Ala144Val	missense
CHC155T	ENSG00000183960	KCNH8	3	g.19479854G>A	splicing	intron
CHC1061T	ENSG00000120457	KCNJ5	11	g.128786453T>C	p.Cys363Arg	missense
CHC1061T	ENSG00000173338	KCNK7	11	g.65361108_65361134del	p.Val178_Pro186del	deletion
CHC433T	ENSG00000075043	KCNQ2	20	g.62044812A>C	p.Leu585Arg	missense
CHC433T	ENSG00000120733	KDM3B	5	g.137766069G>T	p.Gln1675His	missense
CHC433T	ENSG00000186280	KDM4D	11	g.94731546A>G	p.Lys337Arg	missense
CHC301T	ENSG00000079999	KEAP1	19	g.10597426C>A	p.Glu593X	nonsense
CHC121T	ENSG00000088247	KHSRP	19	g.6420453G>T	p.Pro152Gln	missense
CHC121T	ENSG00000135709	KIAA0513	16	g.85111142G>T	p.Arg229Leu	missense
CHC051T	ENSG00000164542	KIAA0895	7	g.36396656G>A	p.Ala241Val	missense
CHC614T	ENSG00000005238	KIAA1539	9	g.35107957_35107958del	p.Glu105GlyfsX26	deletion
CHC1061T	ENSG00000163808	KIF15	3	g.44872511G>A	splicing	intron
CHC1053T	ENSG00000112984	KIF20A	5	g.137521219_137521220del	p.Glu649ArgfsX22	deletion
CHC433T	ENSG00000116852	KIF21B	1	g.200945986C>A	p.Gly1441Val	missense
CHC1055T	ENSG00000186638	KIF24	9	g.34256399T>C	p.Glu1069Gly	missense
CHC155T	ENSG00000189013	KIR2DL4	19	g.55317541T>G	p.Leu166Arg	missense
CHC155T	ENSG00000126259	KIRREL2	19	g.36352049G>C	p.Arg361Pro	missense
CHC051T	ENSG00000118263	KLF7	2	g.207988806G>C	p.Pro142Arg	missense
CHC429T	ENSG00000197776	KLHDC1	14	g.50176515G>A	p.Gly86Arg	missense
CHC320T	ENSG00000128607	KLHDC10	7	g.129736848G>A	splicing	intron
CHC302T	ENSG00000172578	KLHL6	3	g.183217510A>T	p.Cys339Ser	missense
CHC1041T	ENSG00000167749	KLK4	19	g.51410260C>G	p.Gly232Ala	missense
CHC614T	ENSG00000162869	KLRAQ1	2	g.48713866C>T	p.Ser472Leu	missense
CHC320T	ENSG00000025800	KPNA6	1	g.32620321_32620329del	p.Gln46ProfsX3	deletion
CHC306T	ENSG00000111615	KRR1	12	g.75905317G>A	p.Gln21X	nonsense
CHC197T	ENSG00000187242	KRT12	17	g.39021093C>A	p.Glu258X	nonsense
CHC429T	ENSG00000198910	L1CAM	X	g.153134061T>C	p.Asn501Asp	missense
CHC155T	ENSG00000101680	LAMA1	18	g.6948416C>A	p.Gly2899Val	missense
CHC1065T	ENSG00000115365	LANCL1	2	g.211305335T>C	p.Tyr226Cys	missense
CHC1053T	ENSG00000132434	LANCL2	7	g.55493113G>A	p.Arg392Gln	missense
CHC1053T	ENSG00000131023	LATS1	6	g.149997395C>A	splicing	intron
CHC433T	ENSG00000187173	LCE2A	1	g.152671515_152671556del	p.Cys51_Gly64del	deletion
CHC1035T	ENSG00000168806	LCMT2	15	g.43620927G>C	p.Tyr587X	nonsense
CHC1065T	ENSG00000183722	LHFP	13	g.39952632G>C	p.Tyr139X	nonsense
CHC1065T	ENSG00000113594	LIFR	5	g.38486026T>G	p.Ile798Leu	missense
CHC433T	ENSG00000174482	LINGO2	9	g.27949012A>T	p.Leu553Gln	missense
CHC301T	ENSG00000188992	LIPI	21	g.15535738A>G	splicing	intron
CHC197T	ENSG00000163431	LMOD1	1	g.201868607A>G	p.Ser512Pro	missense
CHC1065T	ENSG00000188076	SCGB1C1	11	g.193797G>C	p.Glu47Asp	missense
CHC429T	ENSG00000072071	LPHN1	19	g.14266925A>T	p.Ile1046Asn	missense
CHC320T	ENSG00000132793	LPIN3	20	g.39987430T>A	p.Leu827Gln	missense
CHC1061T	ENSG00000197324	LRP10	14	g.23345277T>C	p.Cys374Arg	missense
CHC1041T	ENSG00000172061	LRRC15	3	g.194080760T>C	p.Asn344Ser	missense

Supplementary Table 3. List of all somatic mutations identified in the exome sequencing of 24 HCC

HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic position hg19)	Amino Acid	Mutation Type
CHC1061T	ENSG00000128606	LRRC17	7	g.102574460C>T	p.Arg34Trp	missense
CHC1061T	ENSG00000131409	LRRC4B	19	g.51022137G>A	p.Ser278Leu	missense
CHC197T	ENSG00000033122	LRRC7	1	g.70504700G>T	p.Val1027Phe	missense
CHC197T	ENSG00000133640	LRRIQ1	12	g.85623375C>T	p.Leu1635Phe	missense
CHC1065T	ENSG00000170382	LRRN2	1	g.204588258T>G	p.Lys288Thr	missense
CHC1035T	ENSG00000162951	LRRTM1	2	g.80530291G>T	p.His218Gln	missense
CHC429T	ENSG00000160285	LSS	21	g.47647529C>A	p.Gly86Trp	missense
CHC121T	ENSG00000145220	LYAR	4	g.4270343C>T	splicing	intron
CHC433T	ENSG00000177239	MAN1B1	9	g.140003024C>G	p.Pro694Arg	missense
CHC1052T	ENSG00000172469	MANEA	6	g.96052781T>C	splicing	intron
CHC1061T	ENSG00000069535	MAOB	X	g.43634507C>A	p.Glu384X	nonsense
CHC205T	ENSG00000166963	MAP1A	15	g.43814680C>T	p.Arg337Trp	missense
CHC306T	ENSG00000078018	MAP2	2	g.210574925A>T	p.Lys1674X	nonsense
CHC1065T	ENSG00000139625	MAP3K12	12	g.53875769del	p.Ser814AlafsX95	deletion
CHC614T	ENSG00000107643	MAPK8	10	g.49609777G>A	p.Arg25Gln	missense
CHC301T	ENSG00000127241	MASP1	3	g.186980342T>C	p.Tyr135Cys	missense
CHC433T	ENSG00000171444	MCC	5	g.112440053C>A	splicing	intron
CHC1052T	ENSG00000076003	MCM6	2	g.136610401C>A	p.Asp571Tyr	missense
CHC155T	ENSG00000112559	MDFI	6	g.41617362C>G	p.Pro89Ala	missense
CHC1035T	ENSG00000014641	MDH1	2	g.63832498G>T	p.Val272Phe	missense
CHC155T	ENSG00000135679	MDM2	12	g.69222641T>A	p.Leu205Gln	missense
CHC433T	ENSG00000146834	MEPCE	7	g.100030692C>T	p.Arg608Cys	missense
CHC051T	ENSG00000116688	MFN2	1	g.12052699T>G	p.Ile88Ser	missense
CHC434T	ENSG00000135596	MICAL1	6	g.109771564C>T	p.Arg377His	missense
CHC1053T	ENSG00000155545	MIER3	5	g.56233410A>C	p.Leu144X	nonsense
CHC429T	ENSG00000186260	MKL2	16	g.14311048G>A	p.Asp140Asn	missense
CHC205T	ENSG00000119684	MLH3	14	g.75514768del	p.Ser531ValfsX12	deletion
CHC429T	ENSG00000099953	MMP11	22	g.24124458C>T	p.Pro374Leu	missense
CHC205T	ENSG00000087245	MMP2	16	g.55522491C>T	p.Pro290Leu	missense
CHC433T	ENSG00000137675	MMP27	11	g.102573614T>A	splicing	intron
CHC1061T	ENSG00000149968	MMP3	11	g.102709315T>C	p.Lys399Arg	missense
CHC121T	ENSG00000100985	MMP9	20	g.44639662G>T	p.Glu208X	nonsense
CHC302T	ENSG00000138722	MMRN1	4	g.90874208A>T	p.Tyr1109Phe	missense
CHC1065T	ENSG00000124217	MOCS3	20	g.49576473G>T	p.Cys365Phe	missense
CHC121T	ENSG00000116151	MORN1	1	g.2321390C>T	p.Gly41Glu	missense
CHC320T	ENSG00000130830	MPP1	X	g.154014569T>C	p.Asn196Ser	missense
CHC197T	ENSG00000082126	MPP4	2	g.202545754_202545755del	p.Tyr246ArgfsX6	deletion
CHC1035T	ENSG00000066382	MPPED2	11	g.30433059T>A	p.Asn281Tyr	missense
CHC320T	ENSG00000166902	MRPL16	11	g.59573821T>C	p.X252TrpextX2	missense
CHC433T	ENSG00000116221	MRPL37	1	g.54666230A>G	p.Tyr105Cys	missense
CHC197T	ENSG00000053372	MRTO4	1	g.19584362G>A	p.Arg126Gln	missense
CHC433T	ENSG00000166927	MS4A7	11	g.60156927T>G	p.Leu135Arg	missense
CHC433T	ENSG00000127989	MTERF	7	g.91503452T>G	p.Gln219Pro	missense
CHC1053T	ENSG00000136371	MTHFS	15	g.80181570G>A	p.Arg82Trp	missense
CHC614T	ENSG00000132613	MTSS1L	16	g.70698552T>C	p.Ser474Gly	missense
CHC433T	ENSG00000101057	MYBL2	20	g.42344613G>A	p.Trp663X	nonsense
CHC301T	ENSG00000133454	MYO18B	22	g.26168334C>G	p.Leu576Val	missense
CHC322T	ENSG00000197879	MYO1C	17	g.1383903_1383915del	p.Gln271ProfsX17	deletion
CHC302T	ENSG00000141052	MYOCD	17	g.12666879C>G	p.Pro960Arg	missense
CHC301T	ENSG00000170011	MYRIP	3	g.40231337_40231352del	p.Ser350GlyfsX4	deletion
CHC205T	ENSG00000078177	N4BP2	4	g.40122951A>G	p.Lys1074Glu	missense
CHC155T	ENSG00000164134	NAA15	4	g.140281044A>G	p.Thr469Ala	missense
CHC1061T	ENSG00000102452	NALCN	13	g.102051476A>G	p.Met1?	missense
CHC429T	ENSG00000067798	NAV3	12	g.78574716G>C	p.Lys1839Asn	missense
CHC1052T	ENSG00000151503	NCAPD3	11	g.134062741C>A	p.Asp630Tyr	missense
CHC1053T	ENSG00000146918	NCAPG2	7	g.158437057T>A	p.Arg1102Trp	missense
CHC320T	ENSG00000124160	NCOA5	20	g.44695713C>T	p.Val204Met	missense
CHC433T	ENSG00000196498	NCOR2	12	g.123470536_123470567del	indels	deletion
CHC302T	ENSG00000183091	NEB	2	g.152536496T>C	p.Tyr1028Cys	missense
CHC1035T	ENSG00000100906	NFKBIA	14	g.35871259T>C	p.Tyr305Ser	missense
CHC429T	ENSG00000169760	NLGN1	3	g.173322644G>A	p.Ala86Thr	missense
CHC1061T	ENSG00000087095	NLK	17	g.26488207G>A	p.Met222Ile	missense
CHC433T	ENSG00000167984	NLRC3	16	g.3614016G>A	p.Leu308Phe	missense
CHC121T	ENSG00000182261	NLRP10	11	g.7981542del	p.Cys540ValfsX2	deletion
CHC433T	ENSG00000142405	NLRP12	19	g.54312893C>A	p.Gly674Trp	missense
CHC320T	ENSG00000167634	NLRP7	19	g.55447696C>T	p.Glu745Lys	missense
CHC1052T	ENSG00000132911	NMUR2	5	g.151784262G>T	p.Thr138Asn	missense
CHC433T	ENSG00000112992	NNT	5	g.43609382A>C	p.Lys29Gln	missense
CHC433T	ENSG00000164867	NOS3	7	g.150695503A>T	p.His214Leu	missense
CHC1053T	ENSG00000134250	NOTCH2	1	g.120539757T>C	p.Tyr205Cys	missense
CHC1052T	ENSG00000074181	NOTCH3	19	g.15302568G>T	p.Pro264Thr	missense
CHC205T	ENSG00000255346	NOX5	15	g.69318912C>A	p.Thr32Asn	missense
CHC1055T	ENSG00000151322	NPAS3	14	g.33684497A>T	p.Ile84Phe	missense
CHC1035T	ENSG00000174576	NPAS4	11	g.66192601C>T	p.Ser747Phe	missense
CHC1053T	ENSG00000185551	NR2F2	15	g.96880694T>G	p.Leu363Arg	missense
CHC306T	ENSG00000151623	NR3C2	4	g.149075935A>C	p.Ile711Ser	missense
CHC205T	ENSG00000073969	NSF	17	g.44788380_44788384del	p.Ile508MetfsX3	deletion
CHC1053T	ENSG00000108256	NUFIP2	17	g.27613156T>C	p.Tyr619Cys	missense
CHC307T	ENSG00000126883	NUP214	9	g.134003761T>A	p.Ile95Asn	missense
CHC307T	ENSG00000110713	NUP98	11	g.3756520C>A	p.Gln481His	missense
CHC1035T	ENSG00000089127	OAS1	12	g.113348912G>A	p.Glu176Lys	missense
CHC433T	ENSG00000147162	OGT	X	g.70756182A>G	p.Ile64Met	missense
CHC205T	ENSG00000138315	OIT3	10	g.74690322A>C	p.Gln465Pro	missense
CHC1035T	ENSG00000162600	OMA1	1	g.59002184C>G	splicing	intron
CHC320T	ENSG00000122375	OPN4	10	g.88419072G>T	p.Gly227Val	missense
CHC121T	ENSG00000170782	OR10A4	11	g.6897977G>T	p.Leu33Phe	missense
CHC434T	ENSG00000206474	OR10C1	6	g.29408024C>T	p.Pro78Ser	missense
CHC1052T	ENSG00000177174	OR14C36	1	g.248512710A>G	p.Ile212Val	missense
CHC429T	ENSG00000204700	OR2J2	6	g.29142247T>C	p.Tyr279His	missense
CHC1061T	ENSG00000176200	OR4D11	11	g.59271338G>A	p.Cys97Tyr	missense
CHC1052T	ENSG00000197428	OR51D1	11	g.4661451G>A	p.Arg144His	missense
CHC1041T	ENSG00000167360	OR51Q1	11	g.5444052A>G	p.Ile208Val	missense
CHC121T	ENSG00000180974	OR52E4	11	g.5905850A>T	p.Thr110Ser	missense
CHC614T	ENSG00000174942	OR5R1	11	g.56185444G>A	p.Arg89Cys	missense
CHC1035T	ENSG00000205330	OR6C1	12	g.55714811T>C	p.Val143Ala	missense
CHC121T	ENSG00000150261	OR8K1	11	g.56113963T>A	p.Leu150Gln	missense

Supplementary Table 3. List of all somatic mutations identified in the exome sequencing of 24 HCC

HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic position hg19)	Amino Acid	Mutation Type
CHC1065T	ENSG00000181689	OR8K3	11	g.56086321A>G	p.Asp180Gly	missense
CHC302T	ENSG00000172377	OR9I1	11	g.57886072del	p.Ile282ThrfsX4	deletion
CHC429T	ENSG00000006025	OSBPL7	17	g.45890631C>T	splicing	intron
CHC197T	ENSG00000155719	OTOA	16	g.21726317C>A	p.Phe444Leu	missense
CHC205T	ENSG00000187848	P2RX2	12	g.133198125T>C	p.Val354Ala	missense
CHC306T	ENSG00000090621	PABPC4	1	g.40031047T>C	p.Met326Val	missense
CHC1052T	ENSG00000142619	PADI3	1	g.17596805G>A	p.Gly244Arg	missense
CHC429T	ENSG00000007168	PAFAH1B1	17	g.2570374G>A	p.Trp94X	nonsense
CHC429T	ENSG00000129116	PALLD	4	g.169432738C>T	p.Pro28Leu	missense
CHC1053T	ENSG00000135473	PAN2	12	g.56720433A>C	p.Asp410Glu	missense
CHC434T	ENSG00000183760	PAPL	19	g.39590987G>T	p.Arg209Val	missense
CHC429T	ENSG00000175193	PARL	3	g.183580547C>A	p.Val169Leu	missense
CHC429T	ENSG00000138496	PARP9	3	g.122259427C>T	p.Gly588Arg	missense
CHC1061T	ENSG00000125618	PAX8	2	g.113999185A>C	p.Phe240Leu	missense
CHC433T	ENSG00000108187	PBLD	10	g.70048359C>A	p.Gly191Val	missense
CHC121T	ENSG00000163939	PBRM1	3	g.52702661_52702662del	indels	deletion
CHC1035T	ENSG00000118946	PCDH17	13	g.58208192C>A	p.Asn504Lys	missense
CHC1035T	ENSG00000165194	PCDH19	X	g.99662659C>A	p.Glu313X	nonsense
CHC433T	ENSG00000204970	PCDHA1	5	g.140389516C>A	p.Asp949Glu	missense
CHC205T	ENSG00000124253	PCK1	20	g.56137204_56137205del	p.Thr102SerfsX21	deletion
CHC1052T	ENSG00000160299	PCNT	21	g.47783782G>T	p.Asp848Tyr	missense
CHC320T	ENSG00000100731	PCNX	14	g.71445081G>A	p.Arg676Gln	missense
CHC1055T	ENSG00000169174	PCSK9	1	g.55524200G>C	p.Trp461Cys	missense
CHC1065T	ENSG00000004799	PDK4	7	g.95216389T>C	p.Tyr343Cys	missense
CHC429T	ENSG00000162493	PDPN	1	g.13933683C>T	p.Pro104Leu	missense
CHC197T	ENSG00000181195	PENK	8	g.57353988C>A	p.Arg216Ile	missense
CHC307T	ENSG00000109272	PF4V1	4	g.74719596C>G	p.Ala66Gly	missense
CHC433T	ENSG00000170525	PFKFB3	10	g.6255709A>C	p.Lys67Thr	missense
CHC1052T	ENSG00000154330	PGM5	9	g.71002385T>C	p.Ile193Thr	missense
CHC121T	ENSG00000087495	PHACTR3	20	g.58349374C>T	p.Arg335Trp	missense
CHC1065T	ENSG00000111752	PHC1	12	g.9086508_9086520del	p.Glu648SerfsX15	deletion
CHC433T	ENSG00000134686	PHC2	1	g.33794500T>C	p.Asp798Gly	missense
CHC614T	ENSG00000067177	PHKA1	X	g.71825155C>A	p.Met927Ile	missense
CHC1035T	ENSG00000019144	PHLDB1	11	g.118498522G>C	p.Arg328Pro	missense
CHC433T	ENSG00000116793	PHTF1	1	g.114240991T>C	p.Arg721Gly	missense
CHC1052T	ENSG00000165443	PHYHIPL	10	g.61005035A>G	p.Tyr272Cys	missense
CHC433T	ENSG00000141720	PIP4K2B	17	g.36925987T>A	p.Tyr403Phe	missense
CHC429T	ENSG00000154217	PITPNC1	17	g.65688843C>T	p.Leu280Phe	missense
CHC258T	ENSG00000110697	PITPNM1	11	g.67265000_67265011del	p.Pro641_Ser644del	deletion
CHC433T	ENSG00000107959	PITRM1	10	g.3202086C>A	p.Asp321Tyr	missense
CHC051T	ENSG00000118762	PKD2	4	g.88983119A>T	p.Gln694Leu	missense
CHC155T	ENSG00000105223	PLD3	19	g.40877707A>G	p.Tyr269Cys	missense
CHC155T	ENSG00000076356	PLXNA2	1	g.208213051C>T	p.Gly1472Asp	missense
CHC258T	ENSG00000221866	PLXNA4	7	g.131859679G>C	p.Ala1292Gly	missense
CHC429T	ENSG00000196576	PLXNB2	22	g.50719053 T>A	p.Lys1347Met	missense
CHC121T	ENSG00000175535	PNLIP	10	g.118307955A>G	p.Ile95Met	missense
CHC306T	ENSG00000164087	POC1A	3	g.52179882C>A	p.Arg220Leu	missense
CHC429T	ENSG00000124429	POF1B	X	g.84622772C>T	splicing	intron
CHC429T	ENSG00000186866	POFUT2	21	g.46705622G>T	p.Pro118His	missense
CHC051T	ENSG00000143442	POGZ	1	g.151396685_151396687del	p.Ala421del	deletion
CHC433T	ENSG00000122678	POLM	7	g.44116189C>A	p.Asp252Tyr	missense
CHC433T	ENSG00000130997	POLN	4	g.2214787G>T	p.Ser67X	nonsense
CHC429T	ENSG00000186141	POLR3C	1	g.145609267del	p.Ile24LeufsX5	deletion
CHC322T	ENSG00000166351	POTED	21	g.14987742T>C	p.Cys221Arg	missense
CHC320T	ENSG00000143190	POU2F1	1	g.167358829_167358834del	p.Pro275_Thr276del	deletion
CHC306T	ENSG00000130810	PPAN	19	g.10221193C>G	p.Leu312Val	missense
CHC306T	ENSG00000243207	PPAN-P2RY11	19	g.10221193C>G	p.Leu312Val	missense
CHC302T	ENSG00000112033	PPARD	6	g.35392508G>C	p.Asp344His	missense
CHC433T	ENSG00000155846	PPARGC1B	5	g.149216051A>T	p.Gln678Leu	missense
CHC322T	ENSG00000177380	PPFIA3	19	g.49652918_49652961del	p.Gly1160ArgfsX27	deletion
CHC302T	ENSG00000058272	PPP1R12A	12	g.80266606C>A	p.Gly117Val	missense
CHC1052T	ENSG00000154415	PPP1R3A	7	g.113520138C>G	p.Asp337His	missense
CHC1035T	ENSG00000158528	PPP1R9A	7	g.94539678G>T	p.Ala85Ser	missense
CHC155T	ENSG00000249553	PPP2R2B	5	g.146077602_146077603insA	p.Ile95TyrfsX3	insertion
CHC1061T	ENSG00000149923	PPP4C	16	g.30094740T>A	p.Leu110Gln	missense
CHC1041T	ENSG00000011485	PPP5C	19	g.46890450del	p.Phe335LeufsX15	deletion
CHC433T	ENSG00000110075	PPP6R3	11	g.68337232A>G	p.Tyr382Cys	missense
CHC301T	ENSG00000108946	PRKAR1A	17	g.66526077_66526095del	p.Gln304LysfsX21	deletion
CHC155T	ENSG00000114302	PRKAR2A	3	g.48789654G>A	p.Pro346Ser	missense
CHC614T	ENSG00000166501	PRKCB	16	g.24135258G>A	p.Asp341Asn	missense
CHC1053T	ENSG00000007062	PROM1	4	g.16025950G>T	p.Thr221Asn	missense
CHC1035T	ENSG00000166450	PRTG	15	g.55967863T>C	p.Tyr467Cys	missense
CHC1035T	ENSG00000059915	PSD	10	g.104174840C>A	p.Asp302Tyr	missense
CHC433T	ENSG00000146005	PSD2	5	g.139217341C>A	p.Asp599Glu	missense
CHC433T	ENSG00000156011	PSD3	8	g.18729634G>C	p.Ser247Cys	missense
CHC306T	ENSG00000152104	PTPN14	1	g.214557049_214557051del	p.Glu716del	deletion
CHC205T	ENSG00000070159	PTPN3	9	g.112143978A>T	p.Ile873Asn	missense
CHC433T	ENSG00000144724	PTPRG	3	g.62118279A>T	p.Ser207Cys	missense
CHC433T	ENSG00000155093	PTPRN2	7	g.157475495A>T	p.His641Gln	missense
CHC1035T	ENSG00000196090	PTPRT	20	g.41306605G>C	p.Pro352Ala	missense
CHC614T	ENSG00000176894	PXMP2	12	g.133272505A>G	p.Tyr91Cys	missense
CHC429T	ENSG00000109113	RAB34	17	g.27042288C>T	p.Trp203X	nonsense
CHC197T	ENSG00000111540	RAB5B	12	g.56384584A>G	p.Tyr145Cys	missense
CHC1061T	ENSG00000214842	RAD51AP2	2	g.17698119C>A	p.Gly522X	nonsense
CHC433T	ENSG00000002016	RAD52	12	g.1023168G>T	p.Gln363Lys	missense
CHC1035T	ENSG00000164080	RAD54L2	3	g.51691608del	p.Pro1080LeufsX147	deletion
CHC253T	ENSG00000188559	RALGAPA2	20	g.20507002_20507014del	indels	deletion
CHC434T	ENSG00000075391	RASAL2	1	g.178412048dup	p.Asp390GlyfsX4	duplication
CHC433T	ENSG00000165105	RASEF	9	g.85613331A>T	p.Val585Glu	missense
CHC155T	ENSG00000198774	RASSF9	12	g.86199412A>T	p.Trp126Arg	missense
CHC1053T	ENSG00000162775	RBM15	1	g.110882914G>A	p.Gly296Asp	missense
CHC121T	ENSG00000091009	RBM27	5	g.145609449G>A	p.Asp189Asn	missense
CHC306T	ENSG00000188739	RBM34	1	g.235301490C>A	splicing	intron
CHC301T	ENSG00000056586	RC3H2	9	g.125621361T>C	p.Thr624Ala	missense
CHC433T	ENSG00000167771	RCOR2	11	g.63679989_63679999del	p.Tyr347LeufsX39	deletion
CHC302T	ENSG00000084093	REST	4	g.57798059A>T	p.His1012Leu	missense

Supplementary Table 3. List of all somatic mutations identified in the exome sequencing of 24 HCC

HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic position hg19)	Amino Acid	Mutation Type
CHC121T	ENSG00000108370	RGS9	17	g.63221138C>T	p.Pro476Ser	missense
CHC433T	ENSG00000153561	RMND5A	2	g.86968076C>T	p.Leu57Phe	missense
CHC433T	ENSG00000180537	RNF182	6	g.13977482T>A	p.Cys44X	nonsense
CHC1052T	ENSG00000152193	RNF219	13	g.79190319C>A	p.Ser526Ile	missense
CHC1061T	ENSG00000137075	RNF38	9	g.36356380G>A	p.Pro277Ser	missense
CHC1052T	ENSG00000069667	RORA	15	g.60797803del	p.Lys315AsnfsX10	deletion
CHC258T	ENSG00000136643	RPS6KC1	1	g.213303065del	p.Arg223LeufsX8	deletion
CHC1061T	ENSG00000198208	RPS6KL1	14	g.75373288G>C	p.His530Gln	missense
CHC1055T	ENSG00000189306	RRP7A	22	g.42910686_42910687insT	indels	insertion
CHC306T	ENSG00000114767	RRP9	3	g.51968546C>A	p.Arg401Leu	missense
CHC051T	ENSG00000132026	RTBDN	19	g.12939741T>C	p.Thr98Ala	missense
CHC320T	ENSG00000160753	RUSC1	1	g.155296579G>T	p.Gln690His	missense
CHC155T	ENSG00000163785	RYK	3	g.133921646 A>C	p.Val235Gly	missense
CHC155T	ENSG00000232040	SCAND3	6	g.28540650G>A	p.Leu1006Phe	missense
CHC433T	ENSG00000136531	SCN2A	2	g.166223828A>T	p.Asn1208Tyr	missense
CHC121T	ENSG00000153253	SCN3A	2	g.165947448C>T	p.Gly1739Arg	missense
CHC205T	ENSG00000111319	SCNN1A	12	g.6465044T>C	p.Asn352Ser	missense
CHC1053T	ENSG00000168447	SCNN1B	16	g.23359963C>G	p.Gln15Glu	missense
CHC121T	ENSG00000175356	SCUBE2	11	g.9043424T>C	p.Lys921Arg	missense
CHC205T	ENSG00000165525	SDCCAG1	14	g.50295058 T>C	p.Lys480Arg	missense
CHC1053T	ENSG00000073578	SDHA	5	g.256525_256533del	p.Ser663X	deletion
CHC320T	ENSG00000166562	SEC11C	18	g.56816776_56816783del	p.Val41CysfsX15	deletion
CHC1052T	ENSG00000101310	SEC23B	20	g.18513307G>T	splicing	intron
CHC1041T	ENSG00000187742	SECISBP2	9	g.91972406A>G	p.Lys732Glu	missense
CHC121T	ENSG00000170381	SEMA3E	7	g.83035340C>A	p.Lys283Asn	missense
CHC197T	ENSG00000111897	SERINC1	6	g.122775025G>T	p.Ala160Asp	missense
CHC121T	ENSG00000021355	SERPINB1	6	g.2840750G>T	p.Pro24Gln	missense
CHC429T	ENSG00000183431	SF3A3	1	g.38449882G>T	p.His143Asn	missense
CHC1035T	ENSG00000087365	SF3B2	11	g.65835682G>A	p.Glu832Lys	missense
CHC322T	ENSG00000189091	SF3B3	16	g.70582331G>T	p.Arg463Leu	missense
CHC205T	ENSG00000164023	SGMS2	4	g.108824469T>A	p.His218Gln	missense
CHC434T	ENSG00000148341	SH3GLB2	9	g.131783430C>T	p.Glu92Lys	missense
CHC1041T	ENSG00000172985	SH3RF3	2	g.110015263 C>T	p.Thr388Met	missense
CHC302T	ENSG00000161681	SHANK1	19	g.51189537G>T	p.Ala845Glu	missense
CHC051T	ENSG00000182199	SHMT2	12	g.57626053A>G	p.Glu191Gly	missense
CHC1053T	ENSG00000168779	SHOX2	3	g.157817738C>A	splicing	intron
CHC1055T	ENSG00000105366	SIGLEC8	19	g.51955889T>C	splicing	intron
CHC301T	ENSG00000129450	SIGLEC9	19	g.51628458C>A	p.Thr76Lys	missense
CHC1035T	ENSG00000160584	SIK3	11	g.116744237T>C	p.Lys508Arg	missense
CHC051T	ENSG00000197555	SIPA1L1	14	g.72139195G>T	p.Gly987Val	missense
CHC433T	ENSG00000100625	SIX4	14	g.61180349C>A	p.Val708Phe	missense
CHC614T	ENSG00000182628	SKA2	17	g.57196831T>C	p.Glu49Gly	missense
CHC301T	ENSG00000174327	SLC16A13	17	g.6941603_6941614del	p.Gln160_Leu163del	deletion
CHC433T	ENSG00000118596	SLC16A7	12	g.60168617T>A	p.Leu181Met	missense
CHC307T	ENSG00000105143	SLC1A6	19	g.15065076G>A	p.Thr412Ile	missense
CHC1065T	ENSG00000144136	SLC20A1	2	g.113420482 G>T	p.Lys640Asn	missense
CHC320T	ENSG00000170482	SLC23A1	5	g.138713965_138713966insC	p.Leu423AlafsX7	insertion
CHC1053T	ENSG00000004864	SLC25A13	7	g.95761164_95761165insAT	p.Pro496PhefsX14	insertion
CHC1035T	ENSG00000155287	SLC25A28	10	g.101371024C>T	p.Arg226His	missense
CHC433T	ENSG00000197496	SLC2A10	20	g.45358052G>A	p.Gly491Asp	missense
CHC302T	ENSG00000170385	SLC30A1	1	g.211749293_211749294del	p.Val322CysfsX15	deletion
CHC205T	ENSG00000164756	SLC30A8	8	g.118165285C>A	p.Ser125X	nonsense
CHC433T	ENSG00000138459	SLC35A5	3	g.112299965dup	p.Leu334PhefsX19	duplication
CHC1035T	ENSG00000160190	SLC37A1	21	g.43994977G>T	p.Trp491Cys	missense
CHC1061T	ENSG00000139974	SLC38A6	14	g.61449305G>A	p.Gly62Asp	missense
CHC320T	ENSG00000141424	SLC39A6	18	g.33703604T>C	p.Ile332Val	missense
CHC1053T	ENSG00000149150	SLC43A1	11	g.57268779G>A	p.Gln60X	nonsense
CHC1052T	ENSG00000167703	SLC43A2	17	g.1479025C>T	p.Gly528Asp	missense
CHC155T	ENSG00000164889	SLC4A2	7	g.150772379G>A	p.Gly1029Ser	missense
CHC301T	ENSG00000117834	SLC5A9	1	g.48698175G>A	splicing	intron
CHC301T	ENSG00000151012	SLC7A11	4	g.139106331C>T	p.Ala287Thr	missense
CHC614T	ENSG00000183023	SLC8A1	2	g.40366760A>G	p.Tyr776His	missense
CHC1041T	ENSG00000090020	SLC9A1	1	g.27434217T>G	p.Thr402Pro	missense
CHC205T	ENSG00000066230	SLC9A3	5	g.492032_492033insC	p.Ile123HisfsX79	insertion
CHC121T	ENSG00000166750	SLFN5	17	g.33586053C>A	p.Ser115Tyr	missense
CHC1052T	ENSG00000184347	SLIT3	5	g.168096806C>T	p.Gly1440Ser	missense
CHC433T	ENSG00000178235	SLITRK1	13	g.84454111A>T	p.Val511Glu	missense
CHC302T	ENSG00000102038	SMARCA1	X	g.128649922C>T	p.Glu160Lys	missense
CHC1041T	ENSG00000080503	SMARCA2	9	g.2039655del	p.Arg183GlufsX5	deletion
CHC1053T	ENSG00000163104	SMARCAD1	4	g.95191952A>G	p.Ile519Val	missense
CHC301T	ENSG00000099956	SMARCB1	22	g.24145583G>T	p.Arg201Leu	missense
CHC1055T	ENSG00000100796	SMEK1	14	g.91937183A>G	p.Leu540Ser	missense
CHC614T	ENSG00000138041	SMEK2	2	g.55816053T>G	p.Thr321Pro	missense
CHC320T	ENSG00000143740	SNAP47	1	g.227946961G>A	p.Val300Met	missense
CHC121T	ENSG00000163788	SNRK	3	g.43344873C>G	p.Leu60Val	missense
CHC433T	ENSG00000249481	SPATS1	6	g.44344131G>T	p.Leu265Phe	missense
CHC197T	ENSG00000065526	SPEN	1	g.16259206dup	p.Pro2158AlafsX26	duplication
CHC1035T	ENSG00000152377	SPOCK1	5	g.136314446del	p.Pro406GlnfsX8	deletion
CHC306T	ENSG00000121067	SPOP	17	g.47696415G>C	p.Phe136Leu	missense
CHC1061T	ENSG00000169474	SPRR1A	1	g.152957738del	p.Pro12HisfsX10	deletion
CHC1055T	ENSG00000161011	SQSTM1	5	g.179260586G>A	splicing	intron
CHC301T	ENSG00000080603	SRCAP	16	g.30744772T>A	splicing	intron
CHC205T	ENSG00000174780	SRP72	4	g.57337912A>G	p.Tyr86Cys	missense
CHC1052T	ENSG00000116350	SRSF4	1	g.29481412C>A	p.Arg125Leu	missense
CHC320T	ENSG00000144057	ST6GAL2	2	g.107459971del	p.Glu155SerfsX19	deletion
CHC1041T	ENSG00000004866	ST7	7	g.116830931G>A	p.Glu399Lys	missense
CHC1055T	ENSG00000148488	ST8SIA6	10	g.17365104T>C	p.Thr230Ala	missense
CHC121T	ENSG00000138134	STAMBPL1	10	g.90665347A>T	p.Arg60Trp	missense
CHC121T	ENSG00000170581	STAT2	12	g.56745235C>A	splicing	intron
CHC121T	ENSG00000124214	STAU1	20	g.47734596A>C	p.Ser409Arg	missense
CHC205T	ENSG00000040341	STAU2	8	g.74495040C>A	p.Gly396Val	missense
CHC433T	ENSG00000125834	STK35	20	g.2097579T>G	p.Val387Gly	missense
CHC429T	ENSG00000101109	STK4	20	g.43623818G>A	p.Ala205Thr	missense
CHC1052T	ENSG00000068781	STON1-GTF2A1L	2	g.48872191C>G	p.Ala812Gly	missense
CHC434T	ENSG00000165730	STOX1	10	g.70644659G>T	p.Leu369Phe	missense
CHC121T	ENSG00000125695	STRADA	17	g.61784056C>G	p.Gly266Ala	missense

Supplementary Table 3. List of all somatic mutations identified in the exome sequencing of 24 HCC

HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic position hg19)	Amino Acid	Mutation Type
CHC051T	ENSG00000079950	STX7	6	g.132785152A>G	p.Ser225Pro	missense
CHC614T	ENSG00000060140	STYK1	12	g.10782124C>T	p.Asp201Asn	missense
CHC197T	ENSG00000135316	SYNCRIP	6	g.86346836T>G	p.Asp172Ala	missense
CHC051T	ENSG00000146383	TAAR6	6	g.132891657C>A	p.Pro66Gln	missense
CHC1035T	ENSG00000237110	TAAR9	6	g.132860372A>T	p.Tyr315Phe	missense
CHC1053T	ENSG00000122728	TAF1L	9	g.32631796T>A	p.Lys1261Met	missense
CHC433T	ENSG00000106290	TAF6	7	g.99709773C>G	p.Glu263Asp	missense
CHC614T	ENSG00000177565	TBL1XR1	3	g.176765120C>T	p.Gly278Arg	missense
CHC121T	ENSG00000121075	TBX4	17	g.59543205A>T	p.Lys103X	nonsense
CHC433T	ENSG00000165929	TC2N	14	g.92264242T>A	p.Arg248X	nonsense
CHC155T	ENSG00000148737	TCF7L2	10	g.114912162_114912163insT	p.Met411IlefsX12	insertion
CHC301T	ENSG00000176148	TCP11L1	11	g.33087377C>T	p.Thr325Ile	missense
CHC306T	ENSG00000111077	TENC1	12	g.53453654_53453661del	p.His754CysfsX5	deletion
CHC205T	ENSG00000070759	TESK2	1	g.45811097_45811106del	p.Lys375ValfsX3	deletion
CHC302T	ENSG00000138336	TET1	10	g.70333249A>G	p.His385Arg	missense
CHC1061T	ENSG00000091513	TF	3	g.133476673G>T	p.Asp311Tyr	missense
CHC1035T	ENSG00000042832	TG	8	g.133900392G>T	p.Gln780His	missense
CHC1061T	ENSG00000198959	TGM2	20	g.36775212C>A	p.Gly256Cys	missense
CHC434T	ENSG00000115970	THADA	2	g.43779021G>A	p.Leu952Phe	missense
CHC433T	ENSG00000172673	THEMIS	6	g.128134048C>A	p.Asp580Tyr	missense
CHC1055T	ENSG00000151923	TIAL1	10	g.121337183A>G	p.Tyr225His	missense
CHC433T	ENSG00000104980	TIMM44	19	g.7999948A>G	splicing	intron
CHC434T	ENSG00000104067	TJP1	15	g.29997948G>A	p.Pro1618Ser	missense
CHC301T	ENSG00000146872	TLK2	17	g.60679446A>C	p.Lys588Asn	missense
CHC205T	ENSG00000103534	TMC5	16	g.19501748C>T	p.Arg869X	nonsense
CHC197T	ENSG00000118600	TMEM5	12	g.64196101G>T	p.Gly220Val	missense
CHC197T	ENSG00000126106	TMEM53	1	g.45120629G>A	p.Pro146Ser	missense
CHC1065T	ENSG00000164953	TMEM67	8	g.94792905G>T	p.Ala267Ser	missense
CHC1041T	ENSG00000116857	TMEM9	1	g.201104822G>T	p.Thr174Lys	missense
CHC433T	ENSG00000198092	TMPRSS11F	4	g.68934471A>T	p.Val207Asp	missense
CHC434T	ENSG00000041982	TNC	9	g.117836008G>A	p.Gln1030X	nonsense
CHC1061T	ENSG00000120889	TNFRSF10B	8	g.22880326C>A	p.Gly394Val	missense
CHC121T	ENSG00000240505	TNFRSF13B	17	g.16843685G>A	p.Gln196X	nonsense
CHC433T	ENSG00000127863	TNFRSF19	13	g.24234562A>C	p.Arg223Ser	missense
CHC121T	ENSG00000118194	TNNT2	1	g.201328756C>G	p.Gln279His	missense
CHC1053T	ENSG00000079308	TNS1	2	g.218677154G>C	p.Leu1553Val	missense
CHC197T	ENSG00000136205	TNS3	7	g.47342994A>T	p.Leu1004Gln	missense
CHC301T	ENSG00000168477	TNXB	6	g.32029976C>A	p.Gly2376Cys	missense
CHC197T	ENSG00000141232	TOB1	17	g.48941255_48941316del	p.Arg22AlafsX5	deletion
CHC1035T	ENSG00000115705	TPO	2	g.1440130G>T	p.Arg152Ser	missense
CHC253T	ENSG00000116176	TPSG1	16	g.1272273G>A	p.Arg194Trp	missense
CHC121T	ENSG00000170638	TRABD	22	g.50635960C>G	p.Ser205Cys	missense
CHC197T	ENSG00000131323	TRAF3	14	g.103371846_103371858del	p.Arg479MetfsX12	deletion
CHC433T	ENSG00000183763	TRAIP	3	g.49879373C>T	splicing	intron
CHC301T	ENSG00000167632	TRAPPC9	8	g.141460993C>A	p.Glu258Asp	missense
CHC121T	ENSG00000186439	TRDN	6	g.123714817C>A	p.Gly353X	nonsense
CHC429T	ENSG00000204613	TRIM10	6	g.30126187C>A	p.Glu249X	nonsense
CHC429T	ENSG00000168930	TRIM49	11	g.89536959C>A	p.Glu138Asp	missense
CHC433T	ENSG00000125733	TRIP10	19	g.6744824T>C	p.Leu268Pro	missense
CHC429T	ENSG00000083067	TRPM3	9	g.73233817C>T	p.Gly763Asp	missense
CHC1055T	ENSG00000070985	TRPM5	11	g.2441602C>T	p.Gly167Ser	missense
CHC434T	ENSG00000144481	TRPM8	2	g.234847747G>A	p.Ala152Thr	missense
CHC1065T	ENSG00000126467	TSKS	19	g.50251699C>A	p.Ala143Ser	missense
CHC433T	ENSG00000113312	TTC1	5	g.159476614A>G	p.Tyr212Cys	missense
CHC1055T	ENSG00000171853	TTC15	2	g.3428301G>A	p.Trp428X	nonsense
CHC320T	ENSG00000198677	TTC37	5	g.94852850C>G	p.Arg764Thr	missense
CHC307T	ENSG00000101407	TTI1	20	g.36642037T>G	p.Lys61Thr	missense
CHC433T	ENSG00000155657	TTN	2	g.179623870T>A	p.Lys3382X	nonsense
CHC433T	ENSG00000251297	TUBB4Q	4	g.190903858C>A	p.Glu375X	nonsense
CHC1035T	ENSG00000086288	TXNDC3	7	g.37904023del	p.Ile177LeufsX8	deletion
CHC1053T	ENSG00000156521	TYSND1	10	g.71899684A>C	p.Leu566Arg	missense
CHC1055T	ENSG00000033178	UBA6	4	g.68562417_68562443del	indels	deletion
CHC301T	ENSG00000130560	UBAC1	9	g.138845556_138845557insC	p.Lys102GlnfsX4	insertion
CHC155T	ENSG00000177889	UBE2N	12	g.93804509C>A	splicing	intron
CHC121T	ENSG00000110344	UBE4A	11	g.118267042C>A	p.Pro1037Thr	missense
CHC433T	ENSG00000127481	UBR4	1	g.19468160T>G	p.His2764Pro	missense
CHC1052T	ENSG00000198722	UNC13B	9	g.35378318A>T	p.Lys615X	nonsense
CHC1041T	ENSG00000135093	USP30	12	g.109511319_109511344del	p.Cys234X	deletion
CHC1052T	ENSG00000170832	USP32	17	g.58282831T>C	p.Ile1076Val	missense
CHC121T	ENSG00000170242	USP47	11	g.11971500A>T	p.Glu1070Val	missense
CHC1053T	ENSG00000170236	USP50	15	g.50793033del	p.Asn313ThrfsX69	deletion
CHC429T	ENSG00000156697	UTP14A	X	g.129054452A>C	p.Lys258Gln	missense
CHC433T	ENSG00000026025	VIM	10	g.17277300C>G	p.Arg381Gly	missense
CHC1055T	ENSG00000223501	VPS52	6	g.33219393G>A	p.Arg643Cys	missense
CHC1061T	ENSG00000120688	WBP4	13	g.41639199del	p.Arg43GlyfsX31	deletion
CHC1052T	ENSG00000138442	WDR12	2	g.203757417C>G	p.Asp222His	missense
CHC433T	ENSG00000065183	WDR3	1	g.118492616A>T	splicing	intron
CHC1065T	ENSG00000158023	WDR66	12	g.122395042T>C	p.Val533Ala	missense
CHC253T	ENSG00000133316	WDR74	11	g.62606991C>G	p.Gly18Arg	missense
CHC155T	ENSG00000140527	WDR93	15	g.90260173T>C	p.Leu263Ser	missense
CHC121T	ENSG00000075035	WSCD2	12	g.108618534del	p.Gly235AlafsX15	deletion
CHC429T	ENSG00000206579	XKR4	8	g.56436337G>A	p.Gly502Ser	missense
CHC197T	ENSG00000221947	XKR9	8	g.71593349T>C	p.Val19Ala	missense
CHC253T	ENSG00000196419	XRCC6	22	g.42052974_42052993del	p.Ala454GlnfsX7	deletion
CHC1061T	ENSG00000100811	YY1	14	g.100743917A>G	p.Lys409Glu	missense
CHC433T	ENSG00000163374	YY1AP1	1	g.155646500G>A	p.His193Tyr	missense
CHC1052T	ENSG00000169064	ZBBX	3	g.166958663G>A	p.Ser774Phe	missense
CHC320T	ENSG00000185670	ZBTB3	11	g.62519564A>T	p.X575LysextX6	missense
CHC307T	ENSG00000166860	ZBTB39	12	g.57397116_57397122del	p.Met527SerfsX124	deletion
CHC433T	ENSG00000204859	ZBTB48	1	g.6649028C>T	p.Pro608Leu	missense
CHC322T	ENSG00000083223	ZCCHC6	9	g.88924865T>C	p.Tyr1149Cys	missense
CHC320T	ENSG00000102383	ZDHHC15	X	g.74698796G>T	p.Ala63Asp	missense
CHC197T	ENSG00000186908	ZDHHC17	12	g.77220773G>T	p.Trp328Leu	missense
CHC1035T	ENSG00000091656	ZFHX4	8	g.77620035A>T	p.Asn949Tyr	missense
CHC433T	ENSG00000062370	ZFP112	19	g.44831839T>A	p.Glu830Val	missense
CHC155T	ENSG00000204644	ZFP57	6	g.29640818G>T	p.Thr357Asn	missense

Supplementary Table 3. List of all somatic mutations identified in the exome sequencing of 24 HCC

HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic position hg19)	Amino Acid	Mutation Type
CHC155T	ENSG00000169946	ZFPM2	8	g.106814470G>T	p.Arg720Ser	missense
CHC051T	ENSG00000005889	ZFX	X	g.24229375T>C	p.Ile767Thr	missense
CHC205T	ENSG00000165156	ZHX1	8	g.124265860A>T	p.Ile776Lys	missense
CHC302T	ENSG00000043355	ZIC2	13	g.100635295T>G	p.Val326Gly	missense
CHC1052T	ENSG00000152926	ZNF117	7	g.64439872T>A	p.Asn26Ile	missense
CHC1055T	ENSG00000176293	ZNF135	19	g.58573055C>G	p.Phe59Leu	missense
CHC155T	ENSG00000163848	ZNF148	3	g.124951325T>A	p.Ser749Cys	missense
CHC433T	ENSG00000160321	ZNF208	19	g.22156815A>G	p.Tyr341His	missense
CHC301T	ENSG00000167840	ZNF232	17	g.5013123C>A	p.Glu22X	nonsense
CHC302T	ENSG00000213096	ZNF254	19	g.24288792del	p.Trp27CysfsX15	deletion
CHC306T	ENSG00000090612	ZNF268	12	g.133768187A>G	p.Asn116Ser	missense
CHC205T	ENSG00000182986	ZNF320	19	g.53383988G>T	p.Thr464Asn	missense
CHC1061T	ENSG00000189180	ZNF33A	10	g.38344510G>T	p.Gln486His	missense
CHC322T	ENSG00000169981	ZNF35	3	g.44700400G>C	p.Cys182Ser	missense
CHC1035T	ENSG00000178338	ZNF354B	5	g.178310772G>C	p.Cys440Ser	missense
CHC1053T	ENSG00000198521	ZNF43	19	g.21992119 A>T	p.Asn240Lys	missense
CHC320T	ENSG00000256087	ZNF432	19	g.52537268T>C	p.Tyr555Cys	missense
CHC301T	ENSG00000140987	ZNF434	16	g.3433115C>A	p.Gly399X	nonsense
CHC306T	ENSG00000196263	ZNF471	19	g.57029880T>A	p.Ser64Thr	missense
CHC306T	ENSG00000142528	ZNF473	19	g.50550026C>T	p.His776Tyr	missense
CHC197T	ENSG00000197037	ZNF498	7	g.99217399A>T	p.Gln57Leu	missense
CHC1052T	ENSG00000198633	ZNF534	19	g.52941267C>T	p.Pro198Leu	missense
CHC1053T	ENSG00000172006	ZNF554	19	g.2823070A>G	p.Glu29Gly	missense
CHC302T	ENSG00000198028	ZNF560	19	g.9577515A>T	p.Leu703X	nonsense
CHC429T	ENSG00000189144	ZNF573	19	g.38230055C>G	p.Glu446Gln	missense
CHC614T	ENSG00000189190	ZNF600	19	g.53268984del	p.Phe675LeufsX7	deletion
CHC301T	ENSG00000167554	ZNF610	19	g.52869830A>G	p.Tyr400Cys	missense
CHC614T	ENSG00000160352	ZNF714	19	g.21281677 T>G	p.Trp35Gly	missense
CHC155T	ENSG00000170396	ZNF804A	2	g.185801897_185801907del	p.Ser593GlufsX29	deletion
CHC205T	ENSG00000198783	ZNF830	17	g.33289670C>G	p.Ser362Cys	missense
CHC433T	ENSG00000176371	ZSCAN2	15	g.85165076A>T	p.Arg550Ser	missense
CHC302T	ENSG00000180532	ZSCAN4	19	g.58189906A>G	p.Tyr312Cys	missense
CHC197T	ENSG00000131848	ZSCAN5A	19	g.56733297C>A	p.Gly380Cys	missense
CHC155T	ENSG00000162415	ZSWIM5	1	g.45553765T>A	p.His247Leu	missense

Supplementary Table 4. Correlation between clinical, pathological and genomic features.

Correlation with clinical and pathological features	
HBV infection	IFR2 mutation (P=0.003); no CTNNB1 mutation (P=0.001); High FAA (P=0.01*); Homozygous deletion (P=0.03)
Alcohol intake	ARID1A mutation (P=0.002)
No etiology	HNF1A mutation (P=0.008)
Age < 60 years	IRF2 mutation (P =0.002), no CTNNB1 mutation (P=0.05)
Poor tumor differentiation (Edmondson III-IV)	High FAA (P=0.04*); High ploidy (P=0.03*) ; Homozygous deletion (P=0.04)
Well tumor differentiation (Edmondson I-II)	High level G>T transversion (P=0.01*); HNF1A mutation (P=0.03)
Non-cirrhotic liver	High FAA (P=0.04*); high level G>T transversion (P=0.01*); RPS6KA3 mutation (P=0.05)
Large tumors (>50 mm)	High FAA (P=0.004*)
High serum Alpha Foeto Protein (≥24 ng/ml)	High ploidy (P=0.01*); High FAA (P=0.03*); no CTNNB1 mutation (P=0.03); Homozygous deletion (P=0.008)
Microscopic vascular invasion	Homozygous deletion (P=0.009)
Correlation between gene alterations	
High FAA	High ploidy (P=1E-07*); G1-G3 transcriptomic (P=6E-05*); TP53 mutation (P=0.003*); AXIN1 mutation (P=0.02*); IRF2 mutation (P=0.01*); Homozygous deletion (P=0.00001*)
CTNNB1 mutation	G5-G6 transcriptomic (P<1E-9); NFE2L2 mutation (P=0.01); ARID1A mutation (P=0.05); no TP53 mutation (P=0.0001); no AXIN1 mutation (P=0.006)
TP53 mutation	G3 transcriptomic (P=0.0001)
RPS6KA3 mutation	AXIN1 mutation (P=0.02)
IRF2 mutation	G2 transcriptomic (P=0.0002)
IL6ST mutation	G6 transcriptomic (P=0.02)
HNF1A mutation	G4 transcriptomic (P=0.04)

*Kruskal Wallis test

Supplementary Table 5: Focal Amplifications

#HCC-ID	Copy number	Start position (in bp)	End position (in bp)	Cytoband	Genes
CHC014T	6	73776674	73959878	1p31.1	
CHC014T	6	80208060	80416986	1p31.1	
CHC304T	7	115862255	115922523	1p13.2	
CHC309T	5	154750817	155186728	1q21.3	ADAM15,DPM3,RAG1AP1,TRIM46,THBS3,EFNA4,CKS1B,EFNA1,PMVK,SHC1,MTX1,MUC1,DCST2,PBXIP1,LENEP,KRTCAP2,MIR92B,ZBTB7B,FLAD1,DCST1,EFNA3,PYGO2
CHC794T	6	156300083	156560501	1q22	TTC24,C1orf182,C1orf61,IQGAP3,RHBG,MEF2D,MIR9-1
CHC314T	5	204440602	204632480	1q32.1	MDM4
CHC961T	6	217085750	217145697	1q41	
CHC205T	6	239587513	239659952	1q43	
CHC031T	5	54708409	55151439	2p16.2	RPL23AP32,SPTBN1
CHC028T	6	126395813	127894614	2q14.3	BIN1,GYPC
CHC028T	6	165047346	167056427	2q24.3	SCN1A,SCN3A,GRB14,GALNT3,SCN2A,COBLL1,SLC38A11,TTC21B,SNORA70F,CSRNP3
CHC1065T	5	192335295	195160637	2q32.3	PCGEM1,SDPR,TMEFF2,OBFC2A
CHC1052T	6	189910073	190237100	3q28	TMEM207,CLDN16,CLDN1
CHC1055T	6	11425013	12099334	4p15.33	
CHC1055T	5	13265682	13484419	4p15.33	HSP90AB2P
CHC1055T	4	13940962	14099570	4p15.33	
CHC254T	8	55108295	55257610	4q12	
CHC339T	6	57368167	58136697	4q12	REST,HOPX,IGFBP7,SPINK2,ARL9,C4orf14,POLR2B
CHC018T	6	66431910	67459960	4q13.1	
CHC1154T	6	2866347	3104266	5p15.33	
CHC1154T	6	3126446	4907777	5p15.33	IRX1
CHC1065T	4	29342141	29625795	5p13.3	
CHC1154T	6	42483694	43899601	5p13.1	PAIP1,SEPP1,HMGCS1,CCL28,C5orf34,CCDC152,ZNF131,MGC42105,C5orf28,NNT,LOC153684,C5orf39
CHC211T	5	65186000	66518705	5q12.3	ERBB2IP,CD180,LOC100303749,MAST4,SFRS12
CHC211T	6	73710425	76147233	5q13.3	C5orf37,GFM2,HMGCR,HEXB,ANKRD31,ENC1,NSA2,COL4A3BP,GCNT4,FAM169A,SV2C,IQGAP2,F2RL2,POLK,F2R,F2RL1,NCRUPAR
CHC304T	6	1374278	2064263	6p25.3	FOXC1,FOXF2
CHC097T	6	27835931	27847516	6p22.1	HIST1H3I,HIST1H4L
CHC794T	5	43187767	43900442	6p21.1	XPO5,SLC22A7,POLH,VEGFA,ABCC10,YIPF3,RSPH9,CRIP3,DLK2,MAD2L1BP,C6orf108,ZNF318,C6orf154,POLR1C,GTPBP2,MRPS18A,TTBK1,TJAP1
CHC033T	8	63961693	64269846	6q12	LGSN
CHC301T	5	64269848	65171418	6q12	PHF3,PTP4A1
CHC237T	5	66746844	67995170	6q12	
CHC242T	5	18864041	18935766	7p21.1	
CHC303T	8	70145074	70209636	7q11.22	
CHC303T	8	70387954	70521775	7q11.22	
CHC314T	5	79730562	80354228	7q21.11	GNAI1,CD36,GNAT3
CHC121T	6	81176805	81273755	7q21.11	
CHC154T	5	128169980	128866388	7q32.1	FLJ45340,IRF5,LOC407835,LOC286016,ATP6V1F,CALU,TNPO3,SMO,OPN1SW,FLNC,CCDC136,FAM71F1,KCP,FAM71F2,TSPAN33
CHC465T	5	150977228	151926614	7q36.1	RHEB,GALNT11,WDR86,PRKAG2,NUB1,CRYGN,GALNTL5
CHC051T	5	32716484	35319480	8p12	DUSP26,FUT10,MAK16,C8orf41,RNF122
CHC097T	8	34674920	34856370	8p12	
CHC301T	5	34889072	35316787	8p12	
CHC097T	6	35247298	35429072	8p12	
CHC1052T	8	39495326	39587863	8p11.22	
CHC097T	7	40243955	40565815	8p11.21	
CHC1052T	8	42858300	43195671	8p11.21	SGK196,FNTA,HGSNAT
CHC051T	6	53363938	53579553	8q11.23	FAM150A
CHC302T	6	55437525	55476998	8q11.23	
CHC302T	5	56448941	57707933	8q12.1	TGS1,RPS20,SDR16C6,MOS,LYN,PENK,SNORD54,CHCHD7,PLAG1,TMEM68,SDR16C5
CHC302T	5	61984700	63436368	8q12.2	ASPH,CLVS1
CHC327T	7	80264466	82017371	8q21.13	ZBTB10,TPD52,HEY1,STMN2,MRPS28,ZNF704
CHC226T	6	83293873	84974523	8q21.13	
CHC399T	5	88696840	88740928	8q21.3	
CHC154T	5	13588522	13854996	10p13	PRPF18
CHC033T	8	114966497	115807015	10q25.3	CASP7,C10orf81,NHLRC2,HABP2,ADRB1,NRAP,DCLRE1A
CHC033T	8	116040002	116519520	10q25.3	AFAP1L2,ABLIM1
CHC1065T	5	117996151	118116033	10q25.3	
CHC129T	6	30246777	30829829	11p14.1	FSHB,MPPED2,C11orf46
CHC245T	8	67479309	69604526	11q13.2	CHKA,SUV420H1,C11orf24,NDUFS8,FGF4,MTL5,CPT1A,ORAOV1,ALDH3B1,IGHMBP2,UNC93B1,MRGPRF,CCND1,TCIRG1,MRPL21,SAPS3,GAL,FGF19,MYEOV,LRP5,TPCN2,LOC645332,MRGPRD
CHC008T	5	68346484	69585786	11q13.2	MTL5,CPT1A,ORAOV1,IGHMBP2,MRGPRF,CCND1,MRPL21,GAL,FGF19,MYEOV,TPCN2,MRGPRD
CHC793T	5	72093615	72276605	11q13.4	
CHC918T	6	117128272	117428277	11q23.3	BACE1,CEP164
CHC226T	7	21531438	22358857	12p12.1	ABCC9,GOLT1B,CMAS,RECQL,KCNJ8,C12orf39,LDHB,PYROXD1,GYS2
CHC031T	8	22945809	23599348	12p12.1	
CHC226T	5	23677561	23700774	12p12.1	
CHC303T	7	53714869	54324068	12q13.13	SP7,SP1,CALCOCO1,AMHR2,NPFF,ATP5G2,PCBP2,ATF7,TARBP2,PRR13,MAP3K12
CHC303T	8	59575431	61320898	12q14.1	SLC16A7
CHC033T	8	82113311	82378975	13q31.1	
CHC033T	8	86071403	88963675	13q31.1	SLITRK5,SLITRK6
CHC961T	5	99527028	99670270	13q32.3	
CHC430T	5	73490925	74130927	16q22.3	
CHC430T	5	76372980	76624462	16q23.1	
CHC430T	5	79460568	79651292	16q23.2	MAF
CHC126T	6	27502030	28479798	17q11.2	GIT1,CRYBA1,ANKRD13B,SSH2,MIR423,NUFIP2,ABHD15,TP53I13,TAOK1,EFCAB5,COR O6
CHC437T	5	28551666	28812119	17q11.2	CPD,TMIGD1,BLMH
CHC1052T	7	37201756	37288064	17q12	

Supplementary Table 5: Focal Amplifications

#HCC-ID	Copy number	Start position (in bp)	End position (in bp)	Cytoband	Genes
CHC126T	8	37770006	40107808	17q12	KRT40,TMEM99,ZPBP2,PPP1R1B,ACLY,CDC6,CASC3,KRT17,KRT10,KRT34,KRT37,KRTAP1-1,KRTAP2-2,KRT13,KRT24,KRT222,KRTAP1-3,RARA,KRT15,KRT23,ERBB2,MED24,KRT12,KRT27,KRTAP3-3,KRTAP3-2,KRTAP3-1,KRTAP1-5,KRTAP4-12,KRTAP4-5,KRTAP4-4,KRTAP4-3,KRTAP4-2,KRTAP4-1,KRTAP9-2,KRTAP9-3,KRTAP9-9,KRTAP9-8,KRTAP9-4,KRTAP17-1,KRT33B,KRT35,KRT32,EIF1,SC65,NT5C3L,ORMDL3,KRT38,KRT9,KRTAP4-7,KRTAP4-11,STARD3,HAP1,NR1D1,TOP2A,PGAP3,C17orf37,KRT19,FKBP10,SMARCE1,IKZF3,GJD3,KLHL10,CSF3,KRT20,PSMD3,GSDMA,JUP,RAPGEFL1,TCAP,GAST,THRA,WIPF2,TNS4,IGFBP4,LOC730755,KLHL11,SNORD124,KRT33A,GSDMB,CCR7,KRT16,PNMT,GRB7,KRT36,KRTAP4-8,KRT28,KRT25,KRTAP4-9,KRTAP2-1,KRT31,KRTAP2-4,KRT14,KRT26,KRT39,MSL1
CHC399T	5	2641036	2817051	18p11.32	SMCHD1
CHC399T	5	13177131	13487484	18p11.21	
CHC399T	5	13590753	13680931	18p11.21	C18orf1
CHC155T	5	64801046	65220233	18q22.1	DSEL
CHC1055T	8	21215213	21277422	19p12	
CHC1055T	4	22779199	23447298	19p12	ZNF99,ZNF492
CHC794T	8	49783102	50301544	19q13.33	CD37,SNORD32A,SNORD35B,PTH2,RRAS,CPT1C,SLC17A7,SNORD35A,RCN3,PIH1D1,FCGRT,SLC6A16,TEAD2,RPL13A,RPS11,NOSIP,TSKS,SNORD33,SCAF1,IRF3,ALDH16A1,PRRG2,SNORD34,BCL2L12,CCDC155,FLT3LG,C19orf76,PRR12,PRMT1,DKKL1,RPL13AP5,MIR150
CHC129T	5	34555834	34612159	21q22.11	
CHC033T	8	18913603	19365285	22q11.21	TSSK2,DGCR2,CLTCL1,DGCR14,GSC2,DGCR5,SLC25A1,DGCR9,DGCR11,DGCR10
CHC033T	8	20854162	21814927	22q11.21	RIMBP3C,PI4KA,MED15,LZTR1,SLC7A4,AIFM3,SNAP29,HIC2,RIMBP3B,MGC16703,P2RX6,CRKL,THAP7,POM121L8P,POM121L4P,TMEM191A,LOC400891,FLJ39582,SERPIND1,P2RX6P

Supplementary Table 6: Homozygous deletion

#HCC-ID	Start position (in bp)	End position (in bp)	Cytoband	Genes
CHC320T	1619542	1680218	1p36.33	SLC35E2,CDK11B,CDK11A,LOC728661,MMP23A
CHC441T	3577322	3616600	1p36.32	TP73
CHC317T	7971079	8652153	1p36.23	ERRFI1,RERE,PARK7,TNFRSF9,SLC45A1
CHC317T	21682435	21766452	1p36.12	
CHC402T	41013016	41054113	1p34.2	ZNF684
CHC218T	50918389	51462438	1p32.3	CDKN2C,FAF1
CHC046T	178665594	178684822	1q25.2	
CHC441T	204231501	204389313	1q32.1	PPP1R15B,PLEKHA6,LOC127841
CHC218T	65524098	65680309	2p14	SPRED2
CHC441T	65561393	65741614	2p14	SPRED2
CHC304T	141466385	142035285	2q22.1	LRP1B
CHC218T	186865607	187084688	2q32.1	
CHC208T	232779224	234694176	2q37.1	ALPP,NPPC,UGT1A5,UGT1A9,UGT1A4,UGT1A8,UGT1A10,KCNJ13,GIGYF2,UGT1A6,SAG,EIF4E2,DGKD,UGT1A3,CHRNG,CHRND,UGT1A7,NEU2,TIGD1,ALPPL2,DNAJB3,NGEF,UGT1A1,INPP5D,C2orf82,USP40,DIS3L2,SCARNA5,SCARNA6,ATG16L1,ALPI,ECEL1,EFHD1,ECEL1P2
CHC254T	233097787	233155565	2q37.1	DIS3L2
CHC218T	65750653	65776339	3p14.1	MAGI1
CHC226T	68512005	68678210	3p14.1	FAM19A1
CHC218T	71074195	71254192	3p13	FOXP1
CHC218T	114034099	114598528	3q13.31	ZBTB20,MIR568
CHC1199T	162123180	162155075	3q26.1	
CHC317T	38980065	39016074	4p14	TMEM156
CHC218T	39496273	39614822	4p14	C4orf34,UGDH
CHC130T	44078423	44093498	4p13	
CHC317T	62416500	62498950	4q13.1	LPHN3
CHC123T	98701199	98809573	4q22.3	C4orf37
CHC304T	108060030	108083470	4q25	
CHC1199T	122281108	122289862	4q27	QRFPR
CHC239T	171252195	171312560	4q33	
CHC239T	184882783	185220261	4q35.1	STOX2,ENPP6
CHC034T	184892635	185370065	4q35.1	STOX2,ENPP6,IRF2
CHC018T	185034184	185382060	4q35.1	ENPP6,IRF2
CHC012T	185148190	185400747	4q35.1	IRF2
CHC239T	185282465	185490725	4q35.1	IRF2
CHC1035T	13201513	13367396	5p15.2	
CHC891T	91575925	91893094	5q14.3	
CHC121T	100995049	101168136	6q16.3	ASCC3
CHC961T	108641306	109574094	6q21	FOXO3,LACE1,SESN1,C6orf182,ARMC2
CHC794T	109863159	109917531	6q21	AKD1
CHC218T	128313089	128691352	6q22.33	PTPRK
CHC218T	148270823	148328366	6q24.3	
CHC609T	166767384	166787242	6q27	BRP44L
CHC301T	169924120	170142385	6q27	WDR27,PHF10,TCTE3,C6orf120
CHC469T	78256343	78492641	7q21.11	MAGI2
CHC218T	110677657	110733716	7q31.1	IMMP2L,LRRN3
CHC218T	111596968	111723487	7q31.1	DOCK4
CHC1055T	3668652	3826044	8p23.2	CSMD1
CHC1055T	3829248	3854986	8p23.2	CSMD1
CHC123T	13185927	13209660	8p22	DLC1
CHC441T	17655407	17748919	8p22	FGL1,MTUS1
CHC031T	17739539	17759862	8p22	FGL1
CHC441T	22210235	22340498	8p21.3	SLC39A14,PIWIL2,PPP3CC
CHC441T	25269103	25318252	8p21.2	DOCK5,GNRH1,KCTD9,CDCA2
CHC441T	38754531	38793681	8p11.22	PLEKHA2
CHC1053T	51029372	51042155	8q11.21	SNTG1
CHC441T	3989790	4310557	9p24.2	GLIS3
CHC304T	9253588	9516347	9p23	PTPRD
CHC254T	12464877	12586943	9p23	
CHC031T	21557407	22207036	9p21.3	CDKN2BAS,CDKN2B,C9orf53,CDKN2A,MTAP,LOC554202
CHC205T	21712194	22081396	9p21.3	CDKN2BAS,CDKN2B,C9orf53,CDKN2A,MTAP
CHC130T	21920347	21997871	9p21.3	CDKN2BAS,C9orf53,CDKN2A
CHC433T	21953138	22044121	9p21.3	CDKN2BAS,CDKN2B,C9orf53,CDKN2A
CHC235T	21954954	22056498	9p21.3	CDKN2BAS,CDKN2B,C9orf53,CDKN2A
CHC1069T	21966222	22028800	9p21.3	CDKN2BAS,CDKN2B,C9orf53,CDKN2A
CHC218T	21980152	22130064	9p21.3	CDKN2BAS,CDKN2B,CDKN2A
CHC793T	21990458	22088259	9p21.3	CDKN2BAS,CDKN2B,CDKN2A
CHC218T	22861228	22963772	9p21.3	
CHC218T	112418912	112924175	9q31.3	PALM2,AKAP2,PALM2-AKAP2
CHC158T	52558493	52616921	10q11.23	A1CF
CHC158T	65000494	65194128	10q21.3	JMJD1C,MIR1296
CHC313T	89406642	89807851	10q23.2	PTEN,PAPSS2,ATAD1,KILLIN,CFLP1
CHC1055T	89495365	89725731	10q23.2	PTEN,PAPSS2,ATAD1,KILLIN,CFLP1
CHC218T	96547464	96682513	10q23.33	CYP2C19
CHC218T	104241684	104531049	10q24.32	SFXN2,SUFU,TRIM8,ARL3,ACTR1A,C10orf26
CHC218T	109453933	109800375	10q25.1	
CHC239T	122762147	122787761	10q26.12	
CHC218T	131361225	131457178	10q26.3	MGMT
CHC014T	25455060	26018892	11p14.3	
CHC441T	46469901	46692869	11p11.2	KIAA0652,AMBRA1,HARBI1
CHC317T	129065881	129115637	11q24.3	
CHC441T	12829915	12912803	12p13.1	APOLD1,GPR19,CDKN1B
CHC014T	28605427	28719699	12p11.22	CCDC91
CHC1199T	45613496	47562926	12q12	SFRS2IP,AMIGO2,SLC38A4,ANO6,ARID2,SLC38A1,SLC38A2,LOC400027
CHC043T	50841058	53094938	12q13.12	ACVRL1,SMAGP,KRT80,KRT71,KRT75,TMPRSS12,LETMD1,DIP2B,CSRNP2,BIN2,SLC4A8,ACVR1B,ANKRD33,GRASP,KRT81,KRT83,KRT85,KRT6C,KRT72,LARP4,KRT6B,KRT6A,NR4A1,KRT2,DAZAP2,METTL7A,KRT7,KRT5,KRT1,POU6F1,KRT86,CELA1,TFCP2,GALNT6,SLC11A2,HIGD1C,ATF1,C12orf44,SCN8A,KRT73,KRT74,KRT77,LOC283404,FIGNL2,KRT84,KRT82
CHC1146T	104845733	104849026	12q23.3	
CHC129T	33678506	33754515	13q13.1	STARD13

Supplementary Table 6: Homozygous deletion

#HCC-ID	Start position (in bp)	End position (in bp)	Cytoband	Genes
CHC158T	48901433	49002353	13q14.2	LPAR6,RB1
CHC137T	56493080	56605491	13q21.1	
CHC242T	70733845	70778216	13q21.33	
CHC226T	75331094	75494108	13q22.1	
CHC441T	58701881	58794000	14q23.1	PSMA3,ARID4A,ACTR10,FLJ31306
CHC226T	44897746	45094018	15q21.1	TRIM69,B2M,SPG11,PATL2
CHC012T	203255	362637	16p13.3	ITFG3,HBA2,AXIN1,HBQ1,ARHGDIG,RGS11,PDIA2,HBA1,HBZ,LUC7L,HBM
CHC031T	265160	341078	16p13.3	ITFG3,AXIN1,ARHGDIG,RGS11,PDIA2,LUC7L
CHC1199T	347185	357139	16p13.3	AXIN1
CHC014T	349222	377793	16p13.3	AXIN1
CHC1154T	19941969	19971789	16p12.3	
CHC018T	20509697	20552074	16p12.3	ACSM2B
CHC081T	65986968	66130755	16q21	
CHC250T	72823076	73087493	16q22.2	ZFHX3
CHC158T	78201954	78504997	16q23.1	WWOX
CHC014T	78817230	79079658	16q23.1	WWOX
CHC130T	89094244	89122738	16q24.3	
CHC469T	2641106	2860023	17p13.3	RAP1GAP2,MIR1253
CHC218T	9097934	9304542	17p13.1	NTN1,STX8
CHC137T	10765210	10830183	17p12	
CHC226T	16068423	16219791	17p11.2	NCOR1,PIGL,MIR1288
CHC441T	25630652	25759163	18q12.1	CDH2
CHC402T	65290715	65318535	18q22.1	
CHC033T	66738930	66758996	18q22.1	
CHC1035T	1	406369	19p13.3	THEG,PPAP2C,C2CD4C,MIER2,FAM138A,FAM138F,FAM138C,FLJ45445,OR4F17,LOC 375690
CHC441T	1124032	1189481	19p13.3	SBNO2
CHC614T	1132638	1238898	19p13.3	C19orf26,SBNO2,STK11
CHC441T	2050824	2221791	19p13.3	MKNK2,MOBKL2A,C19orf36,DOT1L,AP3D1
CHC301T	2141210	2211049	19p13.3	DOT1L,AP3D1
CHC441T	11023435	11146498	19p13.2	CARM1,SMARCA4,YIPF2,C19orf52
CHC235T	43368962	43556842	19q13.2	PSG11,PSG6,PSG7,PSG1
CHC208T	54717302	54759570	19q13.42	LILRB5,LILRB3,LILRA6
CHC304T	15058883	15113007	20p12.1	MACROD2
CHC441T	23348888	23392839	21q21.1	
CHC013T	27336169	27548329	21q21.3	APP
CHC013T	32736170	33090757	21q22.11	SFRS15,SOD1,TIAM1
CHC909T	18624959	18631364	22q11.21	
CHC441T	24707113	24865186	22q11.23	C22orf45,CYTSA,ADORA2A
CHC218T	28411919	29083204	22q12.1	TTC28
CHC239T	6451753	8141016	Xp22.31	HDHD1A,STS,VCX3A,PNPLA4,VCX2,VCX,MIR651
CHC303T	9456802	9543469	Xp22.31	TBL1X
CHC014T	10458876	10621475	Xp22.2	MID1
CHC137T	28770686	29133142	Xp21.3	IL1RAPL1
CHC130T	36786480	37191430	Xp21.1	FAM47C
CHC1192T	53087477	53115704	Xp11.22	GPR173,TSPYL2
CHC307T	82330914	82460172	Xq21.1	
CHC218T	96165910	97165453	Xq21.33	DIAPH2
CHC441T	96441494	96623615	Xq21.33	DIAPH2
CHC218T	104311117	104454049	Xq22.3	IL1RAPL2
CHC218T	111421285	111609731	Xq23	ZCCHC16
CHC034T	134809429	134865393	Xq26.3	CT45A1

Supplementary table 7. Complete list of gene mutations found in a series of validation of 125 HCC.

#HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic hg19)	cDNA	Amino Acid
CHC013T	ENSG00000168036	CTNNB1	3	g.41266124A>G	c.121A>G	p.Thr41Ala
CHC028T	ENSG00000168036	CTNNB1	3	g.41266098A>G	c.95A>G	p.Asp32Gly
CHC037T	ENSG00000168036	CTNNB1	3	g.41266137C>T	c.134C>T	p.Ser45Phe
CHC046T	ENSG00000168036	CTNNB1	3	g.41266103G>A	c.100G>A	p.Gly34Arg
CHC051T	ENSG00000168036	CTNNB1	3	g.41266100T>C	c.97T>C	p.Ser33Pro
CHC059T	ENSG00000168036	CTNNB1	3	g.41266124A>G	c.121A>G	p.Thr41Ala
CHC097T	ENSG00000168036	CTNNB1	3	g.41266136T>C	c.133T>C	p.Ser45Pro
CHC115T	ENSG00000168036	CTNNB1	3	g.41266136T>C	c.133T>C	p.Ser45Pro
CHC121T	ENSG00000168036	CTNNB1	3	g.41266136T>G	c.133T>G	p.Ser45Ala
CHC130T	ENSG00000168036	CTNNB1	3	g.41266101C>T	c.98C>T	p.Ser33Phe
CHC164T	ENSG00000168036	CTNNB1	3	g.41266110A>C	c.107A>C	p.His36Pro
CHC168T	ENSG00000168036	CTNNB1	3	g.41266101C>G	c.98C>G	p.Ser33Cys
CHC197T	ENSG00000168036	CTNNB1	3	g.41266137C>T	c.134C>T	p.Ser45Phe
CHC211T	ENSG00000168036	CTNNB1	3	g.41265926_41266306del	c.14-91_241+62del	deletion exon 3
CHC230T	ENSG00000168036	CTNNB1	3	g.41268766A>T	c.1004A>T	p.Lys335Ile
CHC242T	ENSG00000168036	CTNNB1	3	g.41266136T>C	c.133T>C	p.Ser45Pro
CHC252T	ENSG00000168036	CTNNB1	3	g.41268766A>T	c.1004A>T	p.Lys335Ile
CHC301T	ENSG00000168036	CTNNB1	3	g.41266107T>G	c.104T>G	p.Ile35Ser
CHC302T	ENSG00000168036	CTNNB1	3	g.41266137C>A	c.134C>A	p.Ser45Tyr
CHC303T	ENSG00000168036	CTNNB1	3	g.41266110A>C	c.107A>C	p.His36Pro
CHC317T	ENSG00000168036	CTNNB1	3	g.41266124A>G	c.121A>G	p.Thr41Ala
CHC320T	ENSG00000168036	CTNNB1	3	g.41266113C>G	c.110C>G	p.Ser37Cys
CHC333T	ENSG00000168036	CTNNB1	3	g.41266107T>G	c.104T>G	p.Ile35Ser
CHC335T	ENSG00000168036	CTNNB1	3	g.41266100T>C	c.97T>C	p.Ser33Pro
CHC361TB	ENSG00000168036	CTNNB1	3	g.41265566_41266581del	c.7_378del	p.Thr3_Ala126del
CHC399T	ENSG00000168036	CTNNB1	3	g.41266101C>G	c.98C>G	p.Ser33Cys
CHC429T	ENSG00000168036	CTNNB1	3	g.41266101C>G	c.98C>G	p.Ser33Cys
CHC430T	ENSG00000168036	CTNNB1	3	g.41266136T>C	c.133T>C	p.Ser45Pro
CHC433T	ENSG00000168036	CTNNB1	3	g.41266098A>G	c.95A>G	p.Asp32Gly
CHC437T	ENSG00000168036	CTNNB1	3	g.41266124A>G	c.121A>G	p.Thr41Ala
CHC469T	ENSG00000168036	CTNNB1	3	g.41266103G>A	c.100G>A	p.Gly34Arg
CHC609T	ENSG00000168036	CTNNB1	3	g.41266113C>G	c.110C>G	p.Ser37Cys
CHC614T	ENSG00000168036	CTNNB1	3	g.41266125C>A	c.122C>A	p.Thr41Asn
CHC798T	ENSG00000168036	CTNNB1	3	g.41266101C>G	c.98C>G	p.Ser33Cys
CHC918T	ENSG00000168036	CTNNB1	3	g.41266137C>T	c.134C>T	p.Ser45Phe
CHC983T	ENSG00000168036	CTNNB1	3	g.41274899G>T	c.1149G>T	p.Trp383Cys
CHC983T	ENSG00000168036	CTNNB1	3	g.41242294A>G	c.874A>G	p.Lys292Glu
CHC1040T	ENSG00000168036	CTNNB1	3	g.41266136T>C	c.133T>C	p.Ser45Pro
CHC1041T	ENSG00000168036	CTNNB1	3	g.41266098A>T	c.95A>T	p.Asp32Val
CHC1052T	ENSG00000168036	CTNNB1	3	g.41266129_41266134dup	c.126_131dup	p.Ala43_Pro44dup
CHC1069T	ENSG00000168036	CTNNB1	3	g.41266098A>C	c.95A>C	p.Asp32Ala
CHC1146T	ENSG00000168036	CTNNB1	3	g.41266100T>C	c.97T>C	p.Ser33Pro
CHC008T	ENSG00000141510	TP53	17	g.7578272G>C	c.577C>G	p.His193Asp
CHC013T	ENSG00000141510	TP53	17	g.7577556C>A	c.725G>T	p.Cys242Phe
CHC014T	ENSG00000141510	TP53	17	g.7577534C>A	c.747G>T	p.Arg249Ser
CHC033T	ENSG00000141510	TP53	17	g.7577556C>T	c.725G>A	p.Cys242Tyr
CHC037T	ENSG00000141510	TP53	17	g.7579420dup	c.267dup	p.Ser90LeufsX59
CHC043T	ENSG00000141510	TP53	17	g.7577534C>A	c.747G>T	p.Arg249Ser
CHC046T	ENSG00000141510	TP53	17	g.7577610T>C	c.673-2A>G	splicing
CHC100T	ENSG00000141510	TP53	17	g.7577081T>A	c.857A>T	p.Glu286Val
CHC126T	ENSG00000141510	TP53	17	g.7577085C>T	c.853G>A	p.Glu285Lys
CHC129T	ENSG00000141510	TP53	17	g.7578445A>C	c.485T>G	p.Ile162Ser
CHC137T	ENSG00000141510	TP53	17	g.7574012C>A	c.1015G>T	p.Glu339X
CHC154T	ENSG00000141510	TP53	17	g.7577602del	c.679del	p.Ser227LeufsX20
CHC208T	ENSG00000141510	TP53	17	g.7578190T>G	c.659A>C	p.Tyr220Ser
CHC226T	ENSG00000141510	TP53	17	g.7577534C>A	c.747G>T	p.Arg249Ser
CHC229T	ENSG00000141510	TP53	17	g.7578212G>A	c.637C>T	p.Arg213X
CHC245T	ENSG00000141510	TP53	17	g.7577550C>T	c.731G>A	p.Gly244Asp
CHC254T	ENSG00000141510	TP53	17	g.7577568C>A	c.713G>T	p.Cys238Phe
CHC304T	ENSG00000141510	TP53	17	g.7579398_7579439dup	c.248_289dup	p.Ala83_Ser96dup
CHC314T	ENSG00000141510	TP53	17	g.7578395G>A	c.535C>T	p.His179Tyr
CHC327T	ENSG00000141510	TP53	17	g.7577545T>C	c.736A>G	p.Met246Val
CHC402T	ENSG00000141510	TP53	17	g.7577535C>T	c.746G>A	p.Arg249Lys
CHC793T	ENSG00000141510	TP53	17	g.7573982C>A	c.1045G>T	p.Glu349X
CHC882T	ENSG00000141510	TP53	17	g.7577058C>A	c.880G>T	p.Glu294X
CHC1035T	ENSG00000141510	TP53	17	g.7577534C>A	c.747G>T	p.Arg249Ser
CHC1055T	ENSG00000141510	TP53	17	g.7579502_7579518dup	c.169_185dup	p.Ala63ThrfsX66
CHC1061T	ENSG00000141510	TP53	17	g.7574017C>A	c.1010G>T	p.Arg337Leu
CHC013T	ENSG00000117713	ARID1A	1	g.27106961_27106969del	c.6572_6580del	p.Ser2191_Gly2193del
CHC014T	ENSG00000117713	ARID1A	1	g.27089676C>T	c.2632C>T	p.Gln878X
CHC100T	ENSG00000117713	ARID1A	1	g.27107082_27107094del	c.6693_6705del	p.Met2231IlefsX32
CHC121T	ENSG00000117713	ARID1A	1	g.27023209_27023228del	c.315_334del	p.Asn106ProfsX4
CHC155T	ENSG00000117713	ARID1A	1	g.27056173dup	c.1169dup	p.Met390IlefsX10
CHC205T	ENSG00000117713	ARID1A	1	g.27099939_27099964delinsG	c.3818_3843delinsG	p.Met1273ArgfsX8
CHC211T	ENSG00000117713	ARID1A	1	g.27106934_27106953del	c.6545_6564del	p.Ala2182GlufsX36
CHC230T	ENSG00000117713	ARID1A	1	g.27023381G>A	c.487G>A	p.Ala163Thr
CHC241T	ENSG00000117713	ARID1A	1	g.27089501dup	c.2457dup	p.Asn820GlnfsX52
CHC303T	ENSG00000117713	ARID1A	1	g.27107163_27107181del	c.6774_6792del	p.Leu2259ArgfsX2
CHC320T	ENSG00000117713	ARID1A	1	g.27106640T>A	c.6251T>A	p.Val2084Asp
CHC335T	ENSG00000117713	ARID1A	1	g.27106649G>A	c.6260G>A	p.Gly2087Glu
CHC339T	ENSG00000117713	ARID1A	1	g.27106159delinsAA	c.5770delinsAA	p.Glu1924LysfsX5
CHC433T	ENSG00000117713	ARID1A	1	g.27023909del	c.1015del	p.Ala339LeufsX24
CHC434T	ENSG00000117713	ARID1A	1	g.27023909_27023923del	c.1015_1029del	p.Ala345_Ala349del

Supplementary table 7. Complete list of gene mutations found in a series of validation of 125 HCC.

#HCC-ID	Ensembl Gene ID	Gene symbol	Chromosome	Nucleotide (genomic hg19)	cDNA	Amino Acid
CHC437T	ENSG00000117713	ARID1A	1	g.27097692dup	c.3281dup	p.Gln1095AlafsX10
CHC445T	ENSG00000117713	ARID1A	1	g.27087897_27087911delinsT	c.2184_2198delinsT	p.Pro729GlyfsX83
CHC983T	ENSG00000117713	ARID1A	1	g.27099008C>T	c.3424C>T	p.Gln1142X
CHC1040T	ENSG00000117713	ARID1A	1	g.27056214C>T	c.1210C>T	p.Gln404X
CHC1053T	ENSG00000117713	ARID1A	1	g.27023213_27023222del	c.319_328del	p.Ala107GlyfsX4
CHC018T	ENSG00000103126	AXIN1	16	g.396458G>A	c.568C>T	p.Gln190X
CHC226T	ENSG00000103126	AXIN1	16	g.347764_347765del	c.1741_1742del	p.Ser581CysfsX9
CHC237T	ENSG00000103126	AXIN1	16	g.364557_364563dup	c.999_1005dup	p.Thr336ValfsX17
CHC250T	ENSG00000103126	AXIN1	16	g.347143G>T	c.1868C>A	p.Ser623X
CHC306T	ENSG00000103126	AXIN1	16	g.396233C>A	c.793G>T	p.Gly265X
CHC314T	ENSG00000103126	AXIN1	16	g.360068del	c.1021del	p.Asp341MetfsX73
CHC327T	ENSG00000103126	AXIN1	16	g.348113C>A	c.1393G>T	p.Glu465X
CHC434T	ENSG00000103126	AXIN1	16	g.347772G>T	c.1734C>A	p.Tyr578X
CHC438T	ENSG00000103126	AXIN1	16	g.396962G>A	c.64C>T	p.Arg22X
CHC1052T	ENSG00000103126	AXIN1	16	g.397014T>G	c.12A>C	p.Gln4His
CHC1053T	ENSG00000103126	AXIN1	16	g.347930C>T	c.1576G>A	p.Ala526Thr
CHC1065T	ENSG00000103126	AXIN1	16	g.354326dup	c.1232dup	p.Arg412AlafsX12
CHC1154T	ENSG00000103126	AXIN1	16	g.347929G>A	c.1577C>T	p.Ala526Val
CHC1190T	ENSG00000103126	AXIN1	16	g.347909G>A	c.1597C>T	p.Arg533X
CHC1201T	ENSG00000103126	AXIN1	16	g.347903C>T	c.1603G>A	p.Val535Ile
CHC237T	ENSG00000103126	AXIN1	16	g.348122C>T	c.1384G>A	p.Ala462Thr
CHC018T	ENSG00000177189	RPS6KA3	X	g.20183143_20183145delinsC	c.1636_1638delinsG	p.Leu546ValfsX4
CHC034T	ENSG00000177189	RPS6KA3	X	g.20185706C>T	c.1602+1G>A	splicing
CHC037T	ENSG00000177189	RPS6KA3	X	g.20183078A>T	c.1703T>A	p.Leu568Gln
CHC115T	ENSG00000177189	RPS6KA3	X	g.20206653C>G	c.594-1G>C	splicing
CHC226T	ENSG00000177189	RPS6KA3	X	g.20206644A>G	c.602T>C	p.Leu201Pro
CHC258T	ENSG00000177189	RPS6KA3	X	g.20194611C>A	c.940G>T	p.Gly314X
CHC309T	ENSG00000177189	RPS6KA3	X	g.20181087_20181095delinsC	c.1828_1836delinsG	p.Thr610AspfsX11
CHC429T	ENSG00000177189	RPS6KA3	X	g.20222175T>C	c.290A>G	p.Tyr97Cys
CHC434T	ENSG00000177189	RPS6KA3	X	g.20206044A>T	c.676T>A	p.Tyr226Asn
CHC1044T	ENSG00000177189	RPS6KA3	X	g.20284689C>A	c.62G>T	p.Ser21Ile
CHC1053T	ENSG00000177189	RPS6KA3	X	g.20181154A>C	c.1769T>G	p.Leu590X
CHC1154T	ENSG00000177189	RPS6KA3	X	g.20185727C>A	c.1582G>T	p.Glu528X
CHC1044T	ENSG00000177189	RPS6KA3	X	g.20205954C>T	c.766G>A	p.Val256Met
CHC1053T	ENSG00000177189	RPS6KA3	X	g.20205972C>T	c.748G>A	p.Asp250Asn
CHC154T	ENSG00000135100	HNF1	12	g.121432125dup	c.872dup	p.Gly292ArgfsX25
CHC154T	ENSG00000135100	HNF1	12	g.121432002A>C	c.749A>C	p.Gln250Pro
CHC155T	ENSG00000135100	HNF1	12	g.121437143C>T	c.1574C>T	p.Thr525Ile
CHC196T	ENSG00000135100	HNF1	12	g.121426688A>T	c.379A>T	p.Asn127Tyr
CHC196T	ENSG00000135100	HNF1	12	g.121426804G>T	c.495G>T	p.Trp165Cys
CHC465T	ENSG00000135100	HNF1	12	g.121416642_121416653del	c.71_82del	p.Ile27_Leu30del
CHC465T	ENSG00000135100	HNF1	12	g.121432000_121432017del	c.747_764del	p.Gln250_Gly255del
CHC1061T	ENSG00000135100	HNF1	12	g.121426649_121426652de	c.340_343del	p.Arg114TrpfsX40
CHC1061T	ENSG00000135100	HNF1	12	g.121431485_121431515del	c.689_713+6del	p.Glu230GlyfsX104
CHC059T	ENSG00000116044	NFE2L2	2	g.178098797_178098805del	c.240_248del	p.Gly81_Phe83del
CHC205T	ENSG00000116044	NFE2L2	2	g.178098959T>C	c.86A>G	p.Asp29Gly
CHC317T	ENSG00000116044	NFE2L2	2	g.178098807T>G	c.238A>C	p.Thr80Pro
CHC614T	ENSG00000116044	NFE2L2	2	g.178098789T>A	c.256A>T	p.Ile86Phe
CHC1040T	ENSG00000116044	NFE2L2	2	g.178098799T>G	c.246A>C	p.Glu82Asp
CHC1041T	ENSG00000116044	NFE2L2	2	g.178098807T>G	c.238A>C	p.Thr80Pro
CHC1069T	ENSG00000116044	NFE2L2	2	g.178098803C>A	c.242G>T	p.Gly81Val
CHC1190T	ENSG00000116044	NFE2L2	2	g.178098960C>G	c.85G>C	p.Asp29His
CHC614T	ENSG00000116044	NFE2L2	2	g.178098800T>C	c.245A>G	p.Glu82Gly
CHC123T	ENSG00000189079	ARID2	12	g.46243449G>A	c.1802G>A	p.Arg601Gln
CHC126T	ENSG00000189079	ARID2	12	g.46240646_46240647dup	c.1506_1507dup	p.Ala503GlufsX4
CHC429T	ENSG00000189079	ARID2	12	g.46244040G>T	c.2134G>T	p.Glu712X
CHC614T	ENSG00000189079	ARID2	12	g.46287229C>G	c.5174C>G	p.Ser1725X
CHC725T	ENSG00000189079	ARID2	12	g.46245893_46245894insGTTAGGTGAGATTGGA	c.3987_3988insGTTAGGTGAGATTGGA	p.Leu1330ValfsX3
CHC1044T	ENSG00000189079	ARID2	12	g.46231153C>G	c.1073C>G	p.Thr358Ser
CHC429T	ENSG00000189079	ARID2	12	g.46243361A>G	c.1716-2A>G	splicing
CHC205T	ENSG00000150394	CDH8	16	g.60412498G>C	c.856C>G	p.Pro286Ala
CHC429T	ENSG00000150394	CDH8	16	g.60412513A>G	c.841T>C	p.Tyr281His
CHC1199T	ENSG00000150394	CDH8	16	g.60318497A>C	c.1536+2T>G	splicing
CHC339T	ENSG00000168310	IRF2	4	g.185329422_185329435del	c.412-6_419del	deletion
CHC398T	ENSG00000168310	IRF2	4	g.185339323T>G	c.409A>C	p.Lys137Gln
CHC059T	ENSG00000134352	IL6ST	5	g.55260053_55260055del	c.577_579del	p.Asn193del
CHC469T	ENSG00000134352	IL6ST	5	g.55260061_55260075del	c.557_571del	p.Tyr186_Tyr190del
CHC205T	ENSG00000101292	PROKR2	20	g.5294732A>G	c.284T>C	p.Leu95Pro
CHC429T	ENSG00000101292	PROKR2	20	g.5283292del	c.549del	p.Ile184LeufsX56
CHC037T	ENSG00000133703	KRAS	12	g.25380275T>A	c.183A>T	p.Gln61His
CHC339T	ENSG00000133703	KRAS	12	g.25398285C>T	c.34G>A	p.Gly12Ser
CHC137T	ENSG00000134982	APC	5	g.112175957dup	c.4666dup	p.Thr1556AsnfsX3
CHC205T	ENSG00000134982	APC	5	g.112176007dup	c.4716dup	p.Glu1573X
CHC235T	ENSG00000121879	PIK3CA	3	g.178952085A>G	c.3140A>G	p.His1047Arg
CHC438T	ENSG00000121879	PIK3CA	3	g.178952085A>T	c.3140A>T	p.His1047Leu
CHC469T	ENSG00000147889	CDKN2A	9	g.21971096C>A	c.262G>T	p.Glu88X

Supplementary Table 8: Pathway significantly enriched in the 1150 genes altered by either mutation or homozygous deletion

Pathway Names	p-values	FDR p-values
Phosphatidylinositol signaling system	0.001	0.01
Wnt signaling pathway	0.001	0.01
Long-term potentiation	0.001	0.01
Axon guidance	0.003	0.02
Focal adhesion	0.004	0.02
Cell cycle	0.005	0.02
Complement and coagulation cascades	0.005	0.03
p53 signaling pathway	0.02	0.06
Gap junction	0.02	0.06
ECM-receptor interaction	0.02	0.07
MAPK signaling pathway	0.02	0.07
Apoptosis	0.03	0.09
Adherens junction	0.03	0.1
B cell receptor signaling pathway	0.03	0.1
Insulin signaling pathway	0.03	0.1
Ubiquitin mediated proteolysis	0.03	0.1