

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 <sup>q</sup>	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 <sup>q</sup>	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 <sup>q</sup>	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 <sup>q</sup>	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 <sup>q</sup>	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 <sup>q</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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
RBMX1D	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.

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

<sup>a</sup>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 <sup>a</sup>	PRAMEF11	1	3	27	insC	2
12718307	PRAMEF7	1	2	47	insT	3
17358674 <sup>a</sup>	PADI6	1	9	41	delG	4
17358674 <sup>a</sup>	PADI6	1	9	62	delGT	2
26696284	ARID1A	1	2	19	delC	4
31395890 <sup>a</sup>	SERINC2	1	9	17	insG	3
46770747	CYP4B1	1	8	42	delAT	4
46770748	CYP4B1	1	8	42	delT	4
52949277 <sup>a</sup>	LOC100133211	1	1	42	delG	4
53189215	MAGOH	1	3	25	insA	3
54095320 <sup>a</sup>	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 <sup>a</sup>	PDE4DIP	1	14	80	delG	4
122713730 <sup>a</sup>	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 <sup>a</sup>	RHBG	1	9	40	delC	4
134043234 <sup>a</sup>	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 <sup>a</sup>	ARV1	1	3	146	delCT	1
208315871 <sup>a</sup>	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 <sup>a</sup>	LOC375190	2	8	40	insC	4
254371933	IFT172	2	38	18	insT	3
258505433 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	ZNF806	2	3	50	delC	4
355383457 <sup>a</sup>	ZNF806	2	3	56	insA	4
355383669 <sup>a</sup>	ZNF806	2	3	52	delA	4
361736116	NXP2	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 <sup>a</sup>	SAG	2	10	76	delA	2
463724350	AQP12B	2	1	26	delC	2
479793553 <sup>a</sup>	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 <sup>a</sup>	SLC38A3	3	2	18	insG	4
538148646	GLT8D4	3	6	14	insC	3
538243406 <sup>a</sup>	FLJ10213	3	1	12	insA	2
538564462	PDZRN3	3	10	24	insG	3
540846731 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	CLDN16	3	1	271	delG	2
658673909	PAK2	3	12	16	insT	3
660166378	ZNF595	4	4	17	insA	1
662098266 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	SMAD5	5	6	105	insC	1
985314450 <sup>a</sup>	LOC100288105	5	1	14	delC	4
985640033 <sup>a</sup>	PCDHB9	5	1	32	insA	1
985844899 <sup>a</sup>	PCDHGA8	5	1	27	delC	3
992330379	SCGB3A2	5	1	14	delA	3
994446878 <sup>a</sup>	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 <sup>a</sup>	ZNF187	6	1	33	insG	4
1056096293 <sup>a</sup>	FLJ45422	6	2	18	insT	2
1057247419 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	KIAA0644	7	1	90	delC	4
1222659922 <sup>a</sup>	KIAA0644	7	1	26	insC	3
1226974977	BBS9	7	7	19	insT	1
1228643735 <sup>a</sup>	DPY19L1	7	18	22	delAT	4
1228643736 <sup>a</sup>	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 <sup>a</sup>	FLJ37078	7	14	43	insC	2
1266593512 <sup>a</sup>	ZP3	7	8	51	insG	1
1266763110 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	KRBA1	7	12	76	insC	2
1339973995 <sup>a</sup>	SSPO	7	9	44	insC	1
1340003537 <sup>a</sup>	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 <sup>a</sup>	ATG9B	7	10	49	insC	1
1341434558	SMARCD3	7	10	21	delC	3
1342197228	GALNTL5	7	5	71	delT	4
1342442397 <sup>a</sup>	MLL3	7	14	208	insT	4
1356372261 <sup>a</sup>	XKR5	8	6	55	delAG	1
1374409954 <sup>a</sup>	NEFL	8	3	38	delG	4
1380219728 <sup>a</sup>	UBXN8	8	7	83	insT	1
1380304215	TEX15	8	1	23	insA	3
1388426070 <sup>a</sup>	PLEKHA2	8	11	28	delC	2
1395399601 <sup>a</sup>	PRKDC	8	31	17	insG	1
1398930064	PXDNL	8	14	27	insA	3
1410692513 <sup>a</sup>	YTHDF3	8	4	24	insG	1
1415952398	C8orf34	8	2	32	insG	3
1445261384	LAPTM4B	8	2	16	insC	3
1490189877 <sup>a</sup>	JRK	8	1	12	delCA	3
1490189878 <sup>a</sup>	JRK	8	1	19	delA	2
1491176363	ZNF623	8	1	29	insT	3
1492082552 <sup>a</sup>	RECQL4	8	14	20	delG	3
1498992866	LOC645969	9	1	155	insT	4
1527437913 <sup>a</sup>	C9orf144B	9	4	20	delC	4
1543290663 <sup>a</sup>	FOXDL5	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 <sup>a</sup>	ABO	9	6	117	insC	4
1620006324	GDI2	10	7	14	insG	3
1620254092	IL2RA	10	4	14	insC	3
1621795546 <sup>a</sup>	ITIH5	10	14	23	delC	1
1633127998	NSUN6	10	2	26	insA	3
1647389817	ITGB1	10	13	22	insA	3
1652560241 <sup>a</sup>	LOC340947	10	2	25	delT	1
1653671683 <sup>a</sup>	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 <sup>a</sup>	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 <sup>a</sup>	PNLIPRP2	10	3	52	insG	1