Supplementary Table 3. Continued

Gene	Reference position	Chromosome	Coding sequence	Coverage	Allele change	Amino acid change	Functional predictions by SIFT	Patient no.
TBC1D3B	2384202011	17	5	27	C < T	NS	D	4
TBC1D3E	2384401830	17	9	36	A < T	NS	D	4
TBC1D3D	2385938140	17	2	61	A < G	NS	N	4
TBC1D3D	2385940014	17	4	85	C < A	NS	N	4
TBC1D3D	2385940944	17	6	147	G < A	NS	N	4
ERBB2	2387531879	17	17	51	A < G	NS	N	4
TOP2A	2388219990	17	9	19	T < C	S	N	3
KRT25	2388559828	17	4	159	G < A	S	N	2
KRT26	2388580603	17	1	18	A < T	S	N	3
KRT40	2388787496	17	6	48	A < G	S	N	4
KRTAP3-2	2388808375	17	1	95	T < C	NS	N	4
KRTAP1-1	2388849768	17	1	37	G < C	NS	D	4
KRTAP4-1	2388993082	17	2	33	G < C	NS	N	4
KRTAP4-1	2388993086	17	2	30	A < G	S	N	4
KRTAP9-4	2389058283	17	1	217	C < T	NS	D	4
KRTAP9-4	2389058336	17	1	39	A < C	NS	N	3
KRTAP9-9	2389063986	17	1	44	A < C	NS	N	4
TUBG1	2390418855	17	10	14	C < A	S	N	1
BRCA1	2390878791	17	13	31	C < T	NS	NO	3
NAGS	2391737375	17	6	45	G < A	NS	N	3
CDK5RAP3	2395703185	17	3	61	T < G	NS	D	2
FAM117A	2397445898	17	7	17	G < A	S	N	3
ITGA3	2397801147	17	6	33	T < C	S	N	4
NOG	2404324293	17	1	67	A < C	NS	N	3
MTMR4	2406238200	17	6	13	A < T	NS	NO	3
CSH2	2411602334	17	4	55	C < T	NS	N	4
GH2	2411610386	17	4	18	G < C	NS	N	1
TEX2	2411943294	17	1	21	A < T	NS	D	3
COG1	2420849730	17	7	78	C < T	S	N	4
GPR142[a]	2422019077	17	3	57	A < G	NS	D	1
UNK	2423468317	17	14	19	A < G	S	N	4
QRICH2	2423941144	17	4	44	T < G	NS	N	4
HRNBP3	2426764023	17	1	22	G < A	S	N	4
CBX4	2427461157	17	5	66	C < T	NS	N	2
RNF213	2427979649	17	9	73	G < A	S	N	4
MYL12A	2434375274	18	1	40	G < A	NS	N	3
MYL12A	2434375275	18	1	41	A < T	NS	D	3
AMAC1L1	2442732047	18	1	22	G < A	S	N	2
C18orf1	2444767403	18	5	65	A < G	S	D	3
LOC729774	2445483471	18	2	38	G < T	NS	NR	3
POTEC	2445664872	18	1	68	T < C	NS	N	2
CTAGE1	2448017831	18	1	35	C < T	NS	N	1
KCTD1	2452149054	18	1	18	T < G	NS	N	3
DSG4	2457014977	18	15	41	G < T	NS	NO	3
FAM59A	2457889818	18	4	30	G < T	S	N	3
FAM59A	2457889821	18	4	29	A < C	NS	D	3
MOCOS	2461870479	18	15	143	T < C	NS	N	4
SLC14A2	2471234230	18	4	39	G < A	NS	N	3
KIAA1632	2471505962	18	25	17	A < T	NS	N	3
KIAA1632	2471505963	18	25	17	A < T	NS	NO	3
FUSSEL18	2472796815	18	1	35	A < T	NS	D	1
ZBTB7C	2473578004	18	2	78	T < G	NS	D	4
ZBTB7C	2473588900	18	1	208	T < C	S	N	4
KIAA0427	2474259908	18	6	22	T < A	NS	N	3
CXXC1	2475832249	18	10	67	A < G	S	N	4
TCF4	2480799098	18	12	33	C < A	NS	D	3
TCF4	2481003232	18	3	19	C < A	S	N	3
CCBE1	2485008619	18	4	99	C < T	S	N	2
NETO1[a]	2498404004	18	3	115	A < T	NS	D	1
C19orf6	2506845912	19	4	13	T < G	NS	D	1

Supplementary Table 3. Continued

Gene	Reference position	Chromosome	Coding sequence	Coverage	Allele change	Amino acid change	Functional predictions by SIFT	Patient no.
ABCA7	2506887468	19	25	15	A < G	S	N	4
REXO1	2507659336	19	3	14	C < T	S	N	4
FAM108A1	2507714358	19	2	13	T < C	NS	N	4
PIP5K1C	2509476658	19	13	27	G < A	NS	N	3
MAP2K2	2509934448	19	6	47	C < T	NS	D	4
ACER1	2512145698	19	3	26	T < C	NS	N	4
LASS4	2514105354	19	7	55	T < C	S	N	4
MUC16	2514735984	19	51	113	T < C	NS	N	4
MUC16	2514735995	19	51	104	C < T	NS	N	4
MUC16	2514783318	19	5	66	C < T	NS	N	4
MUC16	2514793493	19	3	59	C < T	NS	N	4
MUC16	2514797580	19	3	46	T < C	S	N	3
ICAM3	2516182922	19	2	22	T < C	NS	N	4
MAST1	2518717997	19	26	18	G < A	S	N	3
CYP4F12	2521526643	19	5	51	T < C	NS	N	4
OR10H2	2521572582	19	1	89	C < T	S	N	4
AP1M1	2522077812	19	11	81	C < G	NS	D	3
CPAMD8	2522819358	19	17	55	G < A	NS	N	3
KIAA1683	2524110904	19	2	62	C < G	NS	N	4
ISYNA1	2524280086	19	7	57	T < C	S	N	4
KIAA0892	2525185534	19	7	61	G < A	S	N	3
ZNF536	2533672403	19	3	28	T < C	S	N	4
GPI	2537503303	19	7	71	C < G	S	N	4
CD22	2538462717	19	5	17	C < G	S	N	3
C19orf15	2541461368	19	1	88	T < C	NS	N	4
MAP4K1	2541732174	19	14	25	G < A	NS	N	4
CAPN12	2541857821	19	18	71	A < G	S	N	4
LGALS4[a]	2541932950	19	3	30	C < A	NS	D	1
ECH1	2541939937	19	9	29	C < T	NS	D	4
PLEKHG2	2542544839	19	12	22	C < T	S	N	3
FCGBP	2543017507	19	21	76	G < A	S	N	4
FCGBP	2543053201	19	6	13	G < T	S	N	1
SNRPA	2543896811	19	2	60	A < G	S	N	4
CYP2F1	2544255597	19	1	31	G < A	S	N	4
ERF	2545386691	19	4	32	G < A	S	N	4
PSG3	2545867483	19	4	156	C < A	S	N	4
PSG8	2545901763	19	2	60	C < A	NS	D	3
CEACAM20	2547650657	19	7	58	T < C	NS	NR	4
ERCC2	2548501717	19	6	71	T < G	S	N	4
EMP3	2551464282	19	2	40	G < T	NS	NO	1
TMEM143	2551479358	19	6	19	A < C	NS	D	3
PTH2	2552559200	19	2	22	G < C	NS	N	3
SHANK1	2553853011	19	2	18	T < C	NS	N	1
ZNF808[a]	2555691982	19	3	39	G < A	NS	N	1
ZNF765	2556544681	19	3	19	C < G	NS	N	1
ZNF765	2556544684	19	3	19	T < C	S	N	1
ZNF761	2556586232	19	2	16	G < A	S	NR	4
LILRB3[a]	2557359732	19	3	208	G < C	NS	N	2
LILRA1	2557740721	19	5	61	T < C	NS	N	2
KIR2DL4	2557949666	19	3	17	C < G	NS	N	3
KIR3DL1	2557963191	19	3	109	A < G	S	N	4
KIR2DS4	2557982650	19	3	37	T < G	S	NR	2
KIR2DS4	2557982701	19	3	36	G < T	NS	NR	2
KIR2DS4	2557982728	19	3	21	G < C	NS	NR	2
RDH13	2558201492	19	1	28	C < T	NS	N	4
RDH13	2558201493	19	1	29	G < T	NS	N	4
ZFP28	2559692350	19	3	33	C < A	S	N	3
ZNF550[a]	2560701027	19	1	67	C < T	NS	D	1
ZSCAN22	2561483213	19	2	17	T < G	NS	N	3
KIR2DS1	2561871082	19	3	153	A < G	S	NR	2

Supplementary Table 3. Continued

Gene	Reference position	Chromosome	Coding sequence	Coverage	Allele change	Amino acid change	Functional predictions by SIFT	Patient no.
SIGLEC1	2565630685	20	3	19	C < T	NS	N	4
PAK7	2571487871	20	4	131	C < T	NS	N	4
FLRT3	2576252200	20	1	17	T < G	NS	D	3
CST9L	2585490888	20	2	216	T < G	NS	N	4
BPI	2595650275	20	11	148	A < G	NS	N	4
LBP	2595672219	20	2	23	G < A	S	N	4
LBP[a]	2595691968	20	10	25	G < T	S	N	1
KIAA1219	2595847726	20	10	14	T < G	NS	D	3
PTPRT	2599404902	20	31	37	C < A	NS	D	3
SEMG2	2602544774	20	2	42	A < G	S	N	4
ZNF335	2603273210	20	21	32	A < G	S	N	4
PCK1	2614832083	20	3	52	A < G	S	N	4
CTSZ	2616266012	20	5	51	A < G	S	N	4
OGFR	2620085220	20	4	20	G < A	S	N	4
KCNQ2	2620689776	20	14	14	C < G	NS	N	4
LOC100132288	2622007697	21	2	24	C < T	NS	NR	4
LOC100288017	2623267208	21	1	18	G < A	NS	NR	2
POTED	2623681322	21	1	60	G < A	NS	N	2
KRTAP13-2	2640442822	21	1	81	A < T	NS	D	3
C21orf66	2642816546	21	12	14	A < C	NS	N	1
C21orf66	2642816547	21	12	14	C < T	NS	N	1
WRB	2649461227	21	2	73	G < T	NS	NO	4
WRB	2649461228	21	2	73	A < T	NS	D	4
DSCAM	2650145634	21	27	116	G < C	S	N	4
PRDM15	2651870131	21	31	65	G < A	S	N	4
PFKL	2654380692	21	4	19	C < T	S	N	4
KRTAP10-6	2654660390	21	1	137	G < A	S	N	4
KRTAP12-2	2654734983	21	1	59	C < T	NS	N	4
KRTAP12-2	2654735333	21	1	71	G < A	S	N	4
KRTAP12-2	2654735334	21	1	69	C < T	NS	N	4
COL6A2	2656200935	21	27	63	C < G	S	N	3
FTCD	2656222648	21	2	55	T < A	NS	D	2
CECR5	2658218162	22	6	14	T < G	NS	D	3
CECR2	2658624712	22	16	25	C < T	S	N	4
LOC100288065	2658662354	22	4	63	A < G	NS	N	4
TBX1	2660347982	22	4	51	C < T	S	N	4
ZNF280B[a]	2663338671	22	1	78	G < A	S	N	2
C22orf30	2672604693	22	3	17	C < T	NS	NO	3
ISX	2675974809	22	2	60	G < A	S	N	1
HMGXB4	2676157665	22	4	42	A < T	S	N	3
APOL1	2677147183	22	2	27	C < T	NS	N	1
TMPRSS6	2677959079	22	17	144	G < A	S	N	4
TMPRSS6	2677959089	22	17	133	A < G	NS	N	4
SSTR3	2678099174	22	1	18	G < A	S	N	4
APOBEC3A	2679853734	22	3	53	C < T	S	N	4
L3MBTL2	2682109341	22	5	24	C < T	S	N	4
NAGA	2682959967	22	3	46	C < T	S	N	4
TTLL12	2684071796	22	5	53	C < T	S	N	3
SCUBE1	2684110469	22	15	48	C < G	S	N	4
LOC100289317	2686220100	22	1	25	A < G	NS	NR	4
CELSR1	2687425845	22	1	58	A < G	NS	N	4
MAPK8IP2	2691494874	22	11	52	G < A	NS	N	4
CD99	2693971425	X	6	16	G < A	NS	D	4
PRKX	2694923444	X	2	88	G < A	S	N	4
ARHGAP6[a]	2702537703	X	4	81	G < A	NS	D	2
DMD	2723711682	X	37	92	T < C	NS	N	4
WAS	2739828502	X	11	13	G < T	NS	N	3
GATA1	2739931290	X	2	14	A < C	NS	N	3
GAGE12E	2740547782	X	1	62	G < T	NS	D	4
PAGE1[a]	2740686656	X	3	37	T < C	S	N	1

Supplementary Table 3. Continued

Gene	Reference position	Chromosome	Coding sequence	Coverage	Allele change	Amino acid change	Functional predictions by SIFT	Patient no.
USP27X	2740875896	X	1	39	G < C	NS	NR	3
TSPYL2	2744246047	X	6	76	A < G	NS	N	3
FAM120C	2745238526	X	14	66	C < A	NS	D	2
ITIH5L	2745914425	X	8	22	G < A	NS	N	3
MSN	2752987418	X	9	47	G < A	S	N	2
OPHN1	2755314567	X	20	47	T < C	NS	N	3
DGAT2L6	2757452592	X	5	20	C < T	S	N	3
LPAR4	2765991350	X	1	46	G < T	NS	D	3
LPAR4	2765991352	X	1	43	C < T	S	N	3
PCDH11X	2779854213	X	7	171	C < A	NS	N	3
SYTL4	2787924130	X	9	24	G < A	S	N	3
SYTL4	2787924131	X	9	24	T < C	NS	D	3
NXF5	2789077402	X	3	81	T < C	NS	D	1
NXF2	2789554971	X	10	19	C < T	S	N	3
CLDN2	2794152808	X	1	26	C < A	NS	N	3
CLDN2	2794152809	X	1	26	C < T	NS	N	3
TRPC5	2799176319	X	1	24	G < A	NS	D	3
TRPC5	2799176320	X	1	24	G < T	NS	N	3
RHOXF2B	2807087244	X	4	29	A < G	NS	N	3
PLAC1	2821580905	X	1	20	A < G	NS	N	3
RBMX	2823837181	X	8	40	G < C	NS	D	4
SLITRK4	2830598721	X	1	56	T < C	NS	N	3
NSDHL	2839816887	X	6	109	A < G	NS	D	3
MPP1	2841799005	X	5	36	T < C	S	N	3
MPP1	2841799006	X	5	36	T < C	NS	N	3
RBMY1D	2863471281	Y	11	23	T < C	S	N	1

SIFT, Sorting Intolerant From Tolerant; N, nonsynonymous mutation; D, deleterious; N, neutral; S, synonymous mutation; NO, nonsense mutation; NR, no record found.

[a]These genes were commonly mutated in the synchronously developed HCCs from patients 1 and 2.

Supplementary Table 4. Functional Relevance of Mutations Detected in HCC Tumors

Patient 1					
HCC 1	No. of mutated genes	51			
	Amino acid change (+)	38 (74.5%)			
	Functional loss[a] (+)	20 (39.2%)			
	KEGG pathway				
	Pathways in cancer	CTNNB1	PDGFRB	TP53	
	Wnt signaling pathway	FBXW11			
	PI3K-Akt signaling pathway	ITGB8			
	Others	ALDH1A1	HDAC9	SORBS2	RYR3
HCC 2	No. of mutated genes	79			
	Amino acid change (+)	58 (73.4%)			
	Functional loss[a] (+)	23 (29.1%)			
	KEGG pathway				
	Viral carcinogenesis	HDAC9	RB1	TP53	
	Wnt signaling pathway	FBXW11			
	PI3K-Akt signaling pathway	ITGB8			
	Others	ALDH1A1	NXF5		
Patient 2					
HCC 1	No. of mutated genes	39			
	Amino acid change (+)	20 (51.3%)			
	Functional loss[a] (+)	10 (25.6%)			
	KEGG pathway				
	Metabolic pathways	DBH			
	Others	AGRN			
HCC 2	No. of mutated genes	70			
	Amino acid change (+)	40 (57.1%)			
	Functional loss[a] (+)	20 (28.6%)			
	KEGG pathway				
	Metabolic pathways	ADSSL1	FTCD	RDH16	
	Others	ABCA13	BTRC	VWF	C4A
		GRM4			
Patient 3					
HCC 1	No. of mutated genes	30			
	Amino acid change (+)	20 (66.7%)			
	Functional loss[a] (+)	6 (20.0%)			
	KEGG pathway				
	Metabolic pathways	CYP1A2			
HCC 2	No. of mutated genes	276			
	Amino acid change (+)	208 (75.3%)			
	Functional loss[a] (+)	90 (32.6%)			
	KEGG pathway				
	Metabolic pathways	ACSM4	ADSS	UGT2B28	DHRS4L2
		GALNT5	ME1	POLE	NSDHL
		PIK3C2G			
	PI3K-Akt signaling pathway	COL6A6	HGF	ANGPT1	LPAR4
	Neuroactive ligand receptor	GLRA2			
	Others	CDK9	CA2	ABCC12	AP1M1
		GNPAT	GLYAT	RUVBL1	GDF9
		MYL12A	MLL3	SLC18A2	MAP4K4
		PRPF8	PIP4K2A	SLC9A4	NUP37
		VCP	TTN		

Supplementary Table 4. Continued

Patient 4					
HCC	No. of mutated genes	364			
	Amino acid change (+)	177 (48.6%)			
	Functional loss[a] (+)	46 (12.6%)			
	KEGG pathway				
	Metabolic pathways	ACSM5	ALPP	PNLIPRP1	
	MAPK signaling pathway	HSPA6	MAP2K2		
	PI3K-Akt signaling pathway	FLT4			
	Others	ECH1	CHI3L1	FURIN	CD99
		KCNJ12	ITGAE	TMPRSS4	REXO1L1
		RBMX	PLOD3	TUBA4A	PGA3

[a]The number of mutated genes predicted to be "damaging (deleterious)" by Sorting Intolerant From Tolerant (SIFT) functional impact predictions (http://provean.jcvi.org/index.php). The genes categorized in multiple pathways are shown in only one representative pathway.

Supplementary Table 5. List of 448 Indels in 409 Genes at a Frequency of >20% of Reads in 7 HCC Tumors From 4 Patients

Reference position	Gene	Chromosome	Coding sequence	Coverage	Allele change	Patient no.
7813482	ERRFI1	1	3	17	insA	3
12628605[a]	PRAMEF11	1	3	27	insC	2
12718307	PRAMEF7	1	2	47	insT	3
17358674[a]	PADI6	1	9	41	delG	4
17358674[a]	PADI6	1	9	62	delGT	2
26696284	ARID1A	1	2	19	delC	4
31395890[a]	SERINC2	1	9	17	insG	3
46770747	CYP4B1	1	8	42	delAT	4
46770748	CYP4B1	1	8	42	delT	4
52949277[a]	LOC100133211	1	1	42	delG	4
53189215	MAGOH	1	3	25	insA	3
54095320[a]	CDCP2	1	4	21	insC	4
62557547	ANGPTL3	1	4	17	insT	3
78876012	ELTD1	1	10	13	insA	3
89014597	GBP1	1	4	17	insA	2
90670304	BARHL2	1	2	20	insC	3
108974106	CLCC1	1	6	84	insG	4
122705624[a]	PDE4DIP	1	14	80	delG	4
122713730[a]	PDE4DIP	1	6	465	delT	1
131401399	DENND4B	1	12	43	insG	3
131474740	NUP210L	1	34	13	insG	3
131951749	SHE	1	3	112	insA	2
133072970	MSTO1	1	11	33	insA	3
133795656	CCT3	1	2	34	insT	3
133844355[a]	RHBG	1	9	40	delC	4
134043234[a]	TTC24	1	3	12	delC	3
136505109	IFI16	1	7	31	insT	3
146999551	F5	1	13	23	insT	3
151907797	GPR52	1	1	18	insA	2
162596811	C1orf25	1	10	26	insT	3
163815430	TPR	1	15	43	delT	3
174374155	CFHR4	1	5	18	insC	3
177507300	NR5A2	1	5	20	insT	3
201685738	NVL	1	6	32	insA	3
203543660	ACBD3	1	2	18	insG	3
208315870[a]	ARV1	1	3	146	delCT	1
208315871[a]	ARV1	1	3	144	delT	1
213162772	LYST	1	3	19	insG	3
214770350	RYR2	1	11	22	insG	3
219641707	PLD5	1	2	102	insA	1
224245114	AHCTF1	1	14	19	insG	3
230467928	RNASEH1	2	8	13	insT	3
236404886	ADAM17	2	19	29	insG	3
251086730[a]	LOC375190	2	8	40	insC	4
254371933	IFT172	2	38	18	insT	3
258505433[a]	SRD5A2	2	1	28	insG	2
267355164	SLC8A1	2	1	15	insG	3
282849120	EFEMP1	2	1	14	insA	3
287714203	PAPOLG	2	15	20	delT	3
288274645	USP34	2	15	14	insC	3
301408194	CCDC142	2	2	27	insC	3
302628924	C2orf3	2	3	22	insA	3
312276713	RETSAT	2	4	55	delC	2
314781292	RGPD2	2	5	27	insT	3
317672121[a]	LOC391405	2	4	43	delA	4
318709414	TRIM43	2	1	22	insA	3
325574912	SLC9A4	2	6	27	insT	3
329490991	RGPD3	2	20	29	insT	3
331565693	GCC2	2	22	18	insC	2
332910299	RGPD5	2	21	25	insA	3
333616906	RGPD7	2	8	21	delA	3

Supplementary Table 5. Continued

Reference position	Gene	Chromosome	Coding sequence	Coverage	Allele change	Patient no.
335725611	SLC20A1	2	8	14	insC	3
336700192	RABL2A	2	4	76	delG	1
340887331	DDX18	2	7	18	insT	3
350555029	IWS1	2	11	62	delG	3
355383031[a]	ZNF806	2	3	50	delC	4
355383457[a]	ZNF806	2	3	56	insA	4
355383669[a]	ZNF806	2	3	52	delA	4
361736116	NXPH2	2	2	48	insT	3
385464478	KCNH7	2	10	41	insT	3
387807820	COBLL1	2	2	23	insA	3
388452944	SCN2A	2	26	57	insT	3
400689016	TTC30A	2	1	32	insA	3
401650351	TTN	2	270	19	insG	3
401670059	TTN	2	242	25	insT	3
401800064	TTN	2	64	26	insA	3
402189048	SESTD1	2	14	31	insG	3
403038177	CWC22	2	11	16	insA	3
418958541	DNAH7	2	34	27	insC	3
439213578	XRCC5	2	13	22	delC	3
446013793	ACSL3	2	14	26	insT	3
446670417	SCG2	2	1	17	insA	3
446671148	SCG2	2	1	30	insC	3
456401277[a]	SAG	2	10	76	delA	2
463724350	AQP12B	2	1	26	delC	2
479793553[a]	GRIP2	3	10	55	insG	4
504388108	TTC21A	3	6	13	insA	3
509772719	ZNF852	3	3	20	delTC	4
509772720	ZNF852	3	3	19	delC	4
511646368	CCR5	3	1	24	insT	3
515483759[a]	SLC38A3	3	2	18	insG	4
538148646	GLT8D4	3	6	14	insC	3
538243406[a]	FLJ10213	3	1	12	insA	2
538564462	PDZRN3	3	10	24	insG	3
540846731[a]	LOC100288801	3	2	39	delG	2
540918687	ZNF717	3	4	18	delC	1
570208682	HHLA2	3	4	18	insT	3
570487430	DZIP3	3	10	45	insT	3
574780156	CD200R1	3	4	24	insA	3
587083495	ZNF148	3	6	14	insG	3
591946859[a]	LOC644974	3	6	36	delC	3
595459401	TOPBP1	3	26	16	insT	3
608303870	PLSCR2	3	4	59	insG	3
611616867	C3orf16	3	5	22	delCT	3
611616868	C3orf16	3	5	21	delT	3
612474548	SELT	3	4	38	insT	4
631967149	PHC3	3	10	13	insT	3
648156647	DGKG	3	2	44	insC	3
652237997[a]	CLDN16	3	1	271	delG	2
658673909	PAK2	3	12	16	insT	3
660166378	ZNF595	4	4	17	insA	1
662098266[a]	POLN	4	23	65	delG	3
696277331	FLJ16686	4	3	53	delC	1
725715810	TMPRSS11F	4	7	30	insA	3
728128121	LOC100129410	4	3	13	insC	2
752860649	UNC5C	4	14	17	insT	3
767688857[a]	EGF	4	24	16	insC	1
779934903	KIAA1109	4	39	17	insT	3
782346647	ANKRD50	4	3	37	insT	3
827268418	NEK1	4	4	17	insT	3
841124368	CDKN2AIP	4	3	16	insA	3
853638502	KIAA0947	5	14	24	insT	3

Supplementary Table 5. Continued

Reference position	Gene	Chromosome	Coding sequence	Coverage	Allele change	Patient no.
889026155[a]	CARD6	5	3	32	insT	2
891727995	PAIP1	5	2	16	insG	2
901348948	MAP3K1	5	13	24	insC	3
909928153	ADAMTS6	5	3	23	insG	3
914509435	SERF1B	5	3	15	insG	3
914509482	SERF1B	5	3	49	insA	3
915509411[a]	GTF2H2	5	13	31	insT	2
919186632	HEXB	5	11	43	insA	3
922917852	SCAMP1	5	7	37	insA	1
928534269	EDIL3	5	7	25	insA	3
931867232	CCNH	5	7	26	insT	3
956697390	EPB41L4A	5	11	13	insT	1
966610635	ZNF474	5	1	39	delT	1
972596345	SLC12A2	5	8	35	insT	3
980635083[a]	SMAD5	5	6	105	insC	1
985314450[a]	LOC100288105	5	1	14	delC	4
985640033[a]	PCDHB9	5	1	32	insA	1
985844899[a]	PCDHGA8	5	1	27	delC	3
992330379	SCGB3A2	5	1	14	delA	3
994446878[a]	TIGD6	5	1	136	delT	1
994476149	HMGXB3	5	6	14	delA	3
998157358	GRIA1	5	11	19	insC	3
1020539380	FAM153B	5	4	23	insC	3
1039337531	C6orf114	6	1	30	insA	3
1052252527	BTN2A2	6	2	44	insG	3
1054107191[a]	ZNF187	6	1	33	insG	4
1056096293[a]	FLJ45422	6	2	18	insT	2
1057247419[a]	MICA	6	5	27	delG	3
1082305754	DST	6	45	18	insT	3
1088830738	EYS	6	6	19	insT	3
1093406718	COL19A1	6	5	16	insA	3
1113248546	MDN1	6	15	14	insC	3
1113280524	MDN1	6	2	40	insA	3
1131602437[a]	FOXO3	6	2	64	insG	3
1133380782	SLC22A16	6	4	20	insA	3
1135037748	C6orf225	6	1	17	delC	3
1153093327	SAMD3	6	7	14	delC	3
1154647636	LOC643854	6	1	26	insT	3
1154648098	LOC643854	6	1	20	insC	3
1159216432	BCLAF1	6	2	13	delT	2
1161156444	PBOV1	6	1	36	insG	3
1182019086	RSPH3	6	6	43	insA	3
1200500350	RSPH10B2	7	19	23	insG	3
1206053594	VWDE	7	19	26	insA	4
1221518316	TAX1BP1	7	13	14	insA	3
1222659823[a]	KIAA0644	7	1	90	delC	4
1222659922[a]	KIAA0644	7	1	26	insC	3
1226974977	BBS9	7	7	19	insT	1
1228643735[a]	DPY19L1	7	18	22	delAT	4
1228643736[a]	DPY19L1	7	18	50	delT	1
1262731853	TYW1B	7	8	142	delA	4
1262954278	TRIM74	7	2	24	insA	2
1265555276	TRIM73	7	2	84	insT	2
1266437261[a]	FLJ37078	7	14	43	insC	2
1266593512[a]	ZP3	7	8	51	insG	1
1266763110[a]	POMZP3	7	5	83	delA	4
1278946055	C7orf62	7	1	20	insC	3
1283360469	HEPACAM2	7	4	29	insT	3
1283589759	CALCR	7	9	26	insT	3
1290893801[a]	ZAN	7	30	28	insG	3
1291366094	MOGAT3	7	2	24	insA	3

Supplementary Table 5. Continued

Reference position	Gene	Chromosome	Coding sequence	Coverage	Allele change	Patient no.
1291722996[a]	EMID2	7	13	20	insG	4
1292538685	LOC100289561	7	1	14	insA	3
1295252926	MLL5	7	12	21	insG	3
1298402792	NRCAM	7	1	17	insT	3
1319055841[a]	KCP	7	10	62	insC	1
1319073009	KCP	7	1	30	delC	2
1333766379	LOC441294	7	1	46	insA	4
1334380185	CTAGE4	7	1	39	insA	3
1334381975	ARHGEF5L	7	1	19	insA	1
1339923632[a]	KRBA1	7	12	76	insC	2
1339973995[a]	SSPO	7	9	44	insC	1
1340003537[a]	SSPO	7	60	15	insC	4
1340012514	SSPO	7	76	23	delA	2
1340015859	SSPO	7	83	14	delC	2
1340525483	C7orf29	7	1	24	delC	1
1341211228[a]	ATG9B	7	10	49	insC	1
1341434558	SMARCD3	7	10	21	delC	3
1342197228	GALNTL5	7	5	71	delT	4
1342442397[a]	MLL3	7	14	208	insT	4
1356372261[a]	XKR5	8	6	55	delAG	1
1374409954[a]	NEFL	8	3	38	delG	4
1380219728[a]	UBXN8	8	7	83	insT	1
1380304215	TEX15	8	1	23	insA	3
1388426070[a]	PLEKHA2	8	11	28	delC	2
1395399601[a]	PRKDC	8	31	17	insG	1
1398930064	PXDNL	8	14	27	insA	3
1410692513[a]	YTHDF3	8	4	24	insG	1
1415952398	C8orf34	8	2	32	insG	3
1445261384	LAPTM4B	8	2	16	insC	3
1490189877[a]	JRK	8	1	12	delCA	3
1490189878[a]	JRK	8	1	19	delA	2
1491176363	ZNF623	8	1	29	insT	3
1492082552[a]	RECQL4	8	14	20	delG	3
1498992866	LOC645969	9	1	155	insT	4
1527437913[a]	C9orf144B	9	4	20	delC	4
1543290663[a]	FOXD4L5	9	1	39	delG	1
1546032104	TRPM3	9	22	19	insT	3
1552818643	VPS13A	9	48	29	insG	3
1574648314	COL15A1	9	13	29	insC	3
1586295095	MUSK	9	1	62	insT	3
1608846803[a]	ABO	9	6	117	insC	4
1620006324	GDI2	10	7	14	insG	3
1620254092	IL2RA	10	4	14	insC	3
1621795546[a]	ITIH5	10	14	23	delC	1
1633127998	NSUN6	10	2	26	insA	3
1647389817	ITGB1	10	13	22	insA	3
1652560241[a]	LOC340947	10	2	25	delT	1
1653671683[a]	LOC642424	10	3	117	delT	1
1657313101	AGAP4	10	7	23	delT	2
1658942495	FAM25G	10	3	48	insC	3
1662197526	LOC100287932	10	6	22	insA	4
1662338998[a]	AGAP6	10	1	50	insC	2
1666373362	PCDH15	10	19	56	insC	3
1673760921	TMEM26	10	6	25	insT	3
1685560504	FAM149B1	10	7	26	insT	3
1701949711	PANK1	10	3	30	insA	3
1708407108	CCNJ	10	3	18	insC	3
1708510568	ZNF518A	10	1	30	insC	1
1708668598	DNTT	10	2	18	insA	3
1709332414	C10orf12	10	1	18	insG	3
1728973932[a]	PNLIPRP2	10	3	52	insG	1