Supplementary Materials

Supplementary table

Table S1. List of orthohepadnavirus sequences

Species	Subclass	Number	Accession number
Human HBV			
	Genotype A	150	FM199977, GU563548, FM199979, HM535205, DQ020002, AF297621, AF297622, AY233290, AY233284, AY233281, AY233288, AY233283, AY233285, FJ692585, HE974363, AB241114, AB116091, AB453986, AB453987, AB241115, AB116088, AB076679, AB116093, AY903452, AB453989, AB453988, AY934771, AY373429, KJ638661, AY934768, AY934767, AY934769, AY934770, AY934772, AY934766, AB116089, AY233274, AF297625, AB116082, AB116087, M57663, AB076678, AB116094, AB116084, AB116086, DQ020003, EF103278, AY161141, AY373432, AF297623, AY233275, AY233276, AY233277, AY233278, AY233279, AY233282, AY233287, AY233289, AF418674, AY161140, AY161138, AB116083, U87742, EU366129, AB116085, FM199974, AY934773, AM494718, AB246335 AB205118, AY233280, AF297624, S50225, V00866, Z35717, X70185, EU594392, EU594390, EU594391, EU594395, EU594394, EU594384, EU594386, EU594383, EU594393, EU594388, EU594389, EU594387, EU594385, AY152726, AY902775, AB116077, AJ012207, AB116078, Z72478, AB116080, L13994, AB116079, X02763, GU563546, AB116081, AB014370, AJ344115, AF090838, X51970, AF090841, AB116076, EU859911, EU859929, GU563554, EU859942, X70185, AB064314, AF090839, AF090840,

			AF536524, AF537371, AF537372, AJ309369, AJ309370, AJ309371, AY034878, AY128092, GQ477461, EU859948 AB194952, AB194951, AB194950, AM184126, AM180623, AM184125, AY934764, FJ692613, FJ692611, FJ692554, FJ692556, FN545831, GQ331047, GQ331046, GQ331048, FN545830, FN545840, FN545839, FN545829, FN545832, FN545837, FN545828, FN545835, FN545833, FN545834
	Genotype B	40	D50521, AB010292, AB073849, AB073852, D23679, D23677, AB073846, D00329, AB073851, AB602818, AB073825, AB073831, AF121244, AB073828, AB073821, AB073833, AB073836, AF100309, AB073822, AB073834, M54923, D00331, AB031266, AB073835, AY033072, DQ463801, DQ463797, AB287314, DQ463799, DQ463787, DQ463795
	Genotype C	168	AB074756, AF068756, AB112408, AB112348, AB112066, AB112471, AB074047, AB205125, AB112065, AB112472, AB074755, AF223959, AF223956, AF223955, AY217371, AJ748098, AB111946, AB074756, AB112063, AF223954, AY167099, AY217374, AF286594, AP011097, AF223960, AF223957, JQ801478, HM011488, GQ924642, GQ377536, JQ801522, JN827423, KM999990, JQ801486, JN827416, JQ801508, HM011491, GQ924658, JQ801500, GQ924609, JQ429078, GQ924616, JQ801493, KC315399, GQ924612, JQ801470, JQ801517, GQ358153, GQ358154, AB205124, AF330110, AY641558, AY641561, AY641563, AY641562, AB205123, AB113876, AB113875, AB113877, AB115417, AY800390, AB033550, X04615, AB033553, D23684, M38636, GQ377535, EU916238, EU939592, GQ377585, AB033556, AY206378, GQ227694, EU939553, EU939536, GQ377514,

			GQ924633, EU916204, FJ899796, FJ562292, FJ562251, FJ787445, EU939557, KM999991, HM750134, EU589345, EU939647, EU589340, JQ040158, EU939587, FJ386586, X01587, AF533983, AP011098, AB202071, AB113879, AY247031, AB014362, AY057947, EU939630, GQ377539, GQ377556, GQ377604, GQ377631, GQ377549, GQ377613, GQ377590, X75656, X75665, AF241410 AB048704, AB048705, AB241109, AB241113, AP011100, AB241110, EU410081, AP011101, EU410080, JN827414, AB241112, KM999992, AB241111, JN827415, EU410079, AP011099, AB493843, AB493840, AB493847, AB493837, AB493842, AB493844, AP011102, AB493838, GQ358156, GQ358155, AB493839, AB493841, AP011103, AB554022, AB554015, AB554021, KM999993, AB554014, EU670263, GU721029, AP011105, AP011104, AP011107, AP011106, EU306671, EU306672, AP011108, AB540583, AB554019, AB554020, AB554025, AB554018, AB560661, GQ358157, AB644285, AB644281, AB644282, AB644280, AB644283, AB644284, HM011493, AB644286, AB644287
	Genotype D	79	AB104709, AB104711, AB104712, AB126581, AB188244, AB222710, AB222711, AB222712, AB222713, AB246347, AB246348, AF121240, AF121241, AF280817, AY161157, AY721605, AY721606, AY721607, AY721608, AY721609, AY721612, AY741797, AY945307, X02496, Y07587, EU594396, EU594397, AB078032, AB078033, AB090270, AB109475, AB109476, AB110075, AB116266, AB120308, AB205126, AB205127, AB210822, AB267090, AJ627220, AJ627223, AY090453, Z35716, EU594403, EU594402, EU594401, EU594400, EU594410,

			EU594409, EU594408, EU594407, EU594416, EU594415, EU594428, EU594399, EU594432, EU594431, EU594425, EU594423, EU594422, EU594421, EU594405, AJ131956, AJ344117, AY233291, AY233292, AY233293, AY233294, AY233295, AY233296, DQ111987, V01460, EU594382, EU594436, EU594434, AB033559, AB048702, AB048703, DQ315779
	Genotype E	38	AB091255, AB091256, AB201288, AB201290, AB201289, AB201287, X75664, X75657, DQ060822, FN594761, FN594764, AM494711, AM494712, AM494714, AM494706, AM494697, FN594754, GQ161783, GQ161811, AB205188, FN594749, DQ060823, DQ060825, AY935700, DQ060824, DQ060829, DQ060830, DQ060826, GQ161790, AB205192, AB194948, AM494713, AB106564, AB194947, FN594752, GQ161828, GQ161791, FN594759
	Genotype F	38	AY090459, AY090461, AY090458, AY090456, AB116552, AF223964, AY179735, AF223963, HM585199, AB116654, AB086397, EU670262, KJ638656, KJ638663, X69798, AY090455, AB116551, AB036920, AB116550, AY179734, AF223962, AB166850, AF223965, AB036915, DQ823090, DQ899148, AY311370, AB036914, AB036919, AB036916, AB036912, AB036911, AB036913, DQ899149, FJ589067, AB036910, X75663, AB116549
	Genotype G	13	AB056513, AF405706, AF160501, AB064310, AP007264, DQ207798, EF634481, AB064313, AB064311, AB056514, AB064312, AB056515, AB375170
	Genotype H	30	AY090454, AY090457, AY090460, AB059661, HM066946, AB059660, AB375161, AB375163, HM117850, AB516394, HM117851, AB064315, AB516395, AB375159, AB375160, AB516393,

			AB375162, AB059659, FJ356716, FJ356715, AB375164, AB266536, EU498228, AB353764, AP007261, AB205010, AB298362, EF157291, AB179747, AB275308
Non-Human Primate HBVs			
	Orangutan HBV	8	AF193864, AF193863, EU155825, EU155824, EU155821, EU155822, EU155827, NC_002168
	Chimpanzee HBV	27	AF242586, AF242585, D00220, AF305327, AF222323, AF222322, FJ798099, FJ798098, AB046525, AJ131575, JQ664509, JQ664508, JQ664507, JQ664506, JQ664505, JQ664504, AM117396, AM117395, AY330911, AF242585, AB032433, AB032432, AM117397, AY330912, HQ018764, AF498266, HQ018763
	Gorilla HBV	6	JQ664503, JQ664502, FJ798097, FJ798095, FJ798096, AJ131567
	Gibbon HBV	27	U46935, AB823656, AB823657, AB823658, AB823659, AB823660, AB823661, AB823662, EU155829, EU155828, AJ131568, AY781183, AY781180, AB037928, AJ131572, AJ131571, AJ131569, AY330913, AY330915, AJ131573, AY077735, AJ131574, AY330914, AJ131568, AY077736, AY330917, AY330916
	WMHBV	1	AF046996
Bat HBVs			
	TBHBV	4	KC79037, KC790379, KC790380, KC790381
	PBHBV	3	KF939648, KF939649, KF939650
	BHBV-C	3	KY905326, KY905327, KY905329
	LBHBV	3	JX941466, JX941467, JX941468
	HBHBV	1	KC790377
	RBHBV	4	KC790373, KC790374, KC790375, KC790376
Rodent HBVs			
	WHV	14	AY334075, AY628095, AY628096, GU734791, J02442, J04514, KF874491, KF874492, KF874493,

			M11082, M18752, M19183, M90520, M18752
	GSHV	1	K02715
	ASHV	1	U29144

Double underlined sequences in human HBV/A and HBV/C correspond to HBV/A (Del) and HBV/C (Del) in Figure 2C, respectively. Underlined bat and rodent HBV sequences are those that were used in the analysis of sequence identity shown in Table 1.

Supplementary figures

Figure S1.

Phylogenetic analysis of orthohepadnaviruses performed by the neighbor-joining method in 33 strains with complete genetic sequences available. Bat and rodent HBV strains used in the phylogenetic analysis are underlined in Table S1.

Figure S1

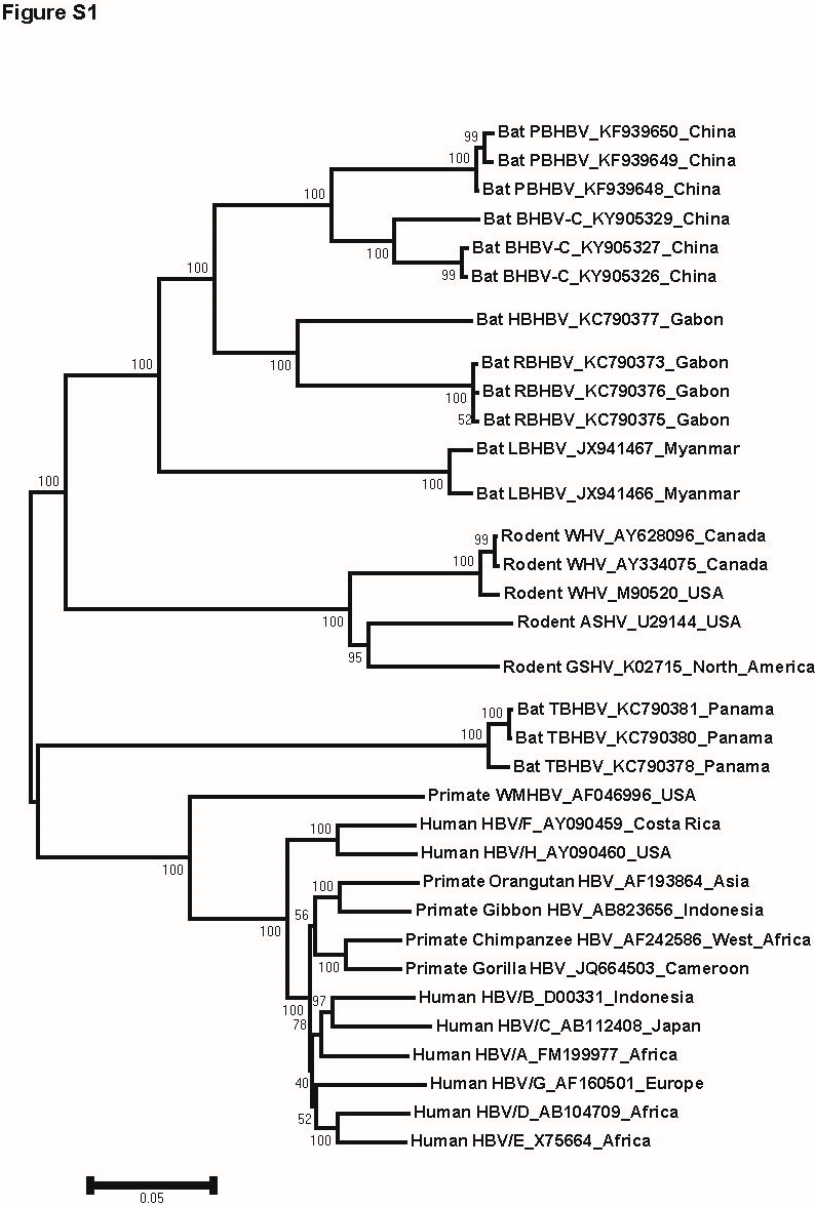


Figure S2. Pair-wise alignments and comparisons of the WMHBV, six bat HBV and three rodent HBV sequences were performed, and 45 patterns of pair-wise data were obtained, of which the first 16 patterns are shown in Figure 3. The remaining 29 patterns are shown in Figure S2A and B. Consensus sequences were used in the analysis. This analysis was performed to clarify partial sequence identity between two species, which may indicate covert conserved genetic segments. Maintenance of % sequence identity was defined as having approximately 65% identity without gaps and a genetic sequence length ≥ 10 bps without sequence gaps, and segments satisfying these conditions are shown in vertical rectangles. Numbers above or below rectangles show the nucleotide positions where high % identity was observed in pair-wise alignment, and % identity of segments.

Figure S2A

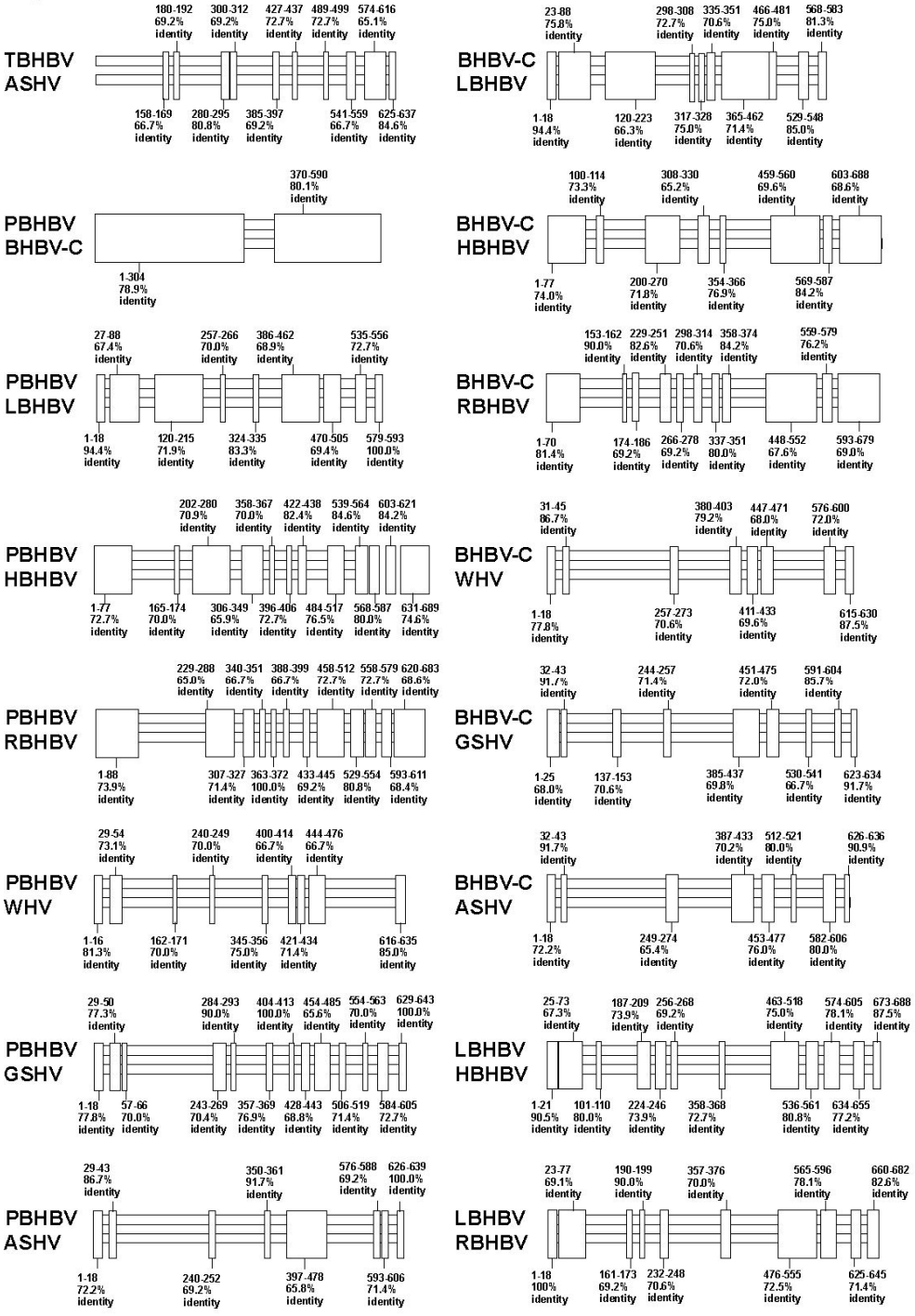

TBHBV
ASHV
180-192 69.2% identity
300-312 69.2% identity
427-437 72.7% identity
489-499 72.7% identity
574-616 65.1% identity
158-169 66.7% identity
280-295 80.8% identity
385-397 69.2% identity
541-559 66.7% identity
625-637 84.6% identity
BHBV-C
LBHBV
23-88 75.8% identity
298-308 72.7% identity
335-351 70.6% identity
466-481 75.0% identity
568-583 81.3% identity
1-18 94.4% identity
120-223 66.3% identity
317-328 75.0% identity
365-462 71.4% identity
529-548 85.0% identity
PBHBV
BHBV-C
370-590 80.1% identity
1-304 78.9% identity
BHBV-C
HBHBV
100-114 73.3% identity
308-330 65.2% identity
459-560 69.6% identity
603-688 68.6% identity
1-77 74.0% identity
200-270 71.8% identity
354-366 76.9% identity
569-587 84.2% identity
PBHBV
LBHBV
27-88 67.4% identity
257-266 70.0% identity
386-462 68.9% identity
535-556 72.7% identity
1-18 94.4% identity
120-215 71.9% identity
324-335 83.3% identity
470-505 69.4% identity
579-593 100.0% identity
BHBV-C
RBHBV
153-162 90.0% identity
229-251 82.6% identity
298-314 70.6% identity
358-374 84.2% identity
559-579 76.2% identity
1-70 81.4% identity
174-186 69.2% identity
266-278 69.2% identity
337-351 80.0% identity
448-552 67.6% identity
593-679 69.0% identity
PBHBV
HBHBV
202-280 70.9% identity
358-367 70.0% identity
422-438 82.4% identity
539-564 84.6% identity
603-621 84.2% identity
1-77 72.7% identity
165-174 70.0% identity
306-349 65.9% identity
396-406 72.7% identity
484-517 76.5% identity
568-587 80.0% identity
631-689 74.6% identity
BHBV-C
WHV
31-45 86.7% identity
380-403 79.2% identity
447-471 68.0% identity
576-600 72.0% identity
1-18 77.8% identity
257-273 70.6% identity
411-433 69.6% identity
615-630 87.5% identity
PBHBV
RBHBV
229-288 65.0% identity
340-351 66.7% identity
388-399 66.7% identity
458-512 72.7% identity
558-579 72.7% identity
620-683 68.6% identity
1-88 73.9% identity
307-327 71.4% identity
363-372 100.0% identity
433-445 69.2% identity
529-554 80.8% identity
593-611 68.4% identity
BHBV-C
GSHV
32-43 91.7% identity
244-257 71.4% identity
451-475 72.0% identity
591-604 85.7% identity
1-25 68.0% identity
137-153 70.6% identity
385-437 69.8% identity
530-541 66.7% identity
623-634 91.7% identity
PBHBV
WHV
29-54 73.1% identity
240-249 70.0% identity
400-414 66.7% identity
444-476 66.7% identity
1-16 81.3% identity
162-171 70.0% identity
345-356 75.0% identity
421-434 71.4% identity
616-635 85.0% identity
BHBV-C
ASHV
32-43 91.7% identity
387-433 70.2% identity
512-521 80.0% identity
626-636 90.9% identity
1-18 72.2% identity
249-274 65.4% identity
453-477 76.0% identity
582-606 80.0% identity
PBHBV
GSHV
29-50 77.3% identity
284-293 90.0% identity
404-413 100.0% identity
454-485 65.6% identity
554-563 70.0% identity
629-643 100.0% identity
1-18 77.8% identity
57-66 70.0% identity
243-269 70.4% identity
357-369 76.9% identity
428-443 68.8% identity
506-519 71.4% identity
584-605 72.7% identity
LBHBV
HBHBV
25-73 67.3% identity
187-209 73.9% identity
256-268 69.2% identity
463-518 75.0% identity
574-605 78.1% identity
673-688 87.5% identity
1-21 90.5% identity
101-110 80.0% identity
224-246 73.9% identity
358-368 72.7% identity
536-561 80.8% identity
634-655 77.2% identity
PBHBV
ASHV
29-43 86.7% identity
350-361 91.7% identity
576-588 69.2% identity
626-639 100.0% identity
1-18 72.2% identity
240-252 69.2% identity
397-478 65.8% identity
593-606 71.4% identity
LBHBV
RBHBV
23-77 69.1% identity
190-199 90.0% identity
357-376 70.0% identity
565-596 78.1% identity
660-682 82.6% identity
1-18 100% identity
161-173 69.2% identity
232-248 70.6% identity
476-555 72.5% identity
625-645 71.4% identity

Figure S2B

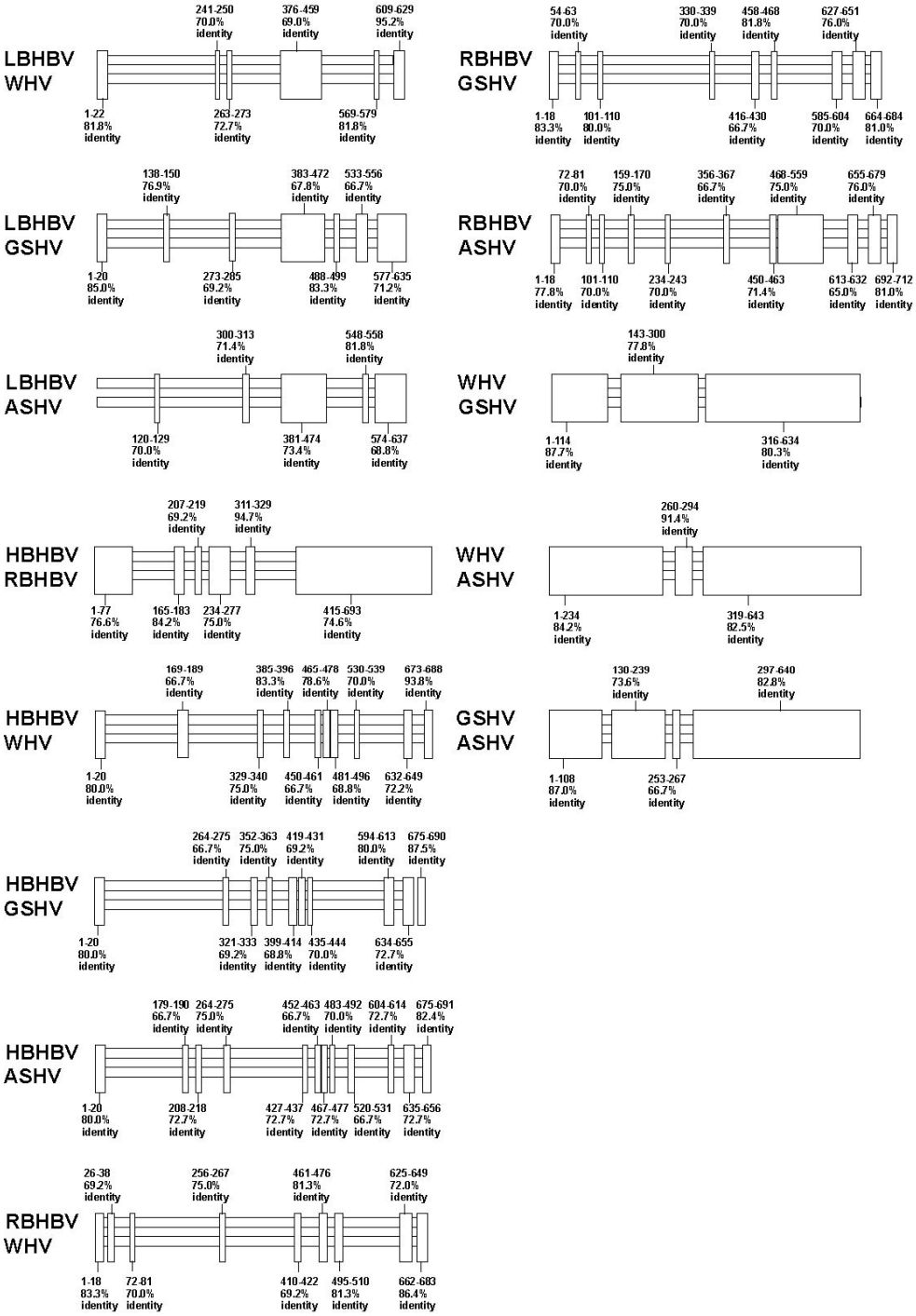

LBHBV
WHV
241-250
70.0%
identity
376-459
69.0%
identity
609-629
95.2%
identity
1-22
81.8%
identity
263-273
72.7%
identity
569-579
81.8%
identity
RBHBV
GSHV
54-63
70.0%
identity
330-339
70.0%
identity
458-468
81.8%
identity
627-651
76.0%
identity
1-18
83.3%
identity
101-110
80.0%
identity
416-430
66.7%
identity
585-604
70.0%
identity
664-684
81.0%
identity
LBHBV
GSHV
138-150
76.9%
identity
383-472
67.8%
identity
533-556
66.7%
identity
1-20
85.0%
identity
273-285
69.2%
identity
488-499
83.3%
identity
577-635
71.2%
identity
RBHBV
ASHV
72-81
70.0%
identity
159-170
75.0%
identity
356-367
66.7%
identity
468-559
75.0%
identity
655-679
76.0%
identity
1-18
77.8%
identity
101-110
70.0%
identity
234-243
70.0%
identity
450-463
71.4%
identity
613-632
65.0%
identity
692-712
81.0%
identity
LBHBV
ASHV
300-313
71.4%
identity
548-558
81.8%
identity
120-129
70.0%
identity
381-474
73.4%
identity
574-637
68.8%
identity
WHV
GSHV
143-300
77.8%
identity
1-114
87.7%
identity
316-634
80.3%
identity
HBHBV
RBHBV
207-219
69.2%
identity
311-329
94.7%
identity
1-77
76.6%
identity
165-183
84.2%
identity
234-277
75.0%
identity
415-693
74.6%
identity
WHV
ASHV
260-294
91.4%
identity
1-234
84.2%
identity
319-643
82.5%
identity
HBHBV
WHV
169-189
66.7%
identity
385-396
83.3%
identity
465-478
78.6%
identity
530-539
70.0%
identity
673-688
93.8%
identity
1-20
80.0%
identity
329-340
75.0%
identity
450-461
66.7%
identity
481-496
68.8%
identity
632-649
72.2%
identity
GSHV
ASHV
130-239
73.6%
identity
297-640
82.8%
identity
1-108
87.0%
identity
253-267
66.7%
identity
HBHBV
GSHV
264-275
66.7%
identity
352-363
75.0%
identity
419-431
69.2%
identity
594-613
80.0%
identity
675-690
87.5%
identity
1-20
80.0%
identity
321-333
69.2%
identity
399-414
68.8%
identity
435-444
70.0%
identity
634-655
72.7%
identity
HBHBV
ASHV
179-190
66.7%
identity
264-275
75.0%
identity
452-463
66.7%
identity
483-492
70.0%
identity
604-614
72.7%
identity
675-691
82.4%
identity
1-20
80.0%
identity
208-218
72.7%
identity
427-437
72.7%
identity
467-477
72.7%
identity
520-531
66.7%
identity
635-656
72.7%
identity
RBHBV
WHV
26-38
69.2%
identity
256-267
75.0%
identity
461-476
81.3%
identity
625-649
72.0%
identity
1-18
83.3%
identity
72-81
70.0%
identity
410-422
69.2%
identity
495-510
81.3%
identity
662-683
86.4%
identity

Figure S3. Based on the pair-wise comparisons of all the strains of orthohepadnaviruses, it was found that PBHBV and BHBV-C, HBHBV and RBHBV, and three rodent HBVs showed high % identities. The nucleotide sequences were separated into segments with high and low sequence similarities with and without gaps. The segments are separated by rectangles; rectangles with solid line show the sequences with no gaps, and shaded rectangles show the sequences with gaps. Numbers below rectangles show the nucleotide positions in pair-wise analysis and % identity of segments. Detailed nucleotide sequence data of S3A, PBHBV and BHBV-C; S3B, HBHBV and RBHBV; and S3C, three rodent HBVs are shown.

Figure S3A

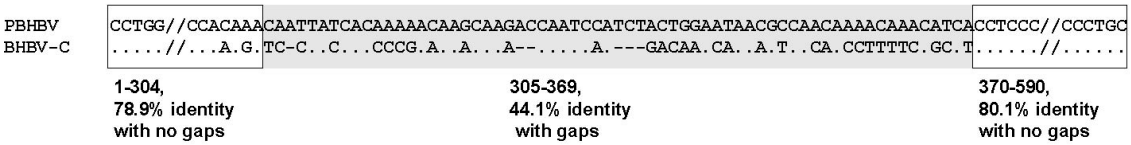


Figure S3B

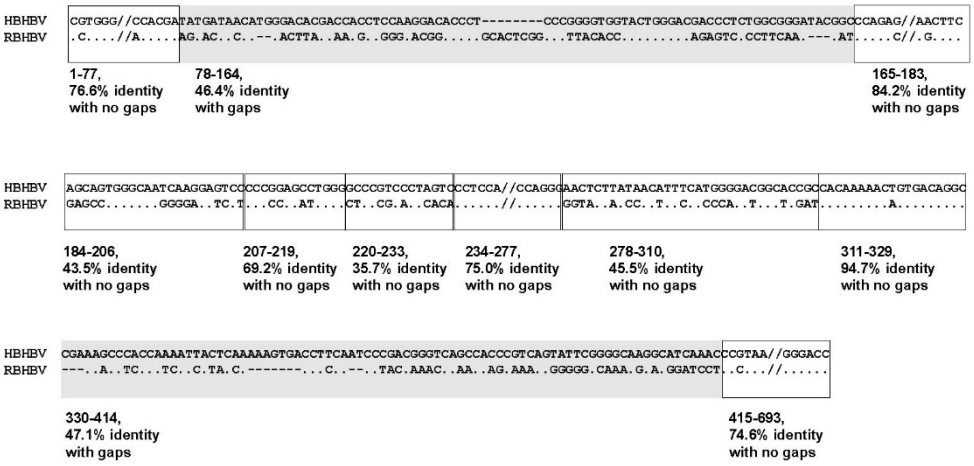
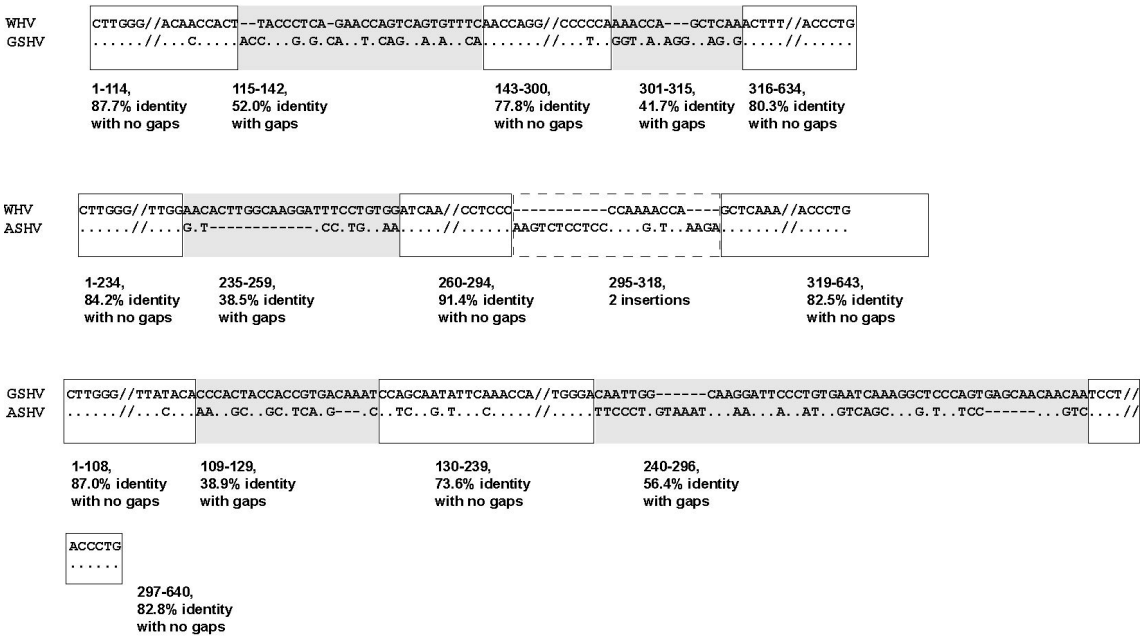


Figure S3C


WHV
GSHV
CTTGGG//ACAACCACT--TACCCTCA-GAACCAGTCAGTGTTTCAACCAGG//CCCCCAAAACCA---GCTCAAACTTT//ACCCTG
1-114, 87.7% identity with no gaps
115-142, 52.0% identity with gaps
143-300, 77.8% identity with no gaps
301-315, 41.7% identity with gaps
316-634, 80.3% identity with no gaps
WHV
ASHV
CTTGGG//TTGGAACACTTGGCAAGGATTTCCTGTGGATCAA//CCTCCC----------CCAAAACCA----GCTCAAA//ACCCTG
1-234, 84.2% identity with no gaps
235-259, 38.5% identity with gaps
260-294, 91.4% identity with no gaps
295-318, 2 insertions
319-643, 82.5% identity with no gaps
GSHV
ASHV
CTTGGG//TTATACACCCACTACCACCGTGACAAATCCAGCAATATTCAAACCA//TGGGACAATTGG------CAAGGATTCCCTGTGAATCAAAGGCTCCCAGTGAGCAACAACAATCCT//
1-108, 87.0% identity with no gaps
109-129, 38.9% identity with gaps
130-239, 73.6% identity with no gaps
240-296, 56.4% identity with gaps
ACCCTG
297-640, 82.8% identity with no gaps