

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	Table S3: HBV DNA Integration Sites*																	
2	patient number	Group	Age	sequence no	clone no.	Clone size	Chrm	Chrm insert sites	gene symbol	insert lccation	Gene polarity	gene to left	distance to left hand gene	gene to left polarity	gene to right	distance to right hand gene	gene to right polarity	cell junction sequence (lower to higher sense)
3	1	1	15	4042	253	2035	X	89717084				CPXCR1	-962300	+	TGIF2LX	204856	+	AGCCATATTTCTGTTCTT--HBV
4	1	1	15	4050			3	150124112				TMEM18 3B	-140746	-	LINC0121 3	114406	+	GCCAGCAGGAGCTTTGCT--HBV
5	1	1	15	3209	185	23	12	102998812				ASCL1	-38296	+	C12orf42	238778	-	AAAATGTAACAAGAGTC--HBV
6	1	1	15	3186	182	282	22	20814502	PI4KA	intron	-							HBV--AGTTTTCGAAGGCTGAGG
7	1	1	15	3183	184	78	1	155314931	FDPS	intron	+							TGGTGGTGGCTGAAACAAGATTG TC-HBV
8	1	1	15	3203	181	165	2	196661734	CCDC15 0	intron	+							HBV--ATTGCCCTTAATAGTACTT
9	1	1	15	3202	183	165	4	6942259	TBC1D1 4	intron	+							ACTGAATTATTTTCATGCCTTC-- HBV
10	1	1	15	3188			7	156990872				NOM1	-17690	+	MXN1	13980	-	HBV-- nnGACTGTGTCTATCATTGGG
11	1	1	15	3191			6	142418190	ADGRG 6	intron	+							TAATCCCAGCTACTACTCn--HBV
12	1	1	15	3199			13	43244958	ENOX1	intron	-							within 130 nts to right if 43244958 HBV--
13	1	1	15	3208			6	114662146				HS3ST5	-599269	-	>1000000			GGTGGTTTAAGCAAATAAAT
14	1	1	15	3334	190	103	19	45113949	PPP1R3 7	intron	+							HBV--TGGCTCTGCTTCTCTTT
15	1	1	15	3337	188	732	2	187112119				ZSWIM2	-262949	-	CALCRL	229843	-	GCAGTTATGTATATGTTTCT--HBV
16	1	1	15	3368	189	1078		0										
17	1	1	15	3339	187	571	1	12184317	TNFRSF 1B	intron	+							HBV--TCATTGTTTAGCCATGAC HBV--
18	1	1	15	3338	186	1223	15	44884789				TRIM69	-117017	+	C15orf43 LINC0098 2	71903 88845	+	AAAAAAGGAAAAAAACTC ATTTGGAGT
19	2	1	17	3296	206	20	1	2970771				TTC34	-181180	-				GCTGATAACAGCCGGGC--HBV
20	2	1	17	3291	205	102	4	84240667	LOC101 928978	intron								HBV--nCCAAACATATAATTGGGAT
21	2	1	17	3274	204	275	1	84772117				SSX2IP	-81560	-	LPAR3	41285	-	CCCGTGTATCATCTAAGAGG-- HBV
22	2	1	17	3260				0										
23	2	1	17	3264			X	97542265	DIAPH2- AS1	intron	-							AGTCAGAAAGTCTTCnnnnnnnnnn nnnnnnnnnnnnnn--HBV
24	2	1	17	3272				0										
25	2	1	17	3276			12	99976747	ANKS1B	intron	-							TTAATAAGAAACATGAT--HBV
26	2	1	17	3278			4	176197346				SPATA4	-1675	-	ASB5	16328	-	TAAAGGGAAAAGTCAAAGTgnnnn nn--HBV
27	2	1	17	3283			3	147148414				PLSCR5	-542198	-	ZIC4	237633	-	GGCACATAGACCAATGGAA--HBV
28	2	1	17	3290				0										
29	2	1	17	3303	200	176	5	45712223				HCN1	-16105	-	>1000000			HBV--TGAATAATATGCTTGC

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
64	3	1	18	3828			11	77870013	AAMDC	intron	+							TACCTAACCC TGAGACA Gnnnnnnnnnnn--HBV
65	3	1	18	3826			X	47283158				USP11	-34830	+	ZNF157	87441	+	HBV--TTTCTGCACATTTGTGTCA
66	3	1	18	3780	223	3024		0										
67	3	1	18	3914	225	34	20	56183987				CBLN4	-178515	-	MC3R	64744	+	HBV-CAATTACCCAGTCTTA
68	3	1	18	3933	224	61	14	76815170				ANGEL1	-2230	-	LRRRC74A	11211	+	HBV--GTATAAACTCTCAATG
69	3	1	18	3940	226	286		0										
70	3	1	18	3913			12	43966271	TMEM11 7	intron	+							AAGAAGGGGATAAGAGn--HBV
71	3	1	18	3938			3	192177304	FGF12	intron	-							HBV--AGGCCTATAAAATTAT
72	3	1	18	3944			13	58018244				PCDH17	-289313	+	LOC1019 26897	147582		HBV--TGGTGACACATACCTGTAGT CTTGCTGACTGCACATATCACATG nn--HBV
73	4	1	18	3572	218	433	22	17962139	MICAL3	intron	-							HBV--GATAACCGACATATAC
74	4	1	18	3592	219	193	5	59451480	PDE4D	intron	-							
75	4	1	18	3567	217	611	2	233776390	MROH2 A	intron	+							HBV--CTGTTGCCAGGCTGGA
76	4	1	18	3566			11	17429330	ABCC8	intron	-							HBV--ATCCACCCTCAAGGCAA
77	4	1	18	3583			1	18438305				IGSF21	-59822	+	KLHDC7A	42624	+	HBV-- GGGCTCAAATCCCTGTTACACGC
78	4	1	18	3584			16	12584020				SNX29	-9731	+	CPPED1	75778	-	HBV-- nCTAAGTGTCCTCTGTGGT
79	4	1	18	3586			1	86733852	SH3GLB 1	intron	+							CTGTGGTGGGAGTATTATA--HBV
80	4	1	18	3588			2	82108916				LOC1005 07201	-641970	-	LOC1720	747886	+	HBV--AATTCTATTGGATTACCC
81	4	1	18	3394	194	103		0										
82	4	1	18	3385	191	102	10	53190646				MBL2	-418946	-	PCDH15	612124	-	TTTCAAAAATTAATTTTTTA--HBV
83	4	1	18	3397	192	433	9	92115984				SPTLC1	-510	-	LOC1001 28076	16849	+	within 40 nts to left of 92115984
84	4	1	18	3383				0										
85	4	1	18	3388			21	30829731	KRTAP7- 1	at beginnin g of exon	-							HBV-- TGTGAAGGGTAAGTTACCCA
86	4	1	18	3389			2	225661861				NYAP2	-7843	+	LOC6467 36	480932	+	HBV--TTACAGACATGCACCAC
87	4	1	18	3391				0										
88	4	1	18	3401				0										
89	4	1	18	3403			7	34592630	NPSR1- AS1	intron	-							within 40 nts to right of nt 34592630
90	4	1	18	3406			5	80192447	SERINC 5	intron	-							within 200 nts to right of nt 80192447
91	4	1	18	3408			8	37724134	LOC101 929622	intron	+							HBV-- ACTCCAGCCCTCTCTGAGC
92	4	1	18	3409				0										
93	4	1	18	3410			X	42702365				CASK	-779331	-	PPP1R2P 9	75000	-	GCTTTCTATATGTTGATGACTn-- HBV
94	4	1	18	3381			15	76549357	SCAPER	intron	-							HBV--CAAATGTCCAACAAT
95	4	1	18	3414	196	103	6	101585725	GRIK2	intron	+							GGAAAAAGGTGACACAT--HBV

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
132	5	1	22	3965	238	89	3	172866200				ECT2	-44726	+	SPATA16	23156	-	GCTTTTATAGTTGAGGCC--HBV TACCTGGGTTTGAACACTGTTnn-- HBV
133	5	1	22	3949	234	102	3	59285332				C3orf67	-543323	-	FHIT	463977	-	
134	5	1	22	3952	237	32	7	34326405				BMPER	-170533	+	NPSR1- AS1	20106	-	HBV--ATCCACAAAACACCTCC
135	5	1	22	3960	236	165	16	13311889				SHISA9	-76479	+	ERCC4	-610142	+	HBV--AAAATTAATGAACATAAAAT HBV-- AGCCCTGCAGGATTTTACAACC
136	5	1	22	3963			2	238285839	PER2	intron	-							
137	5	1	22	3967				0										
138	5	1	22	3972			5	122419019	SNCAIP LOC400 867	intron	+							within 30 nts to right of nt 122419019
139	5	1	22	3977			21	38923345		intron	-							TGTTTCTGAATTACATGTC--HBV GTACCTCTCGCTTACACACAC-- HBV
140	6	1	24	4330	240	89	19	7905028	MAP2K7	intron	+							
141	6	1	24	4316	241	103	2	6468883				LINC012 47	-93461	-	LINC0048 7	260284	-	AAACAACACAGCATTCTCTAAA-- HBV HBV-- CTGCCAAGGCTGGGCAGTCGTT CGATTTCCCTTTGTATTTTATnnnnnn nnnnnnnnn-HBV
142	6	1	24	4332	240	368	9	36836065	PAX5 RALGPS 1	intron	-							
143	6	1	24	4312			9	127214489		intron	+							
144	6	1	24	4321			1	96939372				PTBP2	-124323	+	DPYD	138371	-	within 700 nts to left of nt 96939372
145	6	1	24	4322			1	70708693	LOC101 927244	intron	+							GTCAGACAAGTAATGACTGnnnnn nnn--HBV
146	6	1	24	4325			4	178108873				LINC010 98	-118123	+	>1000000			CTGATTTAATAATGTATATnnnnnnnn nn--HBV
147	6	1	24	4327			2	117314398				>1000000 0			DDX18	500280	+	HBV--TAATTATAGCTTGTCTC
148	6	1	24	4331				0										
149	6	1	24	4265	244	34	4	177597656				AGA	-155153	-	LINC0109 8	131100	+	ACTTAGAAGCTTTACCTC--HBV TGTTACTAGAGTCCCTnnnnnnnn n--HBV
150	6	1	24	4267	244	34	4	6436575	PPP2R2 C	intron	-							
151	6	1	24	4282	244	23	18	35811667				GALNT1 LINC013 43	-99833	+	MIR187	93150	-	TTTATGTCCAACAGAC--HBV AAAAGAAAAAATAACTTAG-- HBV
152	6	1	24	4299	243	281	1	38590990				>1000000 0			RRAGC	260624	-	TTTGGCCATTACAGTATCAGC-- HBV
153	6	1	24	4286	242	1133	10	109779347							XPNPEP1	85418	-	
154	6	1	24	4288				0										
155	6	1	24	4291			3	197076755	DLG1	intron	-							GTACAAAGGCCAGCCTAGCA-- HBV
156	6	1	24	4293			10	37470521				LINC009 93	-123493	+	MTRNR2L 7	130916	-	HBV--AGGCAGGAGAATCGCTTGA TTTTTTGTGTTTTTAAAAAG C-- HBV
157	6	1	24	4248	246	36	15	96814536				SPATA8	-28921	+	LINC0092 3	928079	-	
158	6	1	24	4241	247	42	16	48633860				N4BP1	-23651	-	CBLN1	645543	-	HBV--TGGGTCCAGACCTTAAG HBV--ATCGCACCCTGCACTCC
159	6	1	24	4239	245	381	1	225490526	ENAH	intron	-							
160	6	1	24	4237			2	137801750				THSD7B	-124033	+	LOC1019 28273	77003	-	TTGAGATGTTTTTCAGACT--HBV TGTGTCTGTGTGACGAnnnn-- HBV
161	6	1	24	4238			10	20246294	PLXDC2	intron	+							

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
162	6	1	24	4240			X	42769983				CASK	-846949	-	PPP1R2P 9	7382	-	CACCTCCATAACATACTT--HBV
163	6	1	24	4244			13	109667013				MYO16	-460177	+	LINC0067 6	61260	+	CCCCCGCGTACAGGCACCCC-- HBV
164	6	1	24	4246			3	7363687	GRM7	intron	+							GGTCTCATCCAAT--HBV
165	6	1	24	4257				0										
166	6	1	24	4259			5	160337249	CCNJL	intron	-							GGTCTTGAACCTCTGGGCTG-- HBV
167	6	1	24	4262			X	7273398	STS	intron	+							HBV--CAAGTCATAGGACTGAAAA
168	7	1	28	3092	173	1078	16	10557512	EMP2	intron	-							HBV--nnAAAGTTTTTCTTGG
169	7	1	28	3088	169	1149	1	49161242	AGBL4	intron	-							HBV-- TCTGGAGCCGAGTACATGTTCC T
170	7	1	28	3093	168	2136	X	2621766	CD99P1	intron	-							HBV--TTATTGATTACTCATGTAC
171	7	1	28	3104	172	3730	7	84597817				LOC1019 27378	-13499	+	SEMA3D	397738	-	HBV--ACTATTCCACAATAGCAAAAG
172	7	1	28	3106	170	2919	1	28945637	EPB41	intron	+							AGTGTTTAATATCTGTT--HBV
173	7	1	28	3108	171	3583	4	60356734				>100000 0			MIR548A G1	565884	+	within 40 nts to left of nt 101626622
174	7	1	28	3085			1	101626622				LINC013 07	-249309	+	OLFM3	175944	-	ACACTGCTTCCTGCATCCCAGC-- HBV
175	7	1	28	3087			9	133048728	GTF3C5	intron	+							within 150 nt to left of nt 133048728
176	7	1	28	3089			4	141763033				IL15	-29046	+	INPP4B	265748	-	CTCACACCTGTAATCCTAGCn-- HBV
177	7	1	28	3090				0										
178	7	1	28	3094			X	42098007				CASK	-174973	-	PPP1R2P 9	679358	-	HBV-- nnnnnnnnnnnnTAAACTCGGCC AGTCCTAGTT
179	7	1	28	3096			22	41681252	NHP2L1	intron	-							TCAAAATTTATTTTGTCTTA-- HBV
180	7	1	28	3097			6	37762238				MDGA1	-64248	-	ZFAND3	57292	+	ATTTCTGAGATAGGACTTgnn-- HBV
181	7	1	28	3098			2	58948077	LINC011 22	intron	+							AAATTTGCAT CCACAACCATCATA-- HBV
182	7	1	28	3103			9	83598638				FRMD3	-60205	-	IDNK	24410	+	GAGCCAGGGTCAGAGATGA--HBV
183	7	1	28	3109				0										
184	7	1	28	3115			4	137562796				PCDH18	-30298	-	LINC0061 6	464626	-	HBV--AATTCTCAATCATTTTCTTT TTAATAATTGTTAATATA--HBV
185	7	1	28	3490	212	458	12	45245364	ANO6	intron	-							AGGACCAGCCTGGCCAACTTG-- HBV
186	7	1	28	3468	211	488	3	50252682	GNAI2	intron	+							
187	7	1	28	3456	208	1741	11	2162764				INS	-1555	-	TH	1164	-	CTGAGCCATGCCACAGCnn--HBV
188	7	1	28	3465	209	1910	20	34711080	TP53INP 2	exon	+							GCACCAAGGGAGTGTGCA--HBV
189	7	1	28	3460	210	1826		0										
190	7	1	28	3459	207	2763	4	24192173				PPARGC 1A	-302096	-	MIR573	328018	-	TGGGAAAAATGTTG--HBV
191	7	1	28	3469			2	240851310				KIF1A	-31002	-	AGXT	17434	+	GGTCCTCCTGCCACAT--HBV
192	7	1	28	3473			13	33533086	STARD1 3	intron	-							within 224 nts to right of nt 33533086

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
193	7	1	28	3474			7	81645681	LOC100128317	intron								within 246 nts to left of nt 81645681
194	7	1	28	3476			12	131196616	LINC01257	intron	+							ACAACGTTCACTTTTGTT--HBV
195	7	1	28	3478			4	7378006	SORCS2	intron	+							HBV--TACCCCGATTTTCATGAAG
196	7	1	28	3488			13	88267974				LINC00397	-457454	-	LINC00433	272854	+	HBV--AAAGAGCTTCAGCACAGCA
197	7	1	28	3491			17	77440729	SEPT9	intron	+							GTCTGCACAGGTGCCATC--HBV
198	7	1	28	3493			7	121815754				FAM3C	-419386	-	PTPRZ1	57350	+	HBV--ATTCTGAACATCACTAAT
199	7	1	28	3118	176	282	7	138078614	AKR1D1	intron	+							HBV--CTCAAAGCTATATTCTC
200	7	1	28	3124	177	282	4	73404654	ALB	intron	+							CTAAGGAAAGTGCAAAG--HBV
201	7	1	28	3147	178	283	16	49649494	ZNF423	intron	-							TCAGCACATATTAGGAT--HBV
202	7	1	28	3127	174	484	9	113373775	HDHD3	exon	-							HBV--AATTATCCCCAACATGG
203	7	1	28	3151	175	635	11	9570069				ZNF143	-41545	+	WEE1	3611	+	HBV--AAACAAAACATTGTTAAG
204	7	1	28	3125			8	116876744	RAD21-AS1	exon	+							HBV--nCAGCCATAAAAAAGAAAAA
205	7	1	28	3134			3	34918259	LOC101928135	intron	-							HBV--ATCCCAATAGGAAA
206	7	1	28	3135			3	184416743				CHRD	-26908	+	EPHB3	145055	+	CAGGTGCGCCATAACT--HBV
207	7	1	28	3137				0										
208	7	1	28	3139			4	99319381	ADH1B	intron	-							within 65 nts to right of nt 99319381
209	7	1	28	3143			X	25732927				ARX	-716979	-	MAGEB18	405415	+	AAACCATAATATACTTCT--HBV
210	7	1	28	3145			7	151906852				PRKAG2-AS1	-27629	+	GALNTL5	49526	+	HBV--GGCCATTTTACAATATA
211	7	1	28	3146			4	38669922	KLF3	intron	+							HBV--AAGATGTCCTCTTAA
212	7	1	28	3148				0										
213	7	1	28	3150			19	58353102	A1BG	exon	-							HBV--GAGTCTCCAGGTGGGC
214	8	1	30	2190	89	124	2	26707285	KCNK3	intron	+							CCCTGGAATGGAGTGCG--HBV
215	8	1	30	2198	87	229	3	61826795	PTPRG	intron	+							HBV--TGATAGCCAAATATAAACGTTCT
216	8	1	30	2160	88	220	2	105319156	TGFBRA P1	intron	-							AAAAATAAAAAATCAACAn--HBV
217	8	1	30	2164				0										
218	8	1	30	2166			11	97872304				>1000000			>1000000			GCTGGCTGAGCCAGCA--HBV
219	8	1	30	2168			16	71569561	TAT-AS1	intron	-							HBV--TAACTCCTGCGCTCAAGTG
220	8	1	30	2176			7	5495114	FBXL18	intron	-							HBV--AGGAAAAGGCTCCCACTGC
221	8	1	30	2185			5	141370942	PCDHG B3	exon	+							HBV--AGGAGAACCTGGATGGCAG
222	8	1	30	2281	94	52	2	145043331	TEX41	intron	+							HBV--GAAGTATCCAAGATAACTTCT TTTCTACAGG
223	8	1	30	2301	93	37	6	26933909	GUSBP2	intron	-							TCTGAAGGTGnnnnn--HBV
224	8	1	30	2300	91	320		0										
225	8	1	30	2278	90	1416	2	48690599	LHCGR	intron	-							CGTAGTTCTCTGAATAAGTTCT-- HBV

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
226	8	1	30	2283			X	85244654	ZNF711	intron	+							AACCTTTGGAATGCGCGAGGG-- HBV
227	8	1	30	2310			11	18736493	PTPN5	intron	-							HBV--TTTATGTCTAAATCCTCA
228	8	1	30	2376	99	51	6	29796259	LOC554	intron	+							CCTTGCTAGAAAGAGGTCAT-- HBV
229	8	1	30	2372	97	141		0	223									
230	8	1	30	2385	96	456	2	235320752				SH3BP4	-265038	+	AGAP1	173336	+	HBV--AGAAGAGTAACCTCACGG
231	8	1	30	2371	98	407		0										
232	8	1	30	2365	95	727		0										
233	8	1	30	2394			12	112612606				PTPN11	-102693	+	MIR1302- 1	82427	-	HBV--CCAGGCTGGAGTGCAATGA
234	8	1	30	2401			9	69450228	APBA1	intron	-							within 50 nts to right of 72065144
235	8	1	30	2403			2	105251384				GPR45	-7917	+	TGFBRAP 1	13005	-	HBV--TTGTCTGAGATGTGGGGA
236	8	1	30	2404				0										
237	9	1	39	3498	213	680	X	127219938				PRR32	-398153	+	ACTRT1	831023	-	HBV--CTACATGTTTCCTTTTT
238	9	1	39	3497	215	1030	14	97905846				LOC1001 29345	-219188	-	LINC0155 0	19763	-	TTAGTGTCTCTGCCC--HBV
239	9	1	39	3503	214	621	8	55581800				XKR4	-55649	+	TMEM68	156943	-	within 40 nts to right of nt 55581800
240	9	1	39	3504				0										
241	9	1	39	3507			20	32473272	NOL4L	intron	-							within 40 nts to right of nt 32473272
242	9	1	39	3514			12	70661649	PTPRR	intron	-							HBV-- CCAAACCCAGCACGGGTGAGGG
243	9	1	39	3520			8	107067262				ABRA	-297018	-	ANGPT1	182219	-	CAGGCAACAGGCAATA--HBV
244	9	1	39	3522			17	69641717	LINC014 83	intron	+							TTTGTTTAAGGGGAA--HBV
245	9	1	39	3526			10	82316697	NRG3	intron	+							HBV--TCTACTTCTAAAAAGGA
246	9	1	39	3033	161	89	11	13471813				BTBD10	-8516	-	PTH	20240	-	HBV- nACATTCTCTATGTGAAAGG
247	9	1	39	3035	162	89	5	65472122	ADAMT S6	intron	-							within 40 nts to left of nt 65472122
248	9	1	39	3037	163	89	2	214293678	SPAG16	intron	+							HBV--GTGGAGCTCATGGTTTGCT
249	9	1	39	3014			X	103653329				TCEAL1 CCDC17 9	-22381	+	MORF4L2	22168	-	within 368 nts to right of nt 103653329
250	9	1	39	3019			11	23679528					-819102	-	LUZP2	817441	+	HBV--AAGAGGAGCTTTATTGAG
251	9	1	39	3020			5	7013040				MIR4278	-185119	-	MIR4454	256262	-	HBV--CTTGATGATTAGTCAT
252	9	1	39	3034			19	16397387	EPS15L 1	intron	-							HBV--GCTGTTTGCTATTTTAC
253	9	1	39	3040			15	83141577	HDGFR P3	intron	-							CTCCATGACTGACAGTTTTnnn-- HBV
254	9	1	39	3045			1	211474161				LINC004 67	-41626	+	RD3	2360	-	HBV--GATAGAGTAGTTGGGGACT
255	9	1	39	3047				0										
256	9	1	39	3065	166	238	8	10720956				C8orf74	-20363	+	SOX7	2811	-	HBV-- CAACCCAGCACAAACAATGGAT
257	9	1	39	3055	164	1063	1	227011883	CDC42B PA	intron	-							within 40 nts to right of nt 227011883
258	9	1	39	3082	165	881	10	99810494	ABCC2	intron	+							HBV-- AGTGTGTGGGATTGGGAA

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
259	9	1	39	3068			2	217797054				DIRC3	-40461	-	TNS1	2734	-	HBV-- CTGTCTCGAAAGAAAAAAGAAA A
260	10	2	14	2541	109	52	9	108587789				>100000 0			ACTL7B	266799	-	HBV-- TTTTTCTGAAATTCAGGTGAC
261	10	2	14	2548	108	51	5	118860870	DTWD2	intron	-							HBV--TTAGAAATGATTTTGC ATGTAAGAAAAGATAATTT A-- HBV
262	10	2	14	2551	107	131	5	15736111	FBXL7	intron	+							
263	10	2	14	2535			2	202829835	ICA1L	intron	-							ACTTCTAAGTTTTGCTT--HBV
264	10	2	14	2538			8	59680145				TOX	-560937	-	CA8	508718	-	CTCCAGCATTTTGAGTA--HBV
265	10	2	14	2539			10	79033393	ZMIZ1- AS1	intron	-							HBV--nnACCGGTTTACATCATTCA
266	10	2	14	2543				0										
267	10	2	14	2544			X	80115837				TBX22	-84068	+	CHMP1B2 P	112651	-	TGATTCTCATTCTCTCT--HBV
268	10	2	14	2546			20	30421656				MLLT10P 1	-18194	-	DEFB115	836007	+	TGCATATGGAATGTCTG--HBV
269	10	2	14	2641	114	51	15	56886666	LOC145 783	exon	-							CATAATATAGCACTTTCT--HBV
270	10	2	14	2619	111	187	7	27605977	HIBADH	intron	-							HBV--CAAACAAGTTATTCATCCCA
271	10	2	14	2648	112	187	22	46582920				CELSR1	-45750	-	GRAMD4	43840	+	HBV--CTTCTCTCTCTTTGTCT
272	10	2	14	2639	113	131	4	35618971				>100000			ARAP2	447026	-	HBV-- nnnnnnnnnnGCCTAAAGCCCTTT GTTC
273	10	2	14	2655	110	229	9	113532006	RGS3	intron	+							GAGGAGCTGGGTGTC--HBV
274	10	2	14	2612			15	82533803				GOLGA6 L17P	-7319	+	RPS17	2946	-	HBV--TCAAGCGATCCTCTGCCT
275	10	2	14	2618				0				>100000 0			CHRM3	39525	+	ATATAGTTTTATGTAATTTCC--HBV
276	10	2	14	2633			1	239589547										ACTACTTAAACCTTACC--HBV
277	10	2	14	2634			13	108744898	MYO16	intron	+							within 227 nts to right of nt 163110338
278	10	2	14	2637			4	163110338				MIR4454	-16710	-	NAF1	16369	-	CCTGATGCCT CAGCACCTGCn-- HBV
279	10	2	14	2654			20	64198457	MYT1	intron	+							
280	10	2	14	2714	122	77	1	156213591	PMF1- BGLAP	intron	+							TCCTGCCGCAGCTTCCCAA--HBV
281	10	2	14	2710	123	51	1	220059053	BPNT1	intron	-							TGGATTGTGGTTTTTCTAG--HBV
282	10	2	14	2739	125	187	11	29116520				MIR8068	-638972	-	KCNA4	893220	-	TGCTCTCTACACAGTAAGCAA-- HBV
283	10	2	14	2728	120	220	6	78898764	IRAK1B P1	exon	+							HBV--TTGTAAGACAAAATTT
284	10	2	14	2731	121	297	9	135085520	OLFM1	intron	+							HBV-- TAAGGATTGGGTGCCAGGCA
285	10	2	14	2747	124	642		0										
286	10	2	14	2750	118	622	14	34499424				SPTSSA	-37162	-	EAPP	16504	-	within 40 nts to right of nt 34499424
287	10	2	14	2727	119	938	16	13012870	SHISA9	intron	+							HBV--AACTTCAAAGGGT
288	10	2	14	2751	126	1183	7	55119726	EGFR	intron	+							HBV--AACCCACCTGCCCTGGTT
289	10	2	14	2707			6	116104675	NT5DC1	intron	+							within 73 nts to right of nt 116104675

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
290	10	2	14	2715			19	1594102				MBD3	-1341	-	UQCR11	3052	-	HBV-- CCGGGTTCAAGTAATTCTCTCTG TGGTCAGGGAGCAGCTTTGC-- HBV
291	10	2	14	2732			22	30891961	OSBP2	intron	+							CCTCTTTTGCCCAAGTGGnnn-- HBV
292	10	2	14	2736			12	90641768				LINC009 36	-929816	+	LINC0061 5	276254	+	
293	10	2	14	2744			13	62942327				LINC004 48	-134968		LINC0037 6	240773	-	HBV--TTAATAATTGAAATTAATAATT
294	10	2	14	2749			9	24112457				ELAVL2	-286392	-	IZUMO3	430757	-	HBV--AGTGATTCTCTGCCTCA
295	10	2	14	2753				0										
296	11	2	14	3716	276	69	8	139110753				COL22A 1	-196747	-	KCNK9	490084	-	HBV-- TGGCAACATCCTCAGGCACA
297	11	2	14	3718	277	94	12	84639238				>100000 0			SLC6A15	220249	-	HBV--AGTTACTTCATAAATGTTGA
298	11	2	14	3712			3	93470513				>100000 0			PROS1	402523	-	TTTGATGTAATTTTATATTTT--HBV within ~300 nts to right of nt 48056784
299	11	2	14	3724			17	48056784	NFE2L1	uncertain	+							within ~650 nts to right of nt 56829818
300	11	2	14	3730			1	56829818				C1orf168	-10122	-	C8A	24951	+	
301	11	2	14	3735				0										ACTCCTTCTGCAGGGTGAGTGA-- HBV
302	11	2	14	3680	268	34	19	6696480	C3	intron	-							
303	11	2	14	3678				0										
304	11	2	14	3681				0										
305	11	2	14	3683			21	23640805				D21S208 8E	-255970	-	LOC1019 27869	663744	-	TTTCTTATAATGGTGTATTTAT-- HBV
306	11	2	14	3702	269	69	10	25705185	LINC008 36	intron	+							HBV-- nAGTGGTGAATCTCGGCTCAC
307	11	2	14	3695				0										
308	11	2	14	3696			14	89211096	FOXN3	intron	-							HBV--AGTTTCATTACCTTTCAAC
309	11	2	14	3700			13	109021744	MYO16	intron	+							within 40 nts to left of nt 109021744
310	12	2	16	2581	130	183	3	24420709	THRB	intron	-							HBV-- GGCAAGGTTGCAGAGTAAAGGA
311	12	2	16	2597	132	642	2	23042543				LOC1027 23362	-504256		KLHL29	342883	+	AATAACTCTTTATACAGTTAn--HBV GTGCAGCGGAGAGTGACCCAn-- HBV
312	12	2	16	2666	131	1008	15	35925508				DPH6- AS1	-66507	+	MIR4510	1347	+	
313	12	2	16	2589	129	2000	6	67321866				>100000 0			LOC1027 23883	733484		HBV--nAGGTTAGACTTTTTGGTAC
314	12	2	16	2555	127	1733		0										
315	12	2	16	2567	128	1058	5	163114132				GABRG2	-958593	+	CCNG1	323438	+	ACAGGCAGAATTTCCAAT--HBV
316	12	2	16	2562			11	58955636	GLYATL 1	exon	+							HBV--CAGCTGGATGTCTCTTATTC
317	12	2	16	2570				0										
318	12	2	16	2576				0										
319	12	2	16	2582			3	126580557	TXNRD3 NB	intron	-							TGTGTGGATTCCAATCCCCA-- HBV
320	12	2	16	2583			5	111924181	NREP	intron	-							GCTGGGCCTTGGATTTTGAAA-- HBV
321	12	2	16	2690	137	187	6	70563526				FAM135 A	-2352	+	SDHAF4	3395	+	CTAGGTTGCTGCAGTTTCATn-- HBV

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
322	12	2	16	2667	134	342	8	143235361				GPIHBP 1	-18191	+	ZFP41	11459	+	HBV--nGATTACAGGATCACACACA
323	12	2	16	2682	133	723	2	201601445	ALS2CR 11	intron	-							HBV--AGAGAAGAGCAAGATAGAG ATTGATTTCTCATTTCGTTTT-- HBV
324	12	2	16	2700	135	407	10	105121512	SORCS3	intron	+							within 242 nts to right of nt 130938818
325	12	2	16	2677			3	130938818	ATP2C1	intron	+							
326	12	2	16	2762	144	187	3	98942382				DCBLD2	-41056	-	COL8A1	696213	+	within 40 nts to right of nt 98942382 HBV--
327	12	2	16	2797	140	297	1	167529560				CD247	-10950	-	CREG1	11453	-	nnAGTTGTATTAGCTTTCTATTGC
328	12	2	16	2764	141	643	19	45585702				OPA3	-838	-	GPR4	4062	-	TCAGAAATAAATTTAAGGAC--HBV CTATGAAACCTGTGAATTTnnnnnn nnn--HBV
329	12	2	16	2803	142	1008	6	135385661	AHI1	intron	-							
330	12	2	16	2759	138	4023	9	98882830				GALNT1 2	-32749	+	COL15A1	60882	+	TTTCTTTCCCTGTCTTTTC--HBV ATGCCACTTACTAGGTGGACAAA-- HBV
331	12	2	16	2802	139	1733	18	70984299				GTSCR1	-333442	-	LINC0154 1	535664	-	HBV-- TCTTGCTCACGAGAGTCCTCCC CATCTGTTGGCTCTTGAGAAAn-- HBV
332	12	2	16	2809	143	5596	1	41476045				SCMH1	-233902	-	EDN2	2279	-	
333	12	2	16	2765			2	97732650	ZAP70	intron	+							
334	12	2	16	2768				0										
335	12	2	16	2771				0										
336	12	2	16	2792				0										
337	12	2	16	2810			2	37547391				QPCT	-174564	+	CDC42EP 3	94490	-	HBV-- TCGTGGGGTGACAAAGGGG
338	13	2	17	1959	36	340	X	15162293				MOSPD2	-240956	+	ASB9	81693	-	CCAATAAGCTAGATTCATTnn--HBV
339	13	2	17	1921	34	907	14	106076891				ADAM6	-104622	-	LINC0022 6	210782	+	HBV--ATAAAATGTATATGCA HBV-- CTCTGAAAGTGCTGGGATTA
340	13	2	17	1955	36	1456	22	30596440	PES1	intron	-							
341	13	2	17	1953	35	2000	3	194843049				LOC1005 07391	-60881	+	XXYL1	225234	-	CTGTAATCCCAGCACTTT--HBV approx. HBV-- nCCAGAGTGAAGCAGACATACTG T
342	13	2	17	1918			2	218668259	RNF25	exon	-							
343	13	2	17	1922			6	151518831	CCDC17 0	intron	+							GCAGGTTTTTATTAAGGACT--HBV within 272 nts to right of nt 11034381
344	13	2	17	1925			19	11034381	SMARC A4	intron	+							
345	13	2	17	1926			18	7331602				LRRRC30 >100000 0	-99558	+	PTPRM	236216	+	HBV--nTCTGCCTCCCGGGTTCA
346	13	2	17	1927			X	63317858							SPIN4	29369	-	within 270 nts to left of nt 63317858 ~ATGTACTACTGAGGCCGTA-- HBV
347	13	2	17	1928			X	154096037	MECP2	intron	-							
348	13	2	17	1930			8	104886603				LRP12	-297579	-	ZFPM2	432315	+	AAATCCTCTCTTTAGC--HBV
349	13	2	17	1940			10	42917286				BMS1	-82349	+	LINC0126 4	61730	-	HBV--AAAAAATTGAAAACAGC
350	13	2	17	1943			1	56570009	PPAP2B	intron	-							HBV--CTTATATAGTGTGTGCA

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
351	13	2	17	1952			22	45236843	KIAA0930	intron	-							CCCCTTCTCTGCACCA--HBV AGACCCTTCAGGGACTGCCT-- 21n--HBV
352	13	2	17	1966			11	122647359				MIR100HG	-444297	-	UBASH3B	8330	+	
353	13	2	17	1887	39	938	1	4160502				LINC01346	-207919	+	LOC284661	251548	+	~GTCATGTCTACCCTCTGCAGGG T--HBV
354	13	2	17	1880	40	1456	16	33963253				ENPP7P13	-178978		LINC00273	195331	-	CCCTTGCCCTCTTGGCGC--HBV
355	13	2	17	1895	38	907	12	14259231				GRIN2B	-279143	-	ATF7IP	106400	+	AGGATAACAGTAATAACCGCnn-- HBV
356	13	2	17	1874	37	7967	19	44757015	BCL3	at intron-exon junction	+							HBV--AGACACCGCTCCACCTGG
357	13	2	17	1866			7	144526314	TPK1	intron	-							HBV--TGAAAAAGATTTTGTGATAG
358	13	2	17	1875			5	89178690				MEF2C-AS1	-146314	+	LINC01339	979648		HBV-- GGGCAGAGAAATGTGATATG
359	13	2	17	1876			15	36350632				MIR4510SERPINB8	-423709	+	C15orf41	228970	+	within 95 nts to left of nt 36350632
360	13	2	17	1907			18	64044086					-54712	+	LINC00305	35922	-	HBV--GGTTTGTCTTTCACTGT
361	13	2	17	1914				0										
362	13	2	17	1790	28	187	20	2333235	TGM3	intron	+							TTCTGTCTCCAGAGAAACTGnnnn nnnnnnnnn--HBV
363	13	2	17	1777	25	152		0										
364	13	2	17	1786	27	182	21	8218570	LOC100507412	intron	+							GGATTATGACTGAACGCCTC-- HBV
365	13	2	17	1792	26	327	16	49022236				N4BP1	-412027	-	CBLN1	255681	-	GCGGGATTGGGGTCCCTC--HBV
366	13	2	17	1780				0										
367	13	2	17	1787			9	13895619				LINC01235	-464290	-	LINC00583	32351	+	HBV-- nnnAGCAAGTCACAAAAATTC
368	13	2	17	1795			9	5896764	MLANA	intron	+							CTTTGTGGTAACTGTAAT--HBV
369	13	2	17	1798			20	60862076				MIR548AG2	-297451	+	LOC100506470	216987	+	HBV--nnGATGCTGATTCAGTT
370	13	2	17	1800			22	46675898	GRAMD4	intron	+							GCCCCTGCCTCGGATGC--HBV
371	13	2	17	1806				0										
372	13	2	17	1814			3	56852545	ARHGEF3	intron	-							HBV--TGTTTTTTCAAATTCTCTA
373	14	2	19	1120	11	616	5	166605125				>1000000			CTB-7E3.1	300096	-	HBV--ATAGCCTTATCCTGTGCTT
374	14	2	19	1122	10	1149		0										
375	14	2	19	1090	8	5163	18	6873174	ARHGA P28	intron	+							within 144 nts to right of 6873174
376	14	2	19	1114	9	4450	20	45127011				WFDC12	-2546	-	PI3	47887	+	AATATCTCTTTGGGATCCTG--HBV
377	14	2	19	1106				0										
378	14	2	19	1107			10	94808237	CYP2C19	intron	+							HBV--GGCCAGTATAATGT
379	14	2	19	1126				0										
380	14	2	19	1408	15	1674	6	18042875				KIF13A	-55252	-	NHLRC1	77611	-	HBV--GAAGACCCCTCCGCTGC

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
381	14	2	19	1407			8	30152539				MBOAT4	-7855	-	DCTN6	3757	+	HBV-- nnnGCACGTGCCACCATGCCTCG C
382	14	2	19	1416			2	210601408	CPS1	intron	+							within 102 nts to right of nt 210601408
383	14	2	19	1421			5	165964705							CTB- 7E3.1	940516	-	within 40 nts to right of nt 165964705
384	14	2	19	1426			12	98467233				SLC9A7 P1	-10088	-	LOC6437 70	18310	-	TAAAATTTCTTTCAG--HBV
385	14	2	19	1149	13	1078	2	191820569				NABP1	-132047	+	SDPR	13736	-	TAACATTTTACAGAGCCC--HBV
386	14	2	19	1152	13	1078	3	117825136				LINC009 01	-892898		>1000000			HBV--TGTTAGTGCATCATTTTT
387	14	2	19	1133	12	1272		0										
388	14	2	19	1129			4	82746892	SCD5	intron	-							within 150 nts to right of nt 82746892
389	14	2	19	1131			11	115683192				CADM1	-178669	-	LINC0090 0	72140	-	within 175 nts to left of nt 115683192
390	14	2	19	1141				0										
391	14	2	19	1156			2	162841092				KCNH7	-2345	-	FIGN	768459	-	within 150 nts to right of nt 162841092
392	15	2	23	4037	257	151	9	133881250	VAV2	intron	-							CACAGAGAGATGCGGCCn--HBV
393	15	2	23	4006	255	238	15	48030022				SEMA6D	-255799	+	SLC24A5	90949	+	TTTCAACTCTTCTGCTGCn nnn--HBV
394	15	2	23	4026	257	282		0										
395	15	2	23	4005	256	1149	7	55452043				LANCL2	-18301	+	VOPP1	18564	-	HBV--TACCAATAGTAGGAC
396	15	2	23	3986	254	587	4	48345308	SLAIN2	intron	+							HBV--CAGAGTAAATAATCCCAGTT
397	15	2	23	3997			11	46715331				ZNF408	-9370	+	F2	3861	+	HBV--CCCAGCTATTTGGGAG
398	15	2	23	4007			3	156586391				SSR3	-31191	-	TIPARP- AS1	86779	-	HBV-- GTTTAGGCTTGGCCTCATCACA
399	15	2	23	4021			1	56978586				C8B	-12446	-	DAB1	19319	-	within 40 nts to left of nt 56978586
400	15	2	23	4029			1	47331883				STIL	-17736	-	CMPK1	1913	+	within 450 nts to left of nt 47331883
401	15	2	23	4030			14	103885822				LINC006 37	-27773	+	C14orf2	26465	-	HBV--CCTAGCCCCTACCTTCTC
402	15	2	23	4032			4	180692756				>100000 0			LINC0029 0	371333	-	within 1200 nts to left of nt 180692756
403	15	2	23	4035			10	36055897				PCAT5	-254977	+	>1000000			HBV--GTCCATTCTTCTCATC
404	15	2	23	4038			1	238589902				LOC1001 30331	-661583	+	>1000000			within ~750 nts to right of nt 238589902
405	15	2	23	4065	259	282	3	106417444				CBLB	-548401	-	LINC0088 2	692345	-	HBV-- TGTAACAACATAAAGACGCA
406	15	2	23	4094	262	277	7	46572890				IGFBP3	-651618	-	TNS3	702263	-	HBV--ACCCTGTGAATTATGGTGC
407	15	2	23	4069	264	433	18	35238602				MAPRE2	-95134	+	ZNF397	2427	+	within 162 nts to left of nt 35238602
408	15	2	23	4070	258	1949	5	143874163				HMHB1	-53444	+	YIPF5	288054	+	HBV-- ATAAATCTTGCTGAAGGAAAC
409	15	2	23	4102	260	635		0										
410	15	2	23	4087	261	1149	12	115153653				TBX3	-469489	-	MED13L	804922	-	within 150 nts to left of nt 115153653
411	15	2	23	4096	263	5500	3	41060244				ZNF621	-520449	+	CTNNB1	139208	-	TTGAAGATCAGCTGACTGTAG-- HBV
412	15	2	23	4080			14	50308450	L2HGDH	intron	-							HBV-- ATACACAGATGGCAAAGAAGCAC

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
413	15	2	23	4082			7	74481611	GTF2IRD1	intron	+							within 40 nts to left of nt 74481611
414	15	2	23	4086				0										
415	15	2	23	4098			2	217439396	DIRC3	intron	-							ACAACAACGCAGTGAGATAAA--HBV
416	15	2	23	4101			19	13956220	DCAF15	exon	+							within 40 nts to left of nt 13956220 HBV-
417	15	2	23	4158	266	2000	4	71601151				SLC4A4	-29064	+	GC	140542	-	TTTAAATTAACAGTTTTAGGCA
418	15	2	23	4183	267	2743	3	187060777	ST6GAL1	intron	+							TTGGCAGCTAGAAGTTGAAATT--HBV
419	15	2	23	4152	265	5999	10	95731408	ENTPD1	intron	+							TGTAGCCGACCCTCTG--HBV
420	15	2	23	4162			2	118067070				CCDC93	-52907	-	INSIG2	21403	+	within 75 nts to left of nt 118067070
421	15	2	23	4182			X	122468185				>1000000			GRIA3	716057	+	TGTTTTCCGATAGATnnnn--HBV
422	15	2	23	4184			4	99313535	ADH1B	intron	-							ATTTTTAACTAAAAATTAATAA
423	15	2	23	4185			8	62536589	NKAIN3	intron	+							CTGTGGGGACACATCTAGn--HBV
424	15	2	23	4186			1	235916277				LYST	-32569	-	NID1	59554	-	TCAACCTCTGGAATTTTGA--HBV
425	15	2	23	4189			1	77621722	ZZZ3	intron	-							HBV--CAGGAGGATTTCTGTGCC
426	16	2	25	1327	22	74	8	81218770				PAG1	-106702	-	FABP5	61712	+	ACACCTGGCTAACTTTTTAT--HBV
427	16	2	25	1294	18	92	14	67211985	FAM71D	intron	+							HBV--GCATTCTTCTGCCAGGAGA
428	16	2	25	1293	19	104	10	91904675				TNKS2	-39200	+	FGFBP3	1912	-	HBV--CAGTGCAAAATATTTCTG
429	16	2	25	1307	21	187	16	67667074	C16orf86	intron	+							CGCTCAGACCTCCGAGGTn--HBV
430	16	2	25	1336	20	297	2	123807565				>1000000			CNTNAP5	217721	+	GACACACAGAGCTATGTGG--HBV
431	16	2	25	1295	17	322	8	27291710	TRIM35	intron	-							HBV-nnnnnATAACAATAGTTTATTT
432	16	2	25	1297			22	2083373				>1000000			>1000000			CAAGAGCAAGACTCTACCTCAAnn
433	16	2	25	1299			19	33855613				KCTD15	-39852	+	LSM14A	316833	+	within 68 nts to left of nt 33855613
434	16	2	25	1319			17	51215233	MBTD1	intron	-							TAATCATGTG GTAAGGTTAGn--HBV
435	16	2	25	1322			13	24214004	SPATA1	intron	+							HBV--ATATGTTGGTTTCAGA
436	16	2	25	1342			4	120612857				MAD2L1	-546123	-	PRDM5	79055	-	within 40 nts to right of nt 120612857
437	16	2	25	1447	16	87	4	19740344				>1000000			SLIT2	513219	+	AACAGTATCTCCATTT--HBV
438	16	2	25	1428			6	105969056				PREP	-565932	-	PRDM1	117263	+	TTGTTAATTGCACCACTTC--HBV
439	16	2	25	1430			15	88988718				MFGE8	-75286	-	ABHD2	99431	+	AGGGGAATTGCAATAGAGAAA--HBV
440	16	2	25	1431			7	84719888				LOC101927378	-145045	+	SEMA3D	275667	-	within 19nts to left of nt 84719888
441	16	2	25	1435			13	99366339	UBAC2	intron	+							HBV--GTTTTGAATTTGAGTTTTTCCCCA

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
442	16	2	25	1441			11	59932181				TCN1	-65613	-	OOSP1	10697	+	within 40 nts to right of nt 59932181
443	16	2	25	1449			3	114575127	ZBTB20	intron	-							CAGAAGTAGGACTAGAACT--HBV
444	16	2	25	1452			15	68279727	FEM1B	intron	+							HBV--ATTCTTTTTTAGGTTTAAACA
445	16	2	25	1684	23	51	X	83326924				>1000000			POU3F4	181336	+	GCATGGGAGAACTGAGTTAGC--HBV
446	16	2	25	1670	24	74	11	8636670	TRIM66	intron	-							TCTGATATCTCTTGAATCTTTn--HBV
447	16	2	25	1679	24	32	13	111000244				ANKRD1	-85137	-	ARHGEF7	115282	+	AGCTGNGAAGTCATGCAGCnnnnnnnnnnnnnnnnnnnn--HBV
448	16	2	25	1662			4	166433955				TLL1	-329498	+	SPOCK3	299429	-	AATTAAACTACATGCATTT--HBV
449	16	2	25	1664				0										
450	16	2	25	1671			17	76492339	RHBDF2	intron	-							TGGAGACAGCATAACCCAG--HBV
451	16	2	25	1672			17	51221932	MBTD1	intron	-							TTACAAATCTATGAGAAATCAnnnnnn--HBV
452	16	2	25	1675				0										
453	16	2	25	1689			9	75945996	PCSK5	intron	+							TGTTGATTTGGTGACTGTT--HBV
454	16	2	25	1691			1	33546240	CSMD2	intron	-							HBV--AATCCCATATTTTCAGGGA
455	16	2	25	1696			6	85461810	NT5E	intron	+							HBV--AGGCCTGGCACCCTCTCTCT
456	16	2	25	1700				0										
457	17	2	25	4133	251	23	3	30662750	TGFBR2	intron	+							CTAGAAAATTATCATGGGC--HBV
458	17	2	25	4106	249	39	X	121427083				MIR3672	-56030		>1000000			GTATTATTAGAACCATTATn--HBV
459	17	2	25	4119	250	18	1	15673431				RSC1A1	-11709	+	PLEKHM2	10900	+	TGTTGGCTGTTGTTTCTGC--HBV
460	17	2	25	4123	248	3105	10	83077447				NRG3	-90268	+	>1000000			TTAGGAATTCTAGCAGAACAnnnnnn--HBV
461	17	2	25	4134			17	53822748				C17orf11	-835096	+	KIF2B	129	+	TTTCTCGCATGATCCGGA--HBV
462	17	2	25	4136			3	107279636	LINC0083	intron	+							CAAACAATTTGAAACAGC--HBV
463	17	2	25	4195	252	286	8	29637026				DUSP4	-286748	-	LINC00589	84233	-	ATGGCTAACATGGTGAAACnn--HBV
464	17	2	25	4194			1	22316535				MIR4418	-50235	+	ZBTB40	135315	+	CCCTTAGGTCCTCACAn--HBV
465	17	2	25	4200			3	48634649	SLC26A6	intron	-							HBV--nnAGCTTTCACCAGTCAGGAA
466	17	2	25	4149			13	43863539	CCDC12	intron	-							HBV--AAGAAAGTATAAAGTGT
467	17	2	25	4150			8	34897319				LINC01288	-32521	+	UNC5D	338137	+	CTAGAATTTGGAACTATCT--HBV
468	17	2	25	4151			2	65831213				SPRED2	-398691	-	MIR4778	527035	-	within 40 nts to right of nt 65831213
469	18	2	28	2154			4	99208221	LOC100507053	intron	-							HBV--nAGATTTTTAAGTAACTCC
470	18	2	28	2157			3	228861	CHL1	intron	+							TAATGGTGGA TTTGACCnnnnnnnnn--HBV

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
471	18	2	28	2237	102	561	6	144643887	UTRN	intron	+							HBV-- nnnnnnnnTTTTTAAAATTGCTTTA
472	18	2	28	2232	101	1628	1	152152524				TCHH	-37070	-	RPTN	1070	-	HBV--TCAATAGTCCNNGG
473	18	2	28	2235	103	1976	7	132456666	PLXNA4	intron	-							HBV--CCCAGGATGGGCCAGG
474	18	2	28	2233				0										
475	18	2	28	2322	100	780	14	30602427	G2E3	intron	+							TAATTATTTTTTTGTGTACT--HBV
476	19	2	29	2901	152	187	12	5179216				KCNA5	-133227	+	LOC1019 29584	54779	-	CCATCCTAGACTGTCCTGn--HBV
477	19	2	29	2916	151	295	5	180023238	RNF130	intron	-							HBV-- nTATGTAGATATGCAGGAGTTA
478	19	2	29	2902	149	652	17	13949850				HS3ST3 A1	-348721	-	CDRT15P 1	74647	+	HBV-- nnnCATTGAACCTCCCTGTG
479	19	2	29	2909	150	923	4	141492489				LOC1005 07639	-159872		IL15	144106	+	HBV--AGTCATTCCTGTTCCA AACAGGGAGCATATGGCCTGT-- HBV
480	19	2	29	2904			1	6882297	CAMTA1	intron	+							
481	19	2	29	2906			15	45445807				C15orf48	-12358	+	SLC30A4	36673	-	within 40 nts to left of nt 45445807 AGCATATTCATCCTGGCTGGCn-- HBV
482	19	2	29	2910			13	100363997	PCCA	intron	+							
483	19	2	29	2911			11	134107675	JAM3	intron	+							within 168 nts to right of nt 134107675
484	19	2	29	2919			3	71405086	FOXP1	intron	-							CTTCCAAATTTCCACACA--HBV
485	20	3	23	1242	33	77	19	5695130	LONP1	intron	-							HBV-- nnnnnATGGTATCTTAGATGCCGCT
486	20	3	23	1259	14	5895	14	25412634				STXBP6	-362337	-	>1000000			HBV-- AGTACGGCCGACTCCAGTAGGGA
487	20	3	23	1252			2	209661342	MAP2	intron	+							HBV-- nnTCCACACCAACCCCAAG
488	20	3	23	1261			4	188076224				ZFP42	-71175	+	TRIML2	15047	-	HBV-- CAACTCTCCTGCCTCAGCCT
489	20	3	23	1274			7	2634434	TTYH3	intron	+							CTGCCTCCCTGGTGAGGAGTT GC--HBV
490	20	3	23	1282			20	7007038				BMP2	-226775	+	LINC0142 8	139428	-	within 130 nts to right of nt to right of 7007038
491	20	3	23	1652	47	561	4	104040223				TACR3	-320407	-	CXXC4	428082	-	CTCAGCCCCAAATCTCCTTA--HBV
492	20	3	23	1635	49	1008	8	142522537	ADGRB1	intron	+							TCTGTTGGGGGCTTCAG--HBV
493	20	3	23	1657	48	1171	3	71755312				GPR27	-135	+	PROK2	16342	-	HBV-- nGATTGTACTGACTCCTTTGGG
494	20	3	23	1643	43	878	14	74508971	LTBP2	intron	-							HBV-- GAGGAAGACAGCCGATGGC
495	20	3	23	1637	45	2682	3	160892148	PPM1L	intron	+							CGGAACCTAAAATAAAATAA-- HBV
496	20	3	23	1610	42	5162	1	24169532	IFNLR1	exon	-							HBV-- nnnnCATAGAACATAGCAGCTCCT T
497	20	3	23	1626				0										
498	20	3	23	1639			2	43087375				LOC1027 23854	-47832	-	ZFP36L2	136943	-	HBV-- nCCCAGAAGATTCCTGGATCC

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
530	22	3	26	1550	60	194	X	112390159	ZCCHC1 6	intron	+							HBV-- ATTTAGGATCGTGGCCAGGTG
531	22	3	26	1571	61	642		0										
532	22	3	26	1566	58	2062	1	152568994				LCE3E	-2241	-	LCE3D	10389	-	HBV--TTTTTTTTCTTTAGCACTTTG
533	22	3	26	1536	57	4011	13	86522191				SLITRK6	-722843	-	MIR4500 HG	921795	-	HBV-- CCAGTCAGAACAGCTGGATATTA
534	22	3	26	1581	59	3580	13	84077248				SLITRK1	-195741	-	LINC0033 3	63353	+	HBV--CTTCCCAGAGGATAAAAAGG
535	22	3	26	1541				0										
536	22	3	26	1572			9	133971570	VAV2	intron	-							HBV-- GTGACACTGGCCTCTGCCAG
537	22	3	26	1590			4	88503047	HERC5	intron	+							HBV-- GTTTTCTGTTTCTATTTAT
538	22	3	26	1591			9	130611406	FUBP3	intron	+							TGCCTGATTTGGGGAGA--HBV
539	22	3	26	1596			6	47571362	CD2AP	intron	+							CAAAAAGTAGACTGCACAGG-- HBV
540	22	3	26	1604			1	179363185				SOAT1	-4506	+	AXDND1	2534	+	HBV-- nnnnnnnnAGGAAAATAAGAAAAA AAG
541	23	3	26	1996	80	74	21	21342520	NCAM2	intron	+							AGCCTCTCCAGTATGGCTnnnnnn nnnn--HBV
542	23	3	26	1970	79	2120	9	16239116	C9orf92	intron	-							HBV-- AACCTGGTGGGAAGTAATTGA
543	23	3	26	1983			10	58643783	BICC1	intron	+							within 10 nts to right of nt 58643783
544	23	3	26	1990			5	136506566				TRPC7	-141090	-	SPOCK1	468731	-	HBV-- nnnGGCTAGGGACCTGGAGTCTG
545	23	3	26	2056	83	399	18	38531347				MIR4318	-874132	+	LINC0066 9	675576	-	CATACCCTCTCACCTCCCA-- HBV
546	23	3	26	2016	83	652	2	134257821	MGAT5	intron	+							HBV-- nnnnnATTAGTTTGCAGTCTCTTT T
547	23	3	26	2044	84	1008	20	50917312	ADNP	intron	-							HBV--CAAGTCAGTCAGATGATT
548	23	3	26	2023	81	1241	7	112447138	IFRD1	intron	+							HBV--TGAATCAAAGTCATCAAT
549	23	3	26	2012	82	36781	1	147668340	ACP6	intron	-							TCAACCATAAAGGCAGAAG--HBV
550	23	3	26	2032			9	100084919	ERP44	intron	-							HBV--AAAAAGCTAAGGCAACA
551	23	3	26	2033			7	148773668	CUL1	intron	+							CGCTGCGTGTCTTCTC--HBV
552	23	3	26	2037				0										
553	23	3	26	2041			21	29369825				BACH1 IT2	-7929	+	BACH1- IT2	2675	+	TTCTCAGGCCTGGGTCC--HBV
554	23	3	26	2055			1	17703791	ARHGEF 10L				-5916	+	ACTL8	51521	+	HBV-- GCAGTGGTGCGAACCCGGC
555	23	3	26	2064	86	2000	17	54406378				KIF2B	-581166	+	TOM1L1	494312	+	AAAGATTAATAGTGGTGATT--HBV
556	23	3	26	2088			6	6255684	F13A1	intron	-							AGTGGCAAAGCATGATn--HBV
557	23	3	26	2093			17	9077838	NTN1	intron	+							HBV--GACCGGTGTTCAATGAAT
558	23	3	26	2096			12	91829905				DCN	-646876	-	C12orf79	155070	-	TGCCCACTTTGGCCTCC--HBV
559	24	3	26	2413	104	18469		0										
560	24	3	26	2445			10	89427337				IFIT5	-6335	+	SLC16A1 2	2956	-	~TCCCTTGTGT GAACAGTTc-- HBV
561	24	3	26	2470	105	157	8	138771194	COL22A 1	intron	-							HBV-- nnnnCTCCCTGCACCTCACCAGG
562	24	3	26	2483	106	337	17	43882099	MPP2	intron	-							within 40 nts to right of nt 43882099

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
563	24	3	26	2485			6	97144652	MMS22L	intron	-							ATTTAGGGAAAGTGGCTATnnn-- HBV
564	24	3	26	2490				0										
565	25	3	27	2530	145	25	3	76457907				ZNF717	-672324	-	ROBO2	582235	+	GGTTGGGGCGACTGGGACACAG-- HBV
566	25	3	27	2836	148	57	9	37277108	ZCCHC7	intron	+							CCAAGTATAGACTCATT--HBV HBV- nnnnnnnnGTAGCTGGGATTACAGG CATGT
567	25	3	27	2849	147	1733	X	134523203				HPRT1	-22535	+	MIR450B LOC1019 27701	16981	-	GATAGAGATATAAAATTCTG--HBV
568	25	3	27	2847	146	4320	2	67602716				ETAA1	-192315	+		193337	-	HBV--nAAAAGGACCTAGATA
569	25	3	27	2818			X	3084718	ARSF	intron	+							HBV--AAATATTTTTCCCTGGGA
570	26	3	29	1530	69	340	X	31805791	DMD	intron	-							
571	26	3	29	1497	64	643	20	12456031				BTBD3	-529436	+	LOC1019 29486	409172	-	TAAAGTGTCTAATTCA--HBV HBV-- TGTTGGCTGACAAATTATTTT
572	26	3	29	1503	66	1008	13	102146298	FGF14	intron	-							GAACACTTGTTTTCATCAT--HBV HBV-- CCTCTGCAATCCTCAGGGATA
573	26	3	29	1469	62	2670	5	151860329	GLRA1	intron	-							ACAGAGAGGAAGGGACCTnn-- HBV
574	26	3	29	1495	65	2062	1	31238043	NKAIN1	intron	-							
575	26	3	29	1486			19	48962442				BAX LINC015 26	-644	+	FTL	2866	+	HBV--ACCACACACGGTCAAACAA
576	26	3	29	1516			6	81890783					-76591	-	IBTK	279455	-	
577	26	3	29	1523				0										
578	26	3	29	1525			6	103795610					>100000 0		HACE1	932482	-	HBV-- AAAGAAAAAAAACCCCTATGG
579	26	3	29	1533			12	29009007				CCDC91 MIR548A 1	-458841	+	FAR2 LOC1019 28519	139995	+	GAACCTGTGATTCTATT--HBV
580	26	3	29	1828	78	1008	6	18822120				ATXN1	-250240	+	STMND1	246422	+	ATCACTAATAGGTAATCTATT--HBV TGCCATGCTGGGTTTCA--HBV
581	26	3	29	1823	76	1624	6	17025890					-264400	-		76367	+	HBV--AAAATTCAAACTTGAACT
582	26	3	29	1835	71	3032	X	44242614	EFHC2	intron	-							HBV--AAGAAATCACATTAAGTGT
583	26	3	29	1855	72	2536	1	19390206	CAPZB	intron	-							GTGCCTTTGGATAATTTTAGTCC-- HBV HBV-- nnGACTGTGTCTATCATTGGGTTG GT
584	26	3	29	1821	70	8389	17	55013573	STXBP4	intron	+							
585	26	3	29	1833	154	10501	7	156783566	LMBR1	intron	-							TAGCCATTTTATAGGTTAAA--HBV CTTTCTACTCGATGGGTGCCAA-- HBV
586	26	3	29	1853	74	24258	2	209999103	UNC80	exon	+				SERPINB 5	9169	+	AGATTTACCATTTTAATAAACATG-- HBV
587	26	3	29	1861	73	12438	18	63467741				VPS4B	-45222	-				HBV--ATTATTGTGTATTTTCAGA HBV-- TATATGCAATGATGATAATAAT
588	26	3	29	1830			8	117071845	SLC30A 8	intron	+							
589	26	3	29	1854			11	106701739	GUCY1A 2	intron	-							
590	26	3	29	2964	156	5713	2	62405869				B3GNT2	-181138	+	TMEM17 RBMY1A3 P	94351	-	GTCAGTTCTCACCCCT--HBV
591	26	3	29	2968	155	12556	Y	8834727				TTY11	-17345	-		482333	-	HBV--AGCTACCATTAGACCCAGC
592	26	3	29	2939	153	56293	8	31564713				WRN	-391611	+	NRG1	75038	+	
593	26	3	29	2945				0										
594	26	3	29	2973			4	100034797	LOC256 880	intron								TGTACAATAGTCAGGGATGT--HBV

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
595	<p>*Integration sites are listed by patient age within each patient group (IT, gp1; HBeAg(+) IA, gp2; HBeAg(-), gp3). A "0" in the insert site location means that we were unable to locate a unique integration site based on the cell sequence at the virus/cell junction. A string of n's at the virus/cell junction means that the indicated number of bases differed between the consensus human DNA sequence (GRCh38) and the observed sequence. For instance, HBV--nnGACTGTGTCTATCATTGGGTTGGT means that two bases at the virus/cell junction aligned neither with published HBV sequences nor the human sequence GRCh38. For integrations that did not map to either introns or exons, we determined the distance to the nearest genes to the left or right of the integration (within 1,000,000 base pairs).</p>																	