

表8 HBV Genotype 共通プライマー(100組のみ示す)

Pair ID	Primer ID (Forward)	塩基配列(Forward)	平均位置 (Forward)	Primer ID (Reverse)	塩基配列 (Reverse)	平均位置 (Reverse)	プライマーの degeneracy 指数	予想サイズ
1	1333	TGCACTTGGGTTACCTCTGCACGT	1583	1381	ACCAATTTATGCCTACAGCCTCCTA	1795	0	212
2	191	TGGACTTCTCTCAATTTCTAGGGG	263	238	GATARCCAGGACAARTTGGAGGACA	366	2	103
3	1467	CTTTTACCTCTGCTAATCATCT	1825	1535	CCAAATCTTTATAMGGRTCAATGT	1930	2	105
4	89	CATCAGGAYTCTGTTGGACCCCTKCT	171	138	AAAAATTGAGAGAAGTCCACCACGAG	272	3	101
5	89	CATCAGGAYTCTGTTGGACCCCTKCT	171	144	GAAAAATTGAGAGAAGTCCACCACGGA	273	3	102
6	1148	TYTACGTCCCGTCRGGCTGAATCC	1427	1224	CCGGGTAAAGAGAGGTGGCCGCCGT	1538	3	111
7	1731	TYGGAGTGGATTTCGCACTCCWCC	2274	1790	GGGAGGGAGTGTCTTCKAGGGG	2389	3	116
8	1731	TYGGAGTGGATTTCGCACTCCWCC	2274	1795	GTYTCGAGGGGAGGAGTCTTCT	2397	3	124
9	1816	CCTMGAAGAAGAACCTCCCTGCCTC	2375	1875	CCACCTRTGWTGCCAAGGRATACT	2476	4	101
10	811	TTYTGCCAACTTAYAAARCTTTC	1099	874	CCAGTGGGGTGTGORTCAGCAAAACA	1200	4	101
11	1173	GTCTGCGGTGAATCCHGGGACGAC	1437	1224	CCGGGTAAAGAGAGGTGGCCGCCGT	1538	4	101
12	215	TGTCYTGCCWAAATTYGCACTCC	299	288	AGGAATGATAAAAACGCCGACGAC	400	4	101
13	185	GTCTAGACTGCTGGTGGACTTCTCT	249	219	TGGAGGACARSAGRTTGGTRAGTGA	350	4	101
14	1807	AGAAGAAGCTCCCTGCCTCGGARAC	2381	1891	ARTTCCGACCTRTGWTGCCAAGG	2482	4	101
15	172	GACTGCTGGTGGACTTCTCTCAAT	254	241	ACAARTTGGAGGACARSAGRTTGGT	356	4	102
16	184	GTAGACTGCTGGTGGACTTCTCTCA	251	232	AGGACAARTTGGAGGACARSAGRTT	359	4	108
17	457	GTCAGGAMAMCTCATGTWTCCTC	540	522	ACGGRTGAGGCCACTCCCATAGG	656	4	116
18	1772	CACMAAATGCCCTATCYTATCMAC	2310	1841	ATCTTCTGCGACGGGMATTGAGA	2427	4	118
19	1711	TSTCYTYGGAGTGGATTTCGCACT	2268	1790	GGGAGGGAGTGTCTTCKAGGGG	2389	4	122
20	408	AAGGTATGTTGCCGKTGTCTCTCT	459	473	TGGGAATACARGTGCARTTTCRTCT	603	4	144
21	69	AAYRCATCAGGAYTCTGTTGGACCCC	167	157	TTGAGAGAAGTCCACCACGAGTCTA	268	5	101
22	389	TGGAYTAYCAAGGTATGTTGCCGCT	450	444	GGGAWACATAGAGTKTCCCTTGAGCA	554	5	104
23	1509	TKTCAAGCCTGCAAGCTGTGCCTT	1866	1560	ARAARTCAGAAGGCAAAAAGAGAG	1971	5	105
24	69	AAYRCATCAGGAYTCTGTTGGACCCC	167	144	GAAAAATTGAGAGAAGTCCACCACGGA	273	5	106
25	385	TTGGTTCTCTGGAYTAYCAAGGTA	440	444	GGGAWACATAGAGTKTCCCTTGAGCA	554	5	114
26	1000	TGCCGATCCACTGCGGAACTGCT	1262	1087	CAGCACADCCAGCAGCCATGGRAA	1388	5	126
27	1772	CACMAAATGCCCTATCYTATCMAC	2310	1850	GAGATKSAGATCTTCTGCGACGGG	2436	5	127
28	24	AYYTYCCTGCTGGTGGCTCCAGTTC	54	95	TGTGAGGATYYTGTCAACRAGAAA	230	5	178
29	1345	CTCTGCAGTYRCATGGARACCVCC	1588	1381	ACCAATTTATGCCTACAGCCTCCTA	1795	5	197
30	1330	GCTTCCACTGTCACGTYRCATGGA	1581	1386	GCTGGTGMRCASACCAATTTATGCC	1807	5	216
31	1794	CAGDCCCTMGAAGAAGAACTCC	2368	1877	RTGWTGCCAAGGRATACTAACATTG	2469	6	101
32	207	BGTGTCYTGCCWAAATTYGCACTC	297	293	GAATGATAAAAAGCCGACGACAC	398	6	101
33	1773	YAGAACGMAAATGCCCTATCYTA	2305	1814	GAGAYCTKGTYYTGGAGGGGAGGG	2406	6	102
34	661	GGGCTTCCCCACTGYTGGCTTT	710	711	QAYAMARAAAATGGTAAAGMGG	813	6	103
35	1774	CCCCTATCYTATCMACRMTTCKGGA	2319	1841	ATCTTCTGCGACGGGMATTGAGA	2427	6	109
36	661	GGGCTTCCCCACTGYTGGCTTT	710	723	CCCAVAGYAAMARAAAATGGTAA	819	6	109
37	371	TCATCTCTTCTGGTCTCTGGA	429	432	TKCCTTGAGCARGARTBGTGCAAGT	540	6	111
38	24	AYYTYCCTGCTGGTGGCTCCAGTTC	54	82	AGMAGGGTCCCKAGGARTCCTGATG	187	6	133
39	24	AYYTYCCTGCTGGTGGCTCCAGTTC	54	73	CGAGMAGGGTCCCKAGGARTCCTGA	189	6	135
40	407	GCCCGTKTGTCTCTVMTCCAGGA	469	477	GQATGGGAATACARGTGCARTTCC	606	6	137
41	407	GCCCGTKTGTCTCTVMTCCAGGA	469	483	ATGGGATGGGAATACARGTGCARTT	609	6	140
42	466	GCTCAAGGMAMCTCATGTWTCCTC	539	514	TCCCATAGGWATYTTSCAAAGCCC	640	7	101

43	1039	GCYTYGTYTCTCGCAGCMGGTGTG	1291	1081	TTGGCAGCACADCKAGCAGCCATG	1392	7	101
44	216	MCCRBGTGTYCTGGCCWAAATTYGC	293	264	ATGATAAAACGGCCGACACACATCC	394	7	101
45	158	CCTCACAAATWCCRMAGAGTCTAGAC	232	209	GTRAGTGAYTGGAGRTTKGGGACTG	333	7	101
46	160	ATCCTCACAAATWCCRMAGAGTCTAG	230	205	TRAGTGAYTGGAGRTTKGGGACTGC	332	7	102
47	805	ARGCTTYRYTYTYTCGCCAACTTA	1088	892	GGGTTGCRTCAGCAAACACTTGGGA	1193	7	105
48	1472	CCTCTGCCTAATCATCTYWTGTWCA	1833	1541	YAGWMGCTCCAAATCTTTATAMGG	1938	7	105
49	408	AAGGTATGTTGCCCGTKTGCTCTCT	459	455	WACARCARCADGAGGAWACATAGA	567	7	108
50	805	ARGCTTYRYTYTYTCGCCAACTTA	1088	884	GTGGGGGTTGCRTCAGCAAACACTT	1197	7	109
51	471	GMAMCTGTATGTWCCCTCHTGYTG	546	522	ACGGRCTGAGGCCACTGCCATAGG	656	7	110
52	1179	CRGCGCTGAATCGHCGGACGACGCC	1439	1254	GGMACASRCGGGGAGWCCGGGTAAA	1554	7	115
53	1774	CCCTATCYTATCMACRMTCCKGA	2319	1850	GAGATKSAGATCTTCTGGGAGCGGG	2436	7	118
54	1668	GRCAAYATTTRTGTTGAYATWTC	2202	1757	ATARGATAGGGGCATTTKGTGGTCT	2322	7	120
55	720	TCCTTTWRCKCKTRTTAOCOAATT	787	798	GAAAGGYCTTRTAAGTTGGCGARAA	1115	7	328
56	1913	GGACWCYAAAGTGGGAAATTTTAC	2470	1987	AWGGTGACCCCAAATGAGCCGCT	2824	7	354
57	806	YRYTYTYTCGCCAACTTAYAGRCC	1095	877	TGGGGTTGCRTCAGCAAACACTTG	1196	8	101
58	395	TGGTCTTCTGGAYTAYCAAGGTAT	441	438	GKTKCCTTGAGCARGARTBGTGCAG	542	8	101
59	1745	ACTCCWCCHGCHTAYAGCCACDMAA	2291	1802	CGAGGGGAGGGAGTTCTTCTTKKAG	2392	8	102
60	1782	RMTCCKGARAMRFTCTTTGTTAGA	2335	1850	GAGATKSAGATCTTCTGGGAGCGGG	2436	8	102
61	856	TCGCCACTGTYTGGCTTYAGYTA	716	723	CCCAVAGAYAAMARAAAATGGTAA	819	8	103
62	353	ATCCTGCTGCTATGCCCTCATCTTCT	413	422	TYKGCANKGTCSSGTRCTGKTKGT	516	8	103
63	1529	GCCTCCAAGCTGTGCCCTGGGTGGC	1873	1573	NGAMGRRRARAARTCAGAAGGCAAA	1979	8	106
64	216	MCCRBGTGTYCTGGCCWAAATTYGC	293	285	GGAATGATAAAAAGCCGACGAGA	399	8	106
65	1519	TCAAAGCTCCAAGCTGTGCCCTGGG	1869	1573	NGAMGRRRARAARTCAGAAGGCAAA	1979	8	110
66	1045	GYTYTCTCGCAGCMGGTGTGRRGC	1295	1092	CCCKGHAKGATCGAGTTGGCAGCAC	1407	8	112
67	1677	TATTRTGGTTGAYATWCHTGYGT	2208	1757	ATARGATAGGGGCATTTKGTGGTCT	2322	8	114
68	1000	TGCCGATCCATACTGGGGAAGTCT	1262	1063	CACADCKAGCAGCCATGGRAANGA	1385	8	123
69	385	TTGGTCTTCTGGAYTAYCAAGGTA	440	455	WACARCARCADGAGGAWACATAGA	567	8	127
70	440	RRACCTGGCAVAYCTYCTCAAGG	522	537	GRCTGAGGCCACTCCCATAGGWAT	653	8	131
71	1355	HVTTRYATAAKAGGACTMTTGGACT	1651	1381	ACCAATTTATGCCTACAGCCCTCTA	1795	8	144
72	1355	HVTTRYATAAKAGGACTMTTGGACT	1651	1420	GATGATTAGGCAGAGGTGAAAAGT	1840	8	189
73	1345	CTCTGCACGTYRCATGGARCCVCC	1598	1386	GCTGGTGMRCASACCAATTTATGCC	1807	8	209
74	2014	YTGGAACAMGAKCTACAKCATGGG	2837	2053	CCYTGWMCTGAGGCTCCMCCCA	3092	8	255
75	2008	GGTCACCCWTATWCVTGGGAACAMGA	2824	2053	CCYTGWMCTGAGGCTCCMCCCA	3092	8	268
76	1995	GGQHTCATTTTGGGTCACQWTA	2809	2053	CCYTGWMCTGAGGCTCCMCCCA	3092	8	283
77	433	CAQYACSGGACMMTGCMRRACCTGC	505	477	GGATGGGAATACARGTGCARTTCC	606	9	101
78	628	TGTTCAAGTGGTKCGYMGGGCTTCC	694	700	AAAYAGMGYAWAAAAGGAYTCAMGA	796	9	102
79	437	QYACSGGACMMTGCMRRACCTGCAC	507	483	ATGGATGGGAATACARGTGCARTT	609	9	102
80	1201	ACGACCCBCTCYGKGGYCYTTGGG	1457	1251	CAGATGAGAAGGMACASRCGGGGAG	1564	9	107
81	1001	CWCTGCGGATCCATCTGGGGAAGT	1259	1067	CKAGCAGCCATGGRAANGADGTRTA	1379	9	120
82	1668	GRCAAYATTTRTGTTGAYATWTC	2202	1755	GGAAYGKATARGATAGGGGCAT	2332	9	130
83	1333	TGACTTCGCTTCACTCTGCACGT	1583	1363	TCHKYAAAHAMACAGTYTTGAWGT	1726	9	143
84	1641	TRATGAMYTRGYYWCTGGGGTGGG	2103	1688	GAGTGGGAATCCACACTCCRAARGA	2286	9	183
85	1572	TRCTCTCDTTTTGCTCTCTGAYTT	1953	1662	AWATRTGAAACCAYAARTTGYCT	2217	9	264
86	732	CCAATTTTYTKTRTCTBGGQYAT	806	798	GAAAGGYCTTRTAAGTTGGCGARAA	1115	9	309
87	417	GTTGCCCGTKTGCTCTVMTTCCA	466	455	WACARCARCADGAGGAWACATAGA	567	10	101
88	1828	GCCTCGCARACGMAGRTCTCAATC	2394	1905	TAVAHCCVGTAAARTTCCCACCT	2495	10	101

89	440	RRACCTGCACVAYTCYTGTCTCAAGG	522	516	CCCATAGGWATYTTSCSAAGGCCA	639	10	117
90	427	TTCCAAGGAWNCRACMACCAGYAC	486	477	GGATGGGAATACARGTGCARTTCC	606	10	120
91	784	AATGTGGWTAYCQHGHYTMATGCC	1037	829	CGTTGCCRGCAACGGGGTAAAGGT	1158	10	121
92	1367	ACTGKTDTTTRMDGAVTGGGARGA	1719	1420	GATGATTAGGCAGAGGTGAAAAAGT	1840	10	121
93	427	TTCCAAGGAWNCRACMACCAGYAC	486	483	ATGGGATGGGAATACARGTGCARTT	609	10	123
94	1677	TATRTGGTTTCAYATWCHTGYCT	2208	1755	GGAAYKTKGATARGATAGGGGCAT	2332	10	124
95	1355	HVTTRYATAAKAGGACTMTTGACT	1651	1418	GTGAAAAAGTKRCATGQTGCTGGT	1825	10	174
96	1641	TRATGAMYYTRGCVWCTGGGTGGG	2103	1701	CDGGWGGAGTGCAGATCCACACTCC	2292	10	189
97	1585	TTTTGCCTCTGAYTTYTYCCKTC	1962	1662	AWATRTGAAACGAYAARTTGYCT	2217	10	255
98	1551	TTGAYCCKTATAAAGAAATTTGGAGC	1917	1652	TTARRCCCATRTKARYRTTRACATA	2187	10	270
99	2014	YTGGAACAMGAKCTACAKCATGGG	2837	2077	ACYKVCGATTTGGTRGARGCAGGAGG	3145	10	308
100	720	TCCCTTTWRCCKCTRTTACCAATT	787	800	AAGTTGGCGARAARRYRAAGCYTG	1103	10	316

I: degeneracy を 2 の指数で示した値、黄色のカラムは OE-PCR ゲノムフラグメントを用いた検証対象のプライマーセットを示す

表 9 HBV 共通プライマー検証用ゲノムフラグメント

Genotype	フラグメントの塩基配列
A	TGTGCACTTCGCTTCACTCTGCACGTTGCATGGAGACCACCGTGAACGCCCATCAGATCTGCCAAGGTCTTACATAAAGG GACTCTTGGACTCCAGCAATGTCAACGACCGACCTTGAGGCTACTTCAAAGACTGTGTGTTAAAGGACTGGGAGGAGCTGG GGGAGGAGATTAGGTTAAAGGCTTTGTATTAGGAGGCTGATGGCATAAATTGGTCT
B	TGTGCACTTCGCTTCACTCTGCACGTCGCATGGAGACCACCGTGAACGCCACGGGAGCTTGCCTAAGGCTTGCATAAAGG GACTCTTGGACTTTCAGCAATGTCAACGACCGACCTTGAGGCATACTTCAAAGACTGTGTGTTACTGAATGGGAGGAGTTGGG GGAGGAGGTTAGGTTAATGATCTTTGTAAGGAGGCTGTAGGCATAAATTGGTGT
C	TGTGCACTTCGCTTCACTCTGCACGTCGCATGGAGACCACCGTGAACGCCACCTGGTATTGCCAAGGATTGCATAAAGG GACTCTTGGACTCTCGGCAATGTCAACGACCGACCTTGAGGCATACTTCAAAGACTGTGTGTTAAAGGACTGGGAGGAGCTGGG GGAGGAGATTAGGCTAAAGGCTTTGTACTAGGAGGCTGTAGGCATAAATTGGTCT
D	TGTGCACTTCGCTTCACTCTGCACGTCGCATGGAGACCACCGTGAACGCCACCAATTTGCCAAGGCTTGCATAAAGG GACTCTTGGACTCTCTGTAATGTCAACGACCGACCTTGAGGCATACTTCAAAGACTGTGTTAAAGGACTGGGAGGAGTTGGG GGAGGAGATTAGTAAAGGCTTTGTGTTAGGAGGCTGTAGGCATAAATTGGTCT
E	TGTGCACTTCGCTTCACTCTGCACGTCGCATGGAGACCACCGTGAACGCCACAGATCTTGCCCAAGGCTTACATAAAGG GACTCTTGGACTCTCTGCAATGTCAACGACCGACCTTGAGGCATACTTCAAAGACTGTGTTAAAGGACTGGGAGGAGTTGGG GGAGGAGACTAGATTAATGATCTTTGTAAGGAGGCTGTAGGCATAAATTGGTCT
F	TGTGCACTTCGCTTCACTCTGCACGTCGCATGGAGACCACCGTGAACGCCCCCTGGAGTTGCCAACAGTCTTACATAATAGG ACTATTGGACTTTCAGGACGGTCAATGACCGGTCAATGACCTGGATCGAAGAAATACATCAAAGACTGTGTTAAAGGACTGG GAGGAGTTGGGGAGGAGATTAGGTTAATGATCTTTGTACTAGGAGGCTGTAGGCATAAATTGGTCT
G	TGTGCACTTCGCTTCACTCTGCACGTTACATGAAACCGCCATGAACACCTCTCATCTGCCAAGGCAGTTATATAAGAGG ACTCTTGGACTGTTTGTATGTCAACAACCGGGTGGAGAAATCTTCAAGGACTGTGTTTTGCTGAGTGGGAAGAATTAGGC AATGAGTCCAGGTTAATGACCTTTGTATTAGGAGGCTGTAGGCATAAATTGGTCT
H	TGTGCACTTCGCTTCACTCTGCACGTCGCATGGAGACCACCGTGAACGCCCTTGGAACTTGCACAAACCTTACATAAAGG GACTCTTGGACTCTTATGTAACCGGTCAACGACCTGGATTGAGGAATACATCAAAGACTGTGTTAAAGGACTGGGAGGAGTCT GGGGAGGAGTTAGGTTAATGTTTATGTATTAGGAGGCTGTAGGCATAAATTGGTCT

表 10 HBV ゲノムフラグメント合成用オリゴマー

Genotype	PrimerName	塩基配列	Length	
A	HBV_A1_1	TGTGCACCTTCGCTTCACCTCTGCACGTTGCATGGAGA	37	
	HBV_A1_2	TCTGATGGCGTTTACGGTGGTCTCCATGCAACGTGCAGA	40	
	HBV_A1_3	CCGTGAACGCCCATCAGATCCTGCCAAGGTCTTACATAAG	41	
	HBV_A1_4	CTGGGAGTCCAAGAGTCTCTTATGTAAGACCTTGGGCAGGA	42	
	HBV_A1_5	AGGACTCTTGACTCCCAGCAATGTCAACGACCCGACCTTG	40	
	HBV_A1_6	ACACAGTCTTTGAAGTAGGCCTCAAGGTCCGCTGTTGACATTG	43	
	HBV_A1_7	AGGCCTACTTCAAAGACTGTGTGTTAAAGACTGGGAGGAGCT	43	
	HBV_A1_8	CCTTTAACCTAATCTCCTCCCCAGCTCCTCCAGTCTTAAAC	44	
	HBV_A1_9	GGGGGAGGAGATTAGGTTAAAGGTCTTTGTATTAGGAGGCTGTAGGC	47	
	HBV_A1_10	AGACCAATTTATGCCTACAGCCTCCTAATACAAAGA	36	
B	HBV_B1_1	TGTGCACCTTCGCTTCACCTCT	21	
	HBV_B1_2	GGTGGTCTCCATGCGACGTGCAGAGGTGAAGCGAAGTGCA	40	
	HBV_B1_3	CGTCGCATGGAGACCACCGTGAACGCCACGGGAGCTTGC	40	
	HBV_B1_4	AGAGTCTCTTATGCAAGACCTTGGGCAAGCTCCCGTGGG	40	
	HBV_B1_5	CAAGGTCTTGCCATAAGAGGACTCTTGACTTTCAGCAATGTCAACG	46	
	HBV_B1_6	GAAGTATGCCTCAAGTCCGCTGTTGACATTGCTGAAAGTCCA	43	
	HBV_B1_7	ACCGACCTTGAGGCATACTTCAAAGACTGTGTGTTACTGAATGGG	46	
	HBV_B1_8	CCTCCTCCCCAACTCCTCCCAATCAGTAAACACACAGTCTTT	43	
	HBV_B1_9	AGGAGTTGGGGGAGGAGTTAGGTTAATGATCTTTGTACTAGGAGGC	47	
	HBV_B1_10	ACACCAATTTATGCCTACAGCCTCCTAGTACAAAGATCATTAACCTAA	48	
C	HBV_C1_1	TGTGCACCTTCGCTTCACCTCTGC	23	
	HBV_C1_2	ACGGTGGTCTCCATGCGADGTGCAGAGGTGAAGCGAAGTG	40	
	HBV_C1_3	DGCATGGAGACCACCGTGAACGCCACCTGGTATTGCCCA	40	
	HBV_C1_4	CCAAGAGTCTCTTATGCAATACCTTGGGCAATACCAGTGGG	43	
	HBV_C1_5	AGGTATTGCATAAGAGGACTCTTGACTCTCGGCAATGTCAACGA	45	
	HBV_C1_6	TGAAGTATGCCTCAAGGTCCGCTGTTGACATTGCCGAGAGT	41	
	HBV_C1_7	CCGACCTTGAGGCATACTTCAAAGACTGTGTGTTAAAGACTGGGA	46	
	HBV_C1_8	TCTCCTCCCCAGCTCCTCCAGCTTTAAACACACAGTCTT	42	
	HBV_C1_9	GGAGCTGGGGGAGGAGATTAGGCTAAAGGTCTTTGTACTAGGAG	44	
	HBV_C1_10	AGACCAATTTATGCCTACAGCCTCCTAGTACAAAGACCTTTAGCCTAA	48	
D	HBV_D1_3	CGTCGCATGGAGACCACCGTGAACGCCACCAATTCTTGC	40	
	HBV_D1_4	AGTCCTCTTATGCAAGACCTTGGGCAAGAATTGGTGGCGTT	42	
	HBV_D1_5	CCAAGGTCTTGCCATAAGAGGACTCTTGACTCTCTGTAATGTCAACGA	48	
	HBV_D1_6	TGAAGTATGCCTCAAGGTCCGCTGTTGACATTACAGAGAGTCCAAG	46	
	HBV_D1_7	CCGACCTTGAGGCATACTTCAAAGACTGTTGTTAAAGACTGGGA	46	
	HBV_D1_8	CTAATCTCCTCCCCAACTCCTCCAGTCTTAAACAAACAGTCTT	46	
	HBV_D1_9	GGAGTTGGGGGAGGAGATTAGATTAAGGTCTTTGTATTAGGAGGC	46	
	HBV_D1_10	AGACCAATTTATGCCTACAGCCTCCTAACACAAGACCTTTAAT	44	
	E	HBV_E1_1	TGTGCACCTTCGCTTCACCT	19
		HBV_E1_2	TGGTCTCCATGCGACGTGCAGAGGTGAAGCGAAGTGACA	40
HBV_E1_3		ACGTCGCATGGAGACCACCGTGAACGCCACCGATCTTG	40	
HBV_E1_4		GAGTCTCTTATGTAAGACCTTGGGCAAGACTCGGTGGGCGTTC	44	
HBV_E1_5		CCCAAGGTCTTACATAAGAGGACTCTTGACTCTCTGCAATGTCAAC	47	
HBV_E1_6		AAGTATGCCTCAAGGTCCGCTGTTGACATTGCAGAGAGTCCAA	43	

	HBV_E1_7	GACCGACCTTGAGGCATACTTCAAAGACTGTTTGTTTAAAGACTGGGA	48
	HBV_E1_8	GTCTCCTCCGCCAACTCCTCCAGTCTTTAAACAAACAGTCTTTG	45
	HBV_E1_9	GGAGTTGGGGGAGGAGACTAGATTAATGATCTTTGTACTAGGAGGCT	47
	HBV_E1_10	AGACCAATTTATGCCTACAGCCTCCTAGTACAAAGATCATTAACTA	47
F	HBV_F1_1	TGTGCACTTCGCTTACCTCTGCACGTC	28
	HBV_F1_2	GCGTTCACGGTGGTCTCCATGCGACGTGCAGAGGTGAAGC	40
	HBV_F1_3	GGAGACCACCGTGAAGGCCCCCTGGAGTTTGGCAACAGTC	40
	HBV_F1_4	TCCTGAAAGTCCAATAGTCCATTATGTAAGACTGTTGGCAAACCTCCAGG	50
	HBV_F1_5	TTACATAATAGGACTATTGGACTTTCCAGGACGGTCAATGACCCGGTCA	48
	HBV_F1_6	TGATGTATTCTTCGATCCAGGTCATTGACCCGGTCTATTGACCG	43
	HBV_F1_7	ATGACCTGGATCGAAGAATACATCAAAGACTGTGATTTAAAGACTGGGAGG	52
	HBV_F1_8	ACCTAATCTCCTCCCAACTCCTCCAGCTTTAAATACACAGTCTT	48
	HBV_F1_9	AGTTGGGGGAGGAGATTAGGTTAATGATCTTTGTACTAGGAGGCTGTAG	49
	HBV_F1_10	AGACCAATTTATGCCTACAGCCTCCTAGTACAAAGATCATTAA	42
G	HBV_G1_2	CGGTTTCCATGTAACGTGCAGAGGTGAAGCGAAGTGCACA	40
	HBV_G1_3	CTGCACGTTACATGGAACCGCCATGAACACCTCTCATCATCTG	44
	HBV_G1_4	AAGAGTCTCTTATATAAAGTCCCTGGCAGATGATGAGAGGTGTTTATGG	50
	HBV_G1_5	CCAAAGGCAGTTATATAAGAGGACTCTGGACTGTTTGTATGTAACAACCG	52
	HBV_G1_6	AGTCCTTGAAGTATTTCTCCACCCCGGTTGTGACATAACAAACAGTCC	49
	HBV_G1_7	GGGTGGAGAAACTCTCAAGGACTGTGTTTTGTGCTGAGTGGGAAGAATT	49
	HBV_G1_8	TCATTAACCTGGACTGATTGCTAATCTTCCCACTCAGCAAAAACAC	48
	HBV_G1_9	AGGCAATGAGTCCAGGTTAATGACCTTTGATTAAGGAGGCTGTAGGC	47
	HBV_G1_10	AGACCAATTTATGCCTACAGCCTCCTAATACAAAGG	36
	H	HBV_H1_2	GGGTCTCCATGCGACGTGCAGAGGTGAAGCGAAGTGCACA
HBV_H1_3		ACGTCGCATGGAGACCCCGTGAACGCCCTTGGAACTTG	40
HBV_H1_4		GAGTCTCTTATGTAAGGTTGTTGGCAAGTTCCAAGGGCGGTTT	44
HBV_H1_5		CCAACAACCTTACATAAGAGGACTCTGGACTCTTATGTAACCGGTCAAC	50
HBV_H1_6		CTTTGATGTATTCCTCAATCCAGTCTGTTGACCGTTACATAAGAGTCCAA	51
HBV_H1_7		GACCTGGATTGAGGAATACATCAAAGACTGTGATTTAAAGACTGGGAGG	50
HBV_H1_8		TCAACTCCTCCCGACTCCTCCAGTCTTAAATACACAGT	42
HBV_H1_9		AGTCGGGGGAGGAGTTGAGGTTAATGTTTTATGTATTAGGAGGCTG	46
HBV_H1_10		AGACCAATTTATGCCTACAGCCTCCTAATACATAAACCATTAAACC	45

表 11 HIV-1 Genotype 共通プライマー設計対象ゲノム塩基配列

Accession	Genotype	Definition	Length
EU861977	A	HIV-1 isolate 60000 from Italy complete genome	9781
AY835761	B	HIV-1 isolate 5048-91 clone pbf16 from USA complete genome	9824
AF321523	C	HIV-1 clone MJ4 from Botswana complete genome	9913
AF133821	D	HIV-1 isolate MB2059 from Kenya complete genome	10035
AY173957	F	HIV-1 isolate BZ126 from Brazil complete genome	9030
AF084936	G	HIV-1 subtype G from Democratic Republic of the Congo complete genome	9707
AF190127	H	HIV-1 isolate VI991 from Belgium Gag polyprotein (gag) Pol polyprotein (pol) Vif (vif) Vpr (vpr) truncated Tat (tat) Rev (rev) truncated Vpu (vpu) envelope glycoprotein precursor (env) and Nef (nef) genes complete cds	9056

表 12 HIV-1 Genotype 共通プライマー(上位 228 件のみ表示)

Pair ID	Primer ID (Forward)	塩基配列(Forward)	平均位置 (Forward)	Primer ID (Reverse)	塩基配列 (Reverse)	平均位置 (Reverse)	プライマーの degeneracy 指数 ¹	予想サイズ
1	1834	CTCTGGAAAGGTGAAGGGG	2381	1667	ACCTGCCATCTGTTTCCATA	2436	0	109
6	1834	CTCTGGAAAGGTGAAGGGG	2381	1682	AKCACCTGCCATCTGTTTTC	2452	1	113
8	1834	CTCTGGAAAGGTGAAGGGG	2381	1702	CATCGTGTCTACYGCCACAC	2473	1	137
20	1603	GGAAAGGACCGAARCT	2333	1667	ACCTGCCATCTGTTTCCATA	2436	2	129
27	31	ACTAGCGGAGGCTAGAAGGAGA	93	39	ARCTCYCTGCTTGGCCATAC	154	2	146
30	18	AGGACTCGGCTTGCTGA	41	39	ARCTCYCTGCTTGGCCATAC	154	2	223.625
32	1987	GGCAGGAAGAACGGGA	2894	2007	CGACTRTGCTTCTGCTTTCYCT	2518	2	257.125
43	1603	GGAAAGGACCGAARCT	2333	1682	AKCACCTGCCATCTGTTTTC	2452	3	133
51	1579	GRTACAGTGCASGGGAAAATA	2256	1604	TTKGCTGGTCCCTTCCAAA	2338	3	141
54	523	ACYCTTTGGCARGCACC	810	576	CCTCCAATTCYCGTATGATTT	895	3	147.875
57	31	ACTAGCGGAGGCTAGAAGGAGA	93	44	YARCTCYCTGCTTGGCCA	159	3	149
88	1571	ARATGGCAGTATTCATYCACAAAT	2200	1604	TTKGCTGGTCCCTTCCAAA	2338	3	188
75	1597	MAACTARAGAAYTACAAAAACAAT	2289	1667	ACCTGCCATCTGTTTCCATA	2436	3	201
79	1926	CRRCAAYGACAGAAATAGGCATT	2819	1977	CGGCTTCTGCTGGCAT	2881	3	202
83	507	RCYAGRCCACAGCCG	780	540	CTAATACTGTATGATCTGCTCCTGT	832	3	203.875
96	18	AGGACTCGGCTTGCTGA	41	44	YARCTCYCTGCTTGGCCA	159	3	226.625
100	1721	TGTGQCARGTAGACAGGATGA	2495	1776	CTCCATCKATGGAGACYCC	2574	3	241
102	566	CAGGAGCAGATGATACAGTATTAGA	868	837	TTACYGQYACAGTKCAATAGGACT	1001	3	243
104	1987	GGCAGGAAGAACGGGA	2894	2000	CACRTCTTCTGCTTTCYCTWAT	2911	3	254.125
117	482	RGQYTGTTGQARATGTGG	727	540	CTAATACTGTATGATCTGCTCCTGT	832	3	326.375
125	530	YTCCCTCARATCACTCTTTGG	817	552	TCYCTAATACTGTATGATCTGCTC	845	4	101.875
139	1507	CCTACAAYCCCAAAAYCA	2120	1546	ATACTGCCATYTKACTGCTGTC	2163	4	116
149	806	CCACARQATGGAAAGGATC	1236	836	CTACATAYAARTGATCCATRTATTG	1273	4	117.125
181	1947	CGRGRRGYCAGCCT	2847	1977	CGGCTTCTTCTGCTCAT	2881	4	125.625
186	1949	ATCCRGRRGYCAGCC	2849	1977	CGGCTTCTTCTGCTCAT	2881	4	126.625
195	1463	GGAGMAGRTGCCAGT	2051	1504	GRCTTTGGGGRTTGTAGGG	2116	4	135
213	1217	CAGACTCACARTATGCAWTAGGAAT	1744	1265	TTGTTCAATYCCGCAATYCC	1797	4	147
235	2286	ATAGTGCAACAGCARCAATYTG	3397	2350	TTCCAGAGCARCCCAA	3484	4	160
238	1056	ACTAATGATGTAARRCARTTAACAG	1546	1103	AAACTCCCAAYTCAGGAATCCA	1602	4	180
243	2271	RTTGCTGGHATAGTGCAACAGC	3377	2350	TTCCAGAGCARCCCAA	3484	4	171
245	1507	CCTACAAYCCCAAAAYCA	2120	1574	CTTCCCSGCACTGTAYCC	2243	4	174
246	1384	GGACAAGTAGAYTGTAGYCCAGG	1950	1473	CTGQCCAYCTKCTGCTA	2062	4	175
256	507	RCYAGRCCACAGCCG	780	548	CTGTATCATGCTGCTGTRTCTAA	841	4	197.875
284	506	SAGRCYAGRCCACAGC	779	540	CTAATACTGTATCATCTGCTCCTGT	832	4	205.875
294	1549	GCTGARCACTTARGACAGCAGT	2186	1604	TTKGCTGGTCCCTTCCAAA	2338	4	214
297	590	GATAGRRGGAATTGGAGGYTT	921	656	CCATCCATBCCTGGCTT	1028	4	216
304	2018	GAAAGAGCAAGAGYAGTGMAA	2930	2067	ACARGCATGTTRGCCGA	2999	4	238.5
327	507	RCYAGRCCACAGCCG	780	576	CCTCCAATTCYCGTATGATTT	895	4	261.875
330	1133	GATTCTGARTGGGAGTTTGT	1633	1193	TGAGTCTGYACTATRTTYACTTCT	1717	4	263
341	482	RGQYTGTTGQARATGTGG	727	548	CTGTATCATGCTGCTGTRTCTAA	841	4	320.375
361	1987	GGCAGGAAGAACGGGA	2894	2044	YTGCTGTYCCACACAGG	2963	4	403.625
363	31	ACTAGCGGAGGCTAGAAGGAGA	93	98	YTGRTGATCATTGTCYCTG	239	4	453.5
366	2304	ACRGCTGGGGYATYAARCA	3428	2350	TTCCAGAGCARCCCAA	3484	5	101

369	1133	GATTGCTGARTGGGAGTTTGT	1833	1149	CTGCYCCATOTAGATAQWARGTYTC	1653	5	102
371	1507	CCTAGAAYCCCAAAAGYCA	2120	1539	ACTGCTGTCYTAAGRTGYTCAGC	2156	5	102
377	198	GGRGCCACYYCCACAAGA	348	224	ATTGCGGAGCYTCMTCAATTGA	394	5	106
379	2311	MRGTCACRGCTCTGGGGYAT	3435	2350	TTGGAGAGCARCCCCAA	3484	5	107
383	107	CARGGRCAAATGGTACAYCA	249	156	ATAATGCTGWRRAACATGGGTATTAC	299	5	108
389	1133	GATTGCTGARTGGGAGTTTGT	1833	1152	CTRYTWGCTGCYCCATCTACATAG	1656	5	110
396	1571	ARATGGCAGTATTCATYCACAAAT	2200	1587	TTGTTTTGTARTTCTYTAGTKGT	2275	5	111
469	107	CARGGRCAAATGGTACAYCA	249	182	GGCYCCYCTGATAAATGCTG	329	5	124
478	172	ATACCCGATGTYWAGCATTATCAG	318	224	ATTGCGGAGCYTCMTCAATTGA	394	5	125
488	1217	CAGACTCACARTATGCAWTAGGAAT	1744	1251	YTRRTGYGCTGGTACCCATG	1783	5	127
491	507	RCYAGRGCCAAACAGGCC	780	513	CCAAAGRTGATYTGAGGGA	800	5	127
529	1228	GCAWTAGGAATYATTCARGCACA	1755	1265	TTGTCATTYCCCTCAATYCC	1797	5	135
538	107	CARGGRCAAATGGTACAYCA	249	191	TCTTGGRGTGGCYCC	338	5	138
598	1579	GRTACAGTGCASGGGAAAGAATA	2256	1622	CCTCACCTTCCAGAGDAGYTT	2360	5	158
610	1489	HGCMGTGGTGGGGC	2094	1548	ATACTGCCATYTGKACTGCTGTC	2163	5	161
628	18	AGGACTCGGCTTCTCTGA	41	34	CKYAAACKRATTTTTYCCCA	133	5	166.625
636	568	CAGGAGCAGATGATACAGTATTAGA	868	621	ATTATRTTGAYAGGNGTAGGTCCTA	963	5	169
639	2253	GCAGGAAGYACKATGGGC	3348	2305	AGGACTGTTGYGAGYTG	3429	5	170
645	848	AATAYATGGATGYTTRTATGTAGG	1286	927	ACTGCCATYTRTCAGGATGGAG	1372	5	171
649	1056	ACTAATGATGTAARRCARTTAACAG	1546	1115	GGGGTRTRACAAAACCTCCA	1614	5	172
658	2253	GCAGGAAGYACKATGGGC	3348	2325	TATCTTTCYASAGCYAGGACTCTTG	3450	5	180
667	590	GATAGGRGGAATGGAGGYTT	921	637	TTACYGGYACAGTKCAATAGGACT	1001	5	186
668	198	GGRGCCACYYCCACAAGA	348	266	AGTAGYCCGCTATRTCACTCTCC	451	5	188
683	506	SAGROYAGRGCCAAACAGC	779	548	CTGTATCATCTGCTCCTGTRCTAA	841	5	199.875
684	25	RCWRCGCAAGAGGGCAG	58	39	ARCTCYCTGCTTGCCCATAC	154	5	201.625
687	421	ATGACAGCATGYCARGGAGT	655	462	CCAACARCCOYTTTTYCTAGG	700	5	202.875
690	1038	AAAATCTRAARACAGRAARTATGC	1528	1103	AAACTCCAYTCAGGAATCCA	1602	5	204
693	1571	ARATGGCAGTATTCATYCACAAAT	2200	1622	CCTTCACCTTCCAGAGDAGYTT	2360	5	205
698	1278	TTGAGGRAATGAACAAGTRGATAA	1815	1364	CATGCAWRGCTTCYCCITTT	1917	5	206
727	1463	GCAGGMAGRTGGCCAGT	2051	1539	ACTGCTGTCYTAAGRTGYTCAGC	2156	5	216
734	1592	ATAKCAWCAGAYATACMAACTARAG	2282	1667	ACCTGCCATCTGTTTTCCATA	2436	5	217
739	1489	HGCMGTGGTGGGGC	2094	1574	CTTCCGSGCACTGTAYCC	2243	5	219
742	1507	CCTAGAAYCCCAAAAGYCA	2120	1587	TTGTTTTGTARTTCTYTAGTKGT	2275	5	221
745	1920	TYRYHCATTTCAGAATGGGTG	2802	1977	CGGCTTCTCTCGCCAT	2881	5	224
748	1924	GTTYRYHCATTTCAGAATGGGTG	2806	1977	CGGCTTCTCTCGCCAT	2881	5	226
749	928	CTCCATCCTGAYARATGGACAGT	1373	995	TAGAATYCCCTRTTYCTGCCA	1462	5	226
764	1842	ARGAYAGATGGAACRAGCCC	2886	1906	YGRCAACCAATTCGAAATG	2779	5	236
781	1701	GMTGATWGTGGCARGTAGACA	2472	1776	CTCCATTCATGGAGACYCC	2574	5	247
793	482	RGGYTGTTGARATGTGG	727	513	CCAAAGRTGATYTGAGGGA	800	5	249.5
812	1976	ATYTMCYATGGCAGGAAGAAGC	2880	2007	CGACTRTCTCTGCTCTTTCYCT	2918	5	260.125
820	506	SAGROYAGRGCCAAACAGC	779	576	CCTCOAATTCYGCATCATT	895	5	263.875
830	1133	GATTGCTGARTGGGAGTTTGT	1633	1194	AYTGTGAGTCTGYACTARTTYAC	1720	5	267
844	2476	GGARCCGTGCCTYTTTCAG	3637	2503	AGCCCTGTCTKATCTTSTRGGTAT	3676	5	277.5
845	1899	GGGATACYTGGRRMRRGT	2769	1977	CGGCTTCTCTCGCCAT	2881	5	281
847	483	RGARGMCAICARATGAAAGA	728	540	CTAATACTGTATCATCTGCTCCTGT	832	5	302.375
863	2355	GGGGYGCCTGGAAAA	3489	2421	GTGARTAKCCCTKCCACTACTATT	3578	5	353

875	1987	GGCAGGAAGAACGGGA	2894	2037	YYCCACACAGGHACYCCATA	2955	5	394.625
882	2355	GGGGYTGCTCTGQAAAA	3489	2443	KCTCKCCACTYCTTCTCKAT	3600	5	434
885	1928	CRRCAAYGCAGAAATAGGCATT	2819	2007	CCACTRTCTTGCTGCTTTTCYCT	2918	5	438.125
895	236	AKGARGCTGWCWGAATGGG	406	255	CTAGTAGYTCWCWGTATRTCACTTC	440	6	101
899	175	GARGTAATACCCATGTTYWCAGCA	319	211	AACATTTGGATDGGCTGCTYTG	377	6	101
900	1542	GCTGARCAYCTTARGACAGCAG	2159	1578	ATTATRTCTAYTATTCTTCCOSTG	2253	6	101
910	199	GRGCCACYCCACAAGAYTT	350	224	ATTCWGCAGCYTGMTATTGA	394	6	103
919	143	CTAQRACYTTRAAAYGCATGGGT	286	191	TCTGTGGRTGGCYCC	338	6	105
928	1592	ATAKCAWCAGAYATACMAACTARAG	2282	1804	TTKGCTGGCTCCTTCCAAA	2338	6	107
931	813	GAAAGGATCMCCRCGARTA	1243	836	CTACATAYAARTCATCGATRTATTG	1273	6	107.125
932	2286	ATAGTGCAACAGCARARCAATYTG	3397	2325	TATCTTTCYASAGCYAGGACTCTTG	3450	6	108
935	1587	MAACTARAGAAATACAAAAACAAAT	2289	1622	CGTTCACCTTTCCAGAGDAGYTT	2360	6	108
943	2271	RTTGTCTGGHATAGTGCAACAGC	3377	2305	AGGACTCTTGQYGGGAGYTG	3429	6	109
946	2450	RAATMGAAGAAGRAGGTGGMGA	3608	2463	GGTARCTGAARAGGCACAGG	3624	6	110
967	928	CTCCATCCTGAYARATGGACAGT	1373	975	SRTAAATYGRCTTGCCCA	1438	6	114
971	1228	GCWATAGGAATYATTCARGCACA	1755	1251	YTRTYGCTGGTACCCATG	1783	6	115
976	1316	ATTGGARARCAATGGYAGTGGA	1867	1369	GRCTACARTCTAGTTGCGATGCA	1926	6	115
1012	2271	RTTGTCTGGHATAGTGCAACAGC	3377	2325	TATCTTTCYASAGCYAGGACTCTTG	3450	6	119
1045	1278	TTGGAGGRAATGAACAAGTRGATAA	1815	1310	CACTRRCCATTGYTYTCCAAAT	1860	6	123
1101	506	SAGRCYAGRGCCAACAGC	779	513	CCAAAGRGTGATYTGAGGGA	800	6	129
1115	1384	GGACAAGTAGAYTGAGYCCAGG	1950	1444	TGYCTGYTCTGYTGGRT	2024	6	129
1161	1380	GGATGGACAAGTAGAYTGAGYCC	1946	1444	TGYCTGYTCTGYTGGRT	2024	6	132
1183	1579	GRTACAGTGCASGGGAAAGAATA	2256	1602	GGCTCTTCCAAABWGGRTC	2326	6	134
1203	203	CARGCAGCHATGCAAAATGT	365	266	AGTAGYTCWGTATRTCACTTCCC	451	6	135
1212	806	CCACARGATGGAAAGGATC	1236	841	CTATTTCTAARTCWGANCTACATA	1278	6	135.125
1235	1549	GCTGARCAYCTTARGACAGCAGT	2166	1587	TTGTTTTGTARTCTYTAGTKGT	2275	6	137
1271	848	AATAYATGGATGAYTTRTATGTAGG	1286	892	CATCCAAAGRAATGGGGTTC	1336	6	141
1297	1721	TGTGGCARGTAGACAGGATGA	2495	1742	CTAVTGGTRATGTACTTCTGARCT	2526	6	145
1306	848	AATAYATGGATGAYTTRTATGTAGG	1286	897	ATAHCCCATCCAAAGRAATGG	1341	6	147
1307	1489	HGCMFTGTGGTGGGC	2094	1539	ACTGCTGCTYTAAGRTGYTCAGC	2156	6	147
1313	2253	GCAGGAAGYACKATGGGC	3346	2300	YTRATRCCCAGACYGTGAG	3424	6	149
1322	1402	ATATGGCAAYTRGATTYACMCA	1971	1473	CTGGCCAYCTKCTGCTA	2062	6	151
1338	1248	CATGGGTACCAGRCAYAA	1779	1310	CACTRRCCATTGYTYTCCAAAT	1860	6	153
1343	1278	TTGGAGGRAATGAACAAGTRGATAA	1815	1328	YTTTGTCTACYAYRGGTGGCA	1879	6	154
1351	750	AAARRTCAGTAWCAGTAYTRGATGT	1165	809	GATCCTTTCCATCCYGTGG	1239	6	155.125
1391	2018	GAAAGAGCAGAAGYAGTGGMAA	2930	2044	YTCWCTYCCACACAGG	2963	6	161.5
1401	421	ATGACAGCATGYCARGGAGT	655	453	GYCCTKCYTGCACA	690	6	163.875
1419	1278	TTGGAGGRAATGAACAAGTRGATAA	1815	1337	CAGYTRCYACTATTQYTTTGCTA	1888	6	166
1450	1696	AAAACAGATGGCAGGTGMTG	2467	1742	CTAVTGGTRATGTACTTCTGARCT	2526	6	170
1479	1687	AYTATGGAAAAACAGATGGCAGGT	2458	1742	CTAVTGGTRATGTACTTCTGARCT	2526	6	174
1493	1448	CARCAGARACAGRCARGA	2028	1504	GRCTTTGGGRTTGTAGGG	2116	6	177
1504	198	GGRGCCACYCCACAQA	348	264	CTATRTCACTTCCSTWGGKTC	449	6	180
1509	1571	ARATGGCAGTATTATCYACAATT	2200	1602	GGCTCTTCCAAABWGGRTC	2326	6	181
1522	1248	CATGGGTACCAGRCAYAA	1779	1328	YTTTGTCTACYAYRGGTGGCA	1879	6	184
1525	2431	ATAGAGTYAGMAGGGMTAYTACC	3588	2463	GGTARCTGAARAGGCACAGG	3624	6	185
1529	199	GRGCCACYCCACAAGAYTT	350	266	AGTAGYTCWGTATRTCACTTCCC	451	6	185

1531	1928	CRRCAAYAGCAGAATAGGCATT	2819	1953	CGATRGKARATGCGCTAAGCC	2857	6	186
1533	1801	CAAAAAAATYWMAMAWTTORAA	2299	1667	AGGTGCCATGTGTTTCCATA	2436	6	187
1545	1001	GGCAGARAAAYAGGARATTCTAAA	1468	1049	TTAAYTGYTTACATCATTAGTGTG	1539	6	189
1589	1158	ARACYTWTCTATGTAGATGGRGCAGC	1663	1210	TTCTAWTGCATAYTGTGAGTCTGT	1738	6	192
1572	1783	GGRTCTCCATMGAATGGAG	2586	1812	CCAARTAYTGTARRGATCCTACCTT	2646	6	192
1607	1248	CATGGGTACCAGRCRAYAA	1779	1337	CAGYTRGCYACTATTTTCYTTGCTA	1888	6	196
1615	1851	AGRGARCCMYACAATGAATGG	2708	1906	YGRACCCAAATGCGAAATG	2779	6	197
1617	2253	GCAGGAAGYACKATGGGC	3346	2330	ROTKTTGATCCYKTAGGTATGTTTC	3455	6	197
1621	590	GATAGRRGAATGGAGGYTT	921	641	GGCTTAAKTTACYGGYACAGT	1009	6	198
1623	1158	GAGYAGARACYTWTCTATGTAGATGG	1661	1210	TTCTAWTGCATAYTGTGAGTCTGT	1738	6	198
1628	331	GACATAARACARGRCRCAARGA	540	391	GRCATGCTGCATCATTTCYTC	624	6	198
1632	172	ATACCCATGTTYWCAGCATTATCAG	316	264	CTATRTCACTTCCCSTWGGKTC	449	6	199
1679	25	RCWRCGCAAGAGCCGAG	58	44	YARCTCYCTGCTTGCCCA	159	6	204.825
1684	198	GGRGCCACYCCACAAGA	348	269	TGTTCTYGMAGGCTACTAGTAYTC	454	6	205
1713	568	CAGGAGCAGATGATACAGTATTAQA	868	628	RGTRCARCCMAKYTGAGTCAA	981	6	207
1722	806	CCACARGGATGAAAAGGATC	1238	876	RTCTGGTGRKWRRAATCCCA	1317	6	207.125
1764	407	CAHTAGARAAAATGATGACAGCATG	641	462	CCAAARCCYTTTTTYCTAGG	700	6	211.875
1786	421	ATGACAGCATGYCARGGAGT	655	468	KYCCACATYCCAACARCC	706	6	214.875
1791	1038	AAAATCTRAARACAGGRAARTATGC	1528	1115	GGGTRTRBACAACTCCCA	1614	6	216
1798	732	AGRACTCARGAYTTYGGARGT	1143	809	GATCCTTCCATCCYGTGG	1239	6	218.25
1812	2227	TRARRRACAATTGGAAAGTGAATT	3280	2266	GCTGTTGCACTATDCCAGACAA	3369	6	225
1815	1721	TGTGGCARGTAGACAGGATGA	2495	1774	CMTGCCCARDTGCCA	2571	6	226
1830	1549	GCTGARCACTTARGACAGCAGT	2166	1622	CCTGCACCTTCCGAGGADAGYTT	2360	6	231
1845	933	GGGDTATGARCTCCATCCTGA	1378	985	TAGAATYCCGTRTYCTGGCA	1462	6	238
1850	573	TRYMAGGAARATGAAAACAAA	879	656	CCATCCATBCCTGGCTT	1028	6	239
1875	2016	GRATWAGRGAAGAGCAQAAGAYAG	2928	2067	ACARGCATGTGRGCCA	2999	6	245.5
1885	713	QAGRAAATTRGTARGAYTTCAGRGA	1119	809	GATCCTTCCATCCYGTGG	1239	6	251.25
1890	1124	ARTGGGAGTTGTYYAACCC	1624	1193	TGAGTCTGTACTATRTTYACTTCT	1717	6	254
1898	1978	ATYTMCYATGGCAGGAAGAAGC	2880	2000	CACTRTCTTCTGCTTTTCYCTWAT	2911	6	257.125
1912	1124	ARTGGGAGTTGTYYAACCC	1624	1195	WTGCATAYTGTGAGTCTGTACTAT	1721	6	264
1950	2478	GTGCTYTTCAQYACCRCC	3639	2503	AGCCCTGTCTKATTTSTRGGTAT	3676	6	268.5
1960	1721	TGTGGCARGTAGACAGGATGA	2495	1790	GGYCWGRTCTAYTTGTGTRCTATA	2599	6	271
1993	1896	TCTATRAHMYTATGGGATACYTG	2765	1977	CGCTTCTTCCGCCAT	2881	6	290
1996	483	RGARGMCAYCARATGAAAGA	728	548	CTGTATCATCTGCTCCTGTRCTAA	841	6	296.375
2001	455	GTGGCARRGMAGGRCA	692	513	GCAAAGRGTGATYTGAGGA	800	6	300.5
2012	481	ATGTGGRMRRGARGMCA	725	540	CTAATACTGTATCATCTGCTCTGT	832	6	314.375
2021	1783	GGRTCTCCATMGAATGGAG	2586	1859	CCATTCATTGRKGGYCYCT	2719	6	323
2022	1842	ARGAYAGTGGACRAGCCC	2686	1937	GGATGVTCCAGGGSTC	2834	6	323.375
2044	2511	CCYASAAGAATMAGACAGGGCTT	3697	2544	AAAYARCCOWTCCAGTCCC	3763	6	350.875
2050	1947	CCRGRRGYCAGCCT	2847	2007	CCACTRTCTTCTGCTTTTCYCT	2918	6	359.75
2051	483	RGARGMCAYCARATGAAAGA	728	576	CCTCCAATTCYCGCTATCATT	895	6	360.375
2052	1949	ATCRRGRRGYCAGCC	2849	2007	CCACTRTCTTCTGCTTTTCYCT	2918	6	360.75
2055	442	AGRGWTTRGCTGARGCAATGAG	677	513	GCAAAGRGTGATYTGAGGA	800	6	395.375
2068	1928	CRRCAAYAGCAGAATAGGCATT	2819	2000	CACTRTCTTCTGCTTTTCYCTWAT	2911	6	433.125
2077	2355	GGGGYTGCTTGGAAAA	3489	2449	GYCTYKCTKCCACCTYCT	3607	6	442
2083	2188	AGRGARTTTTTCTAYTGYAATAQA	3202	2266	GCTGTTGCACTATDCCAGACAA	3369	6	497

2085	1323	GYAYGTGAKTTAAAYTGGCCACC	1874	1370	GGRCTACACTACTGTGOCATGC	1928	7	101
2088	900	CHCCATTYCTTTGGATGGG	1344	955	YTTYGTATRTCATTRACAGTCCAG	1415	7	101
2090	1571	ARATGGCAGTATTGATYACAATT	2200	1588	ARTTCTYTAGTTKGTATRTGTGWTG	2274	7	101
2091	362	GAMACCYTGYYTRTCCAAAATG	593	399	CCYTGRCATGCTGCATCA	633	7	101
2092	1589	TACMAACTARAGAAYTACAAAAACA	2277	1612	CAGAGBAGYTTKGTGGTCCCT	2348	7	101
2096	542	GARGCYOTWTTAGAYACAGGAGCA	835	585	TTACYTTRATAAARCCOCCAATTCC	914	7	101
2097	136	ACCTAGRACYTTRAYGATGG	279	194	GRGTGGCYCCYCTGA	341	7	101
2098	1124	ARTGGAGTTTGTAAAYACCCC	1624	1152	CTRYTWGCTGCYCATCTACATAG	1856	7	101
2102	936	CTCCATCCTGAYARATGGACA	1381	965	TGCCGARTTYARTTTYYCCYAC	1427	7	101
2111	2050	GTDOCTGTGTGRRRAGAWGC	2970	2067	ACARGCATGTGTRGCCCA	2999	7	102
2113	2319	TCCRGRCAGAGTCTCTGCG	3444	2368	GCACBYAGTGGTGARAT	3504	7	102
2122	2445	RAGGTGGMGAGMRGRCA	3603	2463	GGTARCTGAARAGGCACAGG	3624	7	102
2161	2324	CARCTCCRGRCAGAGTCCCT	3449	2368	GCACBYAGTGGTGARAT	3504	7	105
2168	1078	TARTYATATGGGAAARAYYCTAA	1574	1103	AAACTCCCAITCAGGAATCCA	1602	7	105
2187	2450	RAATMGAAAGAGRAGTGGMGA	3608	2472	GTARCTGAARAGGCACAGGYTC	3633	7	107
2188	353	RYTGGATGACMGAMACCYTG	584	391	GRCATGCTGTCATCATTTCTYC	624	7	107
2209	1947	CCRGRRRGCACQCT	2947	1953	COATRGRKARATGCCTAAGCC	2857	7	109.625
2219	1949	ATCCRGRRRGCACQCC	2949	1953	COATRGRKARATGCCTAAGCC	2857	7	110.625
2232	1783	QGRGTCTCCATMGAAATGGAG	2586	1805	TYOTTATRCAGWKTCTGMAAAACA	2623	7	111
2241	590	GATAGRRGDAATGGAGGYTT	921	821	ATTATRTTGAYAGNGTAGGTCCTA	963	7	112
2249	237	GARGCTGOWGAATGGGAYAG	412	269	TGTTCTYGMAGGSTACTAGTAGYTC	454	7	112
2259	1752	AAGYTCAGAAAGTACAYATYCCABTA	2538	1776	CTCCATTCKATGGAGACYCC	2574	7	113
2277	2478	QGARCCTGTGCCYTTTCAG	3637	2485	TRAKRSOYTGCCACCQCC	3650	7	114.5
2290	1384	GGAGAAGTAGAYTGTAGYCCAGG	1850	1440	GYYGGRATMACYTCYGGCTTCT	2020	7	116
2320	1380	GCATGGACAAGTAGAYTGTAGYCC	1846	1440	GYYGGRATMACYTCYGGCTTCT	2020	7	119
2367	1483	TTTGGVRTYCCGTACAAAYCC	2102	1546	ATAGTCCCATYTGKAGTGGTGTG	2163	7	125
2370	2286	ATAGTGCAACAGCARARCAATYTG	3397	2330	ROTKTTGATCCYKTAGGTATCTTTTC	3455	7	125
2377	933	GGQDTATGARCTCCATCTGGA	1378	975	SRTAAAYTGRCTTGCCCA	1438	7	126
2390	203	CARGCAGCHATGCAAAATGT	365	264	CTATRTCACTCCSTWGGKTC	449	7	127
2440	762	QDQRTGCATAYTTYTCAGTYCC	1183	809	GATCCTTTCCATCCYTGTTGG	1239	7	131,125
2455	375	CAAAATGCRAAYCCAGAYTG	606	432	GTCATTGCYTCAGYAAWACYCT	667	7	132
2488	1278	TTGGAGGRAATGAACAAGTRGATAA	1815	1318	GGARRTTAAAMTCACTRRCCATTG	1889	7	133
2483	763	GTRGGDGRTGATAYTTYTCAGT	1184	809	GATCCTTTCCATCCYTGTTGG	1239	7	134,125
2493	1448	CARGCAGRACAGGRRCARGA	2028	1486	CCACCAACAKGCDGC	2080	7	135
2496	2271	RTTGTCTGQHATAGTGCAACAGC	3377	2330	ROTKTTGATCCYKTAGGTATCTTTTC	3455	7	136
2499	331	GACATAARACARQRCCAAARGA	540	369	RTCTGRRTYGCAATTTGGA	600	7	136
2584	900	CHCCATTYCTTTGGATGGG	1344	975	SRTAAAYTGRCTTGCCCA	1438	7	144
2588	865	CWGAYTTAGAAATAGGRCARCAYAG	1306	927	ACTGTCCATYTRTCAGGATGGAG	1372	7	144
2600	1463	GCAGGMAGRTGGCCAGT	2051	1516	CYACYACYCCYTRCTTTGG	2131	7	146
2608	1934	GTAGAYCCTARMHWAGASCCCTGG	2830	1977	CCGCTCTTCTGCCAT	2881	7	146.625
2610	862	RAAGCCAGGATGGATGG	1036	685	CAAAATYTGAGGTRTTRTATGGRTT	1087	7	147
2645	18	AGGACTCGGGTCTGCTGA	41	32	TCCGADKYATCTARWYTCQCC	130	7	149.625
2663	2286	ATAGTGCAACAGCARARCAATYTG	3397	2345	CAROGCCAAKYCCYAG	3475	7	152
2665	203	CARGCAGCHATGCAAAATGT	365	269	TGTTCTYGMAGGSTACTAGTAGYTC	454	7	152
2669	2018	GAAAGAGCAGAGAYAGTGGMAA	2930	2037	YYCCACAGGHCACYCCATA	2955	7	152.5
2673	855	ATGTAGQNTCOWQAYTTAGAAATAGG	1295	927	ACTGTCCATYTRTCAGGATGGAG	1372	7	153

2702	143	CTAGRACYTTRAAYGCATGGGT	286	211	AACATTTGCATDGGCTGCTG	377	7	156
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表 13 HIV-1 共通プライマー検証用ゲノムフラグメント

Genotype	Sequence
A	TTATAGGTYCTGATTTAGAAAATAGGGCAGCATAGAAMGAAAAATAGAGGAGYTAAGASCCTATCTATTGAGSTGGGGATTTACYACAC CAGACAAAAAGCATCAGAAAAGAACCTCCATTTCCTTTGGATGGGATATGAACTCCATCCTGACAAAATGGACAGTCCAG TTATAGGATCTGATTTAGAAAATAGGGCAGCATAGAACAAAAATAGAGGAACTGAGACAAACATTTGTTGAGGTGGGGATTTACACAC
B	CAGACAAAAAACATCAGAAAAGAACCTCCATTTCCTTTGGATGGGTTATGAACTCCATCCTGATAAAATGGACAGTACAG TTATAGGATCTGATTTAGAAAATAGGGCAGCATAGAACAAAAATAGAGGAGYTAAGAGAACATCTACTGAAATGGGGATTTACTACAC
F	CAGACAAAAAACATCAGAAAAGAACCTCCATTTCCTTTGGATGGGTTATGAACTCCATCCTGATAAAATGGACAGTACAG TTATAGGATCTGATTTAGAAAATAGGGCAGCATAGAACAAAAATAGAGGAACTGAGAACTCCATCCTGATAAAATGGACAGTACAG
D	CAGACAAAAAGCATCAGAAAAGAACCTCCATTTCCTTTGGATGGGTTATGAACTCCATCCTGATAAAATGGACAGTACAG TTATAGGATCTGATTTAGAAAATAGGCAACATAGAGAAAAAATAGAGAGTTAAGAGCTCATTGTTGAGGTGGGGATTTACCACAC
H	CAGACAAAAAACATCAGAAAAGAACCTCCATTTCCTTTGGATGGGTTATGAACTCCATCCTGATAAAATGGACAGTACAG TTATAGGATCTGATTTAGAAAATAGGGCAACATAGAGCAAAAAATAGAGGAACTTAAAGAACCTATTAAAGTGGGGATTTACCACAC
C	CAGACAAAAAACATCAGAAAAGAACCTCCATTTCCTTTGGATGGGTTATGAACTCCATCCTGATAAAATGGACAGTACAG TTATAGGATCTGATTTAGAAAATAGGGCAACATAGAGCAAAAAATAGAGGAACTTAAAGAACCTATTAAAGTGGGGATTTACCACAC
E	CAGACAAAAAGCATCAGAAAAGAACCTCCATTTCCTTTGGATGGGTTATGAACTCCATCCTGATAAAATGGACAGTACAG TTATAGGATCTGATTTAGAAAATAGGGCAGCAGCAAAATAAAAAATAGAGGAGCTAAGAGCTCATCTATTGAGGTGGGGATTTACTACAC
G	TTATAGGATCTGATTTAGAAAATAGGGCAGCATAGAACAAAAATAGAGGAGYTAAGAGAACATCTACTGAGATGGGGATTTACCACAC CAGATAAGAAACATCAGAAAAGAACCTCCATTTCCTTTGGATGGGTTATGAGCTCCATCCTGACAAAATGGACAGTACAA

表 14 HIV-1 ゲノムフラグメント合成用オリゴマー

Genotype	オリゴマー	塩基配列	Length
A	HIV-1A_T1	TTGTATGTAGGTCCTGATTTAGAAAATAGGGCAGCATAGAA	40
	HIV-1A_T2	TCAATAGATGGGTCTTACTCCTCTATTTTCTCTATGCTGCCCTATTTCTAAATCAGA	58
	HIV-1A_T3	AAAATAGAGGAGTAAGACCCATCTATTGAGTGGGGATTTACACACAGAC	50
	HIV-1A_T4	ATGGAGGTTCTTCTGATGCTTTTTGTCTGGTGTGTAATCCCCAC	46
	HIV-1A_T5	AAAAAGCATCAGAAAAGAACCTCCATTTCCTTTGGATGGGATATGAACTCCAT	50
	HIV-1A_T6	GGCTGGACTGTCCATTTGTCAGGATGGAGTTCATACCCATCCAAAGA	48
B	HIV-1B_T1	TTGTATGTAGGATCTGATTTAGAAAATAGGGCAGCATAGA	39
	HIV-1B_T2	CAAATGTTGCTCAGTTCCTCTATTTTGTCTATGCTGCCCTATTTCTAAATCAGATC	59
	HIV-1B_T3	ACAAAAATAGAGGAACTGAGACAACATTTGTTGAGGTGGGGATTTACACACACC	53
	HIV-1B_T4	ATGGAGGTTCTTCTGATGTTTTTGTCTGGTGTGTAATAATCCCACTCGAA	52
	HIV-1B_T5	AGACAAAAAACATCAGAAAAGAACCTCCATTTCCTTTGGATGGGTTATGAACTCCA	54
	HIV-1B_T6	GGCTGTACTGTCCATTTATCAGGATGGAGTTCATAACCCATCCAAAGGA	49
C	HIV-1C_T1	TTGTATGTAGGATCTGATTTAGAAAATAGGGCAACATAGA	39
	HIV-1C_T2	ACTTTAATAGATGGTTTCTTAATTCCTCTATTTTGTCTATGTTGCCCTATTTCTAAATCAGATC	66
	HIV-1C_T3	GCAAAAAATAGAGGAAATTAAGAAACCATCTATTAAGTGGGGATTTACCACACAGACA	58
	HIV-1C_T4	AATGGGGTTCTTCTGATGTTTTTGTCTGGTGTGTAATAATCCCACTCGAA	46
	HIV-1C_T5	AGAAACATCAGAAAAGAACCTCCATTTCCTTTGGATGGGGTATGAACTCC	48
	HIV-1C_T6	GGCTGTACTGTCCATTTATCAGGATGGAGTTCATAACCCATCCAAAGGA	48
D	HIV-1D_T1	TTGTATGTAGGATCTGACTTAGAAAATAGGGCAGCAT	36
	HIV-1D_T2	TAGGTGTCGCCCTTAATTCCTCTATTTTATCTATGCTGCCCTATTTCTAAGTCAGAT	58
	HIV-1D_T3	AGAATAAAAAATAGAGGAAATTAAGGGACACCTATTGAAAGTGGGGATTTACCACACC	56
	HIV-1D_T4	GTGGTCTTCTCTGATGTTTTTGTCTGGTGTGTAATAATCCCACTCGAA	49
	HIV-1D_T5	AGACAAAAAGCATCAGAAAAGAACCTCCATTTCCTTTGGATGGGTTATGAACTCCAT	55
	HIV-1D_T6	GGCTGTACTGTCCATTTATCAGGATGGAGTTCATAACCCATCCAAAGAAATG	52
F	HIV-1F_T1	TTGTATGTAGGTCCTGACTTAGAAAATAGGGCAGCATAGA	39
	HIV-1F_T2	AGATGTTCTCTTAACCTCTACTTTTGTGATGCTGCCCTATTTCTAAGTCA	54
	HIV-1F_T3	ACAAAAGTAGAGGAGTTAAGAGAACATCTACTGAAATGGGGATTTACTACACCA	54
	HIV-1F_T4	GGGGGTTCTTTTGTGATGTTTTTGTCTGGTGTAGTAAATCCCATTTTCAGT	51
	HIV-1F_T5	GACAAAAAACATCAGAAAAGAACCTCCATTTCCTTTGGATGGGGTATGAACTC	51

	HIV-1F_T6	GGCTGCACCTGTCCATTTATCAGGATGGAGTTCATACCCCATCCAAAGGAAT	51
G	HIV-1G_T1	TTATATGTAGGATCAGACTTAGAAATAGGGCAGCATAGA	39
	HIV-1G_T2	CAGTAGATGTTCTTAACTCTTCTATTTTGGCTCTATGCTGCCOTATTTCTAAGTCT	58
	HIV-1G_T3	GCAAAAAATAGAAGAGTTAAGAGAACATCTACTGAGATGGGATTTACCACACCA	54
	HIV-1G_T4	AATGGAGGTTCTTCTGATGTTTCTTATCTGGTGGTAAATCCCATCT	50
	HIV-1G_T5	QATAAGAAAACATCAGAAAAGAACCTCCATTTCTTTGGATGGGATATGAGCTCG	52
	HIV-1G_T6	GGTTGTAAGTGTCCATTTGTCAGGATGGAGCTCATATCCGATCCAAAGA	48
H	HIV-1H_T1	TTGTATGTAGGATCTGACTTAGAAATAGGACAACATAGA	39
	HIV-1H_T2	TCAACAAATGAGCTCTTAACTCTTCTATTTTCTCTATGTTGCTCTATTCTAAGTCAGATCCTAC	67
	HIV-1H_T3	GAAAAAATAGAAGAGTTAAGAGCTCATTGTTGAGGTGGGATTCACCACACC	53
	HIV-1H_T4	GGGGTCTTCTGATGTTTTGGTCTGGTGGTGAATCCCCACC	45
	HIV-1H_T5	AQACCAAAAACATCAGAAAAGAACCCCATTTCTTTGGATGGGATATGAACTCCAT	55
	HIV-1H_T6	GGCTGTAAGTGTCCATTTGTCAGGATGGAGTTCATATCCGATCCAAAGAAATG	52

表 15 HEV Genotype 共通プライマー設計対象ゲノム塩基配列

ID	Accession	Geno type	Definition	Length
1	AB437319	3	Hepatitis E virus genomic RNA complete genome genotype 3 isolate: JE03-1760F clone: pJE03-1760F/dORF1	6899
150	EU495148	3	Hepatitis E virus isolate TLS25 complete genome	7321
335	AB248522	3	Hepatitis E virus genomic RNA complete genome isolate: swJ12-4	7241
342	AB220979	4	Hepatitis E virus genomic RNA complete genome genotype 4 isolate: HE-JA41	7265
350	AB220971	4	Hepatitis E virus genomic RNA complete genome genotype 4 isolate: HE-JF3	7262
533	AB291964	4	Hepatitis E virus genomic RNA complete genome isolate: JYK-Tok03C	7244
756	AB074920		Hepatitis E virus genomic RNA nearly complete genome isolate: JMY-Haw	7240
888	FJ457024		Hepatitis E virus isolate HEV-H from India complete genome	7217
1142	EU676172	4	Swine hepatitis E virus isolate swGX40 complete genome	7269
1567	AB369690	4	Hepatitis E virus genomic RNA complete genome genotype 4 strain: E067-SIJ05C	7236
1568	AB369689	3	Hepatitis E virus genomic RNA complete genome genotype 3 strain: E088-STM04C	7215
1731	EU366959	4	Hepatitis E virus isolate swGX32 complete genome	7281
2095	EF206691		Avian hepatitis E virus from USA complete genome	6649
2997	AY594199		Swine hepatitis E virus strain swCH25 complete genome	7270
3075	AY115488		Swine hepatitis E virus strain Arkell complete genome	7255

表 16 HEV Genotype 共通プライマー(100組のみ表示)

Pair ID	Primer ID (Forward)	塩基配列(Forward)	平均位置 (Forward)	Primer ID (Reverse)	塩基配列 (Reverse)	平均位置 (Reverse)	プライマーの degeneracy 指数 ¹⁾	子配サイズ
1	81	GGTTCORBGYATHGARAA	4252.6	105	CRCNGARTGYTTCTTCCA	4561.8	13	309.2
2	83	CCNTGGTTCORBGCYAT	4246.6	105	CRCNGARTGYTTCTTCCA	4561.8	13	315.2
3	59	GGYAARGTBGGNCAGGG	4189.6	105	CRCNGARTGYTTCTTCCA	4561.8	13	372.2
4	81	GGTTCORBGYATHGARAA	4252.6	102	YTCRCNGARTGYTTCTTCC	4562.8	14	310.2
5	81	GGTTCORBGYATHGARAA	4252.6	103	GYTCRCNGARTGYTTCTTCC	4563.8	14	311.2
6	83	CCNTGGTTCORBGCYAT	4246.6	102	YTCRCNGARTGYTTCTTCC	4562.8	14	316.2
7	83	CCNTGGTTCORBGCYAT	4246.6	103	GYTCRCNGARTGYTTCTTCC	4563.8	14	317.2
8	86	TNTTYGGMCCNTGGTTCC	4239.6	105	CRCNGARTGYTTCTTCCA	4561.8	14	322.2
9	81	GGTTCORBGYATHGARAA	4252.6	113	YCATTRTCCARAYDGRTRTCCA	4597.8	14	345.2
10	83	CCNTGGTTCORBGCYAT	4246.6	113	YCATTRTCCARAYDGRTRTCCA	4597.8	14	351.2
11	59	GGYAARGTBGGNCAGGG	4189.6	102	YTCRCNGARTGYTTCTTCC	4562.8	14	373.2
12	59	GGYAARGTBGGNCAGGG	4189.6	103	GYTCRCNGARTGYTTCTTCC	4563.8	14	374.2
13	59	GGYAARGTBGGNCAGGG	4189.6	113	YCATTRTCCARAYDGRTRTCCA	4597.8	14	408.2
14	50	TYCARAARGAYTYGRMYAARTTYAC	4150.6	72	GGAACCANGGKCCRAA	4264.6	15	114
15	99	GARAAYGAYTTYTCNGARTTYGA	4378.8	105	CRCNGARTGYTTCTTCCA	4561.8	15	183
16	39	NRRSAARGGYCARGAYGG	4069.6	72	GGAACCANGGKCCRAA	4264.6	15	195
17	38	ATGSTNRRSAARGGYCARGA	4066.6	72	GGAACCANGGKCCRAA	4264.6	15	198
18	40	CYATGSTNRRSAARGGYCA	4063.6	72	GGAACCANGGKCCRAA	4264.6	15	201
19	79	NTGGTTCORBGYATHGA	4249.6	105	CRCNGARTGYTTCTTCCA	4561.8	15	312.2
20	81	GGTTCORBGYATHGARAA	4252.6	108	CVGGYTCRCNGARTG	4570.8	15	318.2
21	86	TNTTYGGMCCNTGGTTCC	4239.6	102	YTCRCNGARTGYTTCTTCC	4562.8	15	323.2
22	83	CCNTGGTTCORBGCYAT	4246.6	108	CVGGYTCRCNGARTG	4570.8	15	324.2
23	86	TNTTYGGMCCNTGGTTCC	4239.6	103	GYTCRCNGARTGYTTCTTCC	4563.8	15	324.2
24	73	TGYGCHYTNTTYGGMCC	4231.6	105	CRCNGARTGYTTCTTCCA	4561.8	15	330.2
25	86	TNTTYGGMCCNTGGTTCC	4239.6	113	YCATTRTCCARAYDGRTRTCCA	4597.8	15	358.2
26	63	GGNCAGGGNATWTCBGC	4198.6	105	CRCNGARTGYTTCTTCCA	4561.8	15	363.2
27	59	GGYAARGTBGGNCAGGG	4189.6	108	CVGGYTCRCNGARTG	4570.8	15	381.2
28	46	GNATHACMTTYTYCARAARGAYTG	4138.6	72	GGAACCANGGKCCRAA	4264.6	16	126
29	136	MVGCSAATGGYGARCC	6317.73	138	WCRTGYTGRTTYVCRARTARTCYTG	6455.73	16	138
30	81	GGTTCORBGYATHGARAA	4252.6	91	RAAYTCNGARAARTORTTYTCAAA	4393.8	16	141.2
31	83	CCNTGGTTCORBGCYAT	4246.6	91	RAAYTCNGARAARTORTTYTCAAA	4393.8	16	147.2
32	99	GARAAYGAYTTYTCNGARTTYGA	4378.8	102	YTCRCNGARTGYTTCTTCC	4562.8	16	184
33	99	GARAAYGAYTTYTCNGARTTYGA	4378.8	103	GYTCRCNGARTGYTTCTTCC	4563.8	16	185
34	98	KGTDTTTCARAAYGAYTTYTCNGA	4372.8	105	CRCNGARTGYTTCTTCCA	4561.8	16	188
35	59	GGYAARGTBGGNCAGGG	4189.6	91	RAAYTCNGARAARTORTTYTCAAA	4393.8	16	204.2
36	99	GARAAYGAYTTYTCNGARTTYGA	4378.8	113	YCATTRTCCARAYDGRTRTCCA	4597.8	16	219
37	79	NTGGTTCORBGYATHGA	4249.6	102	YTCRCNGARTGYTTCTTCC	4562.8	16	313.2
38	79	NTGGTTCORBGYATHGA	4249.6	103	GYTCRCNGARTGYTTCTTCC	4563.8	16	314.2
39	81	GGTTCORBGYATHGARAA	4252.6	104	VGGYTCRCNGARTGYTT	4567.8	16	315.2
40	83	CCNTGGTTCORBGCYAT	4246.6	104	VGGYTCRCNGARTGYTT	4567.8	16	321.2
41	86	TNTTYGGMCCNTGGTTCC	4239.6	108	CVGGYTCRCNGARTG	4570.8	16	331.2
42	73	TGYGCHYTNTTYGGMCC	4231.6	102	YTCRCNGARTGYTTCTTCC	4562.8	16	331.2

43	73	TGYGCHYNTTYGGMCC	4231.6	103	GYTRCCNGARTGYTTCTTC	4563.8	16	332.2
44	70	GCNTGMSYAARACYTTBTG	4216.6	105	CRCCNGARTGYTTCTTCCA	4561.8	16	345.2
45	66	CBGNTGMSYAARACYTT	4213.6	105	CRCCNGARTGYTTCTTCCA	4561.8	16	348.2
46	79	NTGGTTCRBCGYATHGA	4249.6	113	YCATRTTCCARAYDGRTRTCCA	4597.8	16	348.2
47	63	GGNCAGGGNATWTCBGC	4198.6	102	YTRCCNGARTGYTTCTTCC	4562.8	16	364.2
48	63	GGNCAGGGNATWTCBGC	4198.6	103	GYTRCCNGARTGYTTCTTC	4563.8	16	365.2
49	57	AARGTBGGNCAGGGNATWTC	4195.6	105	CRCCNGARTGYTTCTTCCA	4561.8	16	366.2
51	54	GAAARGTBGGNCAGGGNAT	4192.6	105	CRCCNGARTGYTTCTTCCA	4561.8	16	369.2
52	59	GGYAARGTBGGNCAGGG	4189.6	104	VGGYTRCCNGARTGYTT	4567.8	16	378.2
53	63	GGNCAGGGNATWTCBGC	4198.6	113	YCATRTTCCARAYDGRTRTCCA	4597.8	16	399.2
54	50	TYCARAARGAYTYRMYAARTT YAC	4150.6	105	CRCCNGARTGYTTCTTCCA	4561.8	16	411.2
55	39	NRRSAARGGYCARGAYGG	4069.6	105	CRCCNGARTGYTTCTTCCA	4561.8	16	492.2
56	38	ATGSTNRRSAARGGYCARGA	4066.6	105	CRCCNGARTGYTTCTTCCA	4561.8	16	495.2
57	40	CYATGSTNRRSAARGGYCA	4063.6	105	CRCCNGARTGYTTCTTCCA	4561.8	16	498.2
58	50	TYCARAARGAYTYRMYAARTT YAC	4150.6	74	VYGGAAACCANGGKCC	4267.6	17	117
59	50	TYCARAARGAYTYRMYAARTT YAC	4150.6	71	ATRGCVYGGAAACCANGG	4270.6	17	120
60	50	TYCARAARGAYTYRMYAARTT YAC	4150.6	78	YTCDATRGCVYGGAAACCA	4273.6	17	123
61	81	GGTTCRBCGYATHGARAA	4252.6	88	AYTCNGARAARTCRRTTYTCAAHA C	4390.8	17	138.2
62	39	NRRSAARGGYCARGAYGG	4069.6	56	CCCTGNCCVACYTTRCC	4213.6	17	144
63	83	CCNTGGTTCRBCGYAT	4246.6	88	AYTCNGARAARTCRRTTYTCAAHA C	4390.8	17	144.2
64	38	ATGSTNRRSAARGGYCARGA	4066.6	56	CCCTGNCCVACYTTRCC	4213.6	17	147
65	40	CYATGSTNRRSAARGGYCA	4063.6	56	CCCTGNCCVACYTTRCC	4213.6	17	150
66	86	TNTTYGMCNTGGTTC	4239.6	91	RAAYTCNGARAARTCRRTTYTCAA A	4393.8	17	154.2
67	88	KGDTTGTGARAAYGAYTYTCN GA	4372.8	102	YTRCCNGARTGYTTCTTCC	4562.8	17	190
68	86	KGDTTGTGARAAYGAYTYTCN GA	4372.8	103	GYTRCCNGARTGYTTCTTC	4563.8	17	191
69	99	GARAAYGAYTYTCNGARTTYG A	4378.8	108	CVGGYTRCCNGARTG	4570.8	17	192
70	39	NRRSAARGGYCARGAYGG	4069.6	74	VYGGAAACCANGGKCC	4267.6	17	198
72	39	NRRSAARGGYCARGAYGG	4069.6	71	ATRGCVYGGAAACCANGG	4270.6	17	201
73	38	ATGSTNRRSAARGGYCARGA	4066.6	74	VYGGAAACCANGGKCC	4267.6	17	201
74	59	GGYAARGTBGGNCAGGG	4189.6	88	AYTCNGARAARTCRRTTYTCAAHA C	4390.8	17	201.2
75	40	CYATGSTNRRSAARGGYCA	4063.6	74	VYGGAAACCANGGKCC	4267.6	17	204
76	38	ATGSTNRRSAARGGYCARGA	4066.6	71	ATRGCVYGGAAACCANGG	4270.6	17	204
77	38	NRRSAARGGYCARGAYGG	4069.6	78	YTCDATRGCVYGGAAACCA	4273.6	17	204
78	40	CYATGSTNRRSAARGGYCA	4063.6	71	ATRGCVYGGAAACCANGG	4270.6	17	207
79	38	ATGSTNRRSAARGGYCARGA	4066.6	78	YTCDATRGCVYGGAAACCA	4273.6	17	207
80	40	CYATGSTNRRSAARGGYCA	4063.6	78	YTCDATRGCVYGGAAACCA	4273.6	17	210
81	88	KGDTTGTGARAAYGAYTYTCN GA	4372.8	113	YCATRTTCCARAYDGRTRTCCA	4597.8	17	225
82	31	ATHCHGCHMTBAYTYTGA	3176	33	CCCTGNCCVACYTTRCC	3443	17	267
83	79	NTGGTTCRBCGYATHGA	4249.6	108	CVGGYTRCCNGARTG	4570.8	17	321.2
84	75	HYTNTTYGMCNTGGTTC	4238.6	105	CRCCNGARTGYTTCTTCCA	4561.8	17	323.2
85	76	CHYTNTTYGMCNTGGTTC	4237.6	105	CRCCNGARTGYTTCTTCCA	4561.8	17	324.2
86	86	TNTTYGMCNTGGTTC	4239.6	104	VGGYTRCCNGARTGYTT	4567.8	17	328.2
87	77	ACYTTBTGYGCHYNTTYGG	4228.6	105	CRCCNGARTGYTTCTTCCA	4561.8	17	333.2
88	73	TGYGCHYNTTYGGMCC	4231.6	108	CVGGYTRCCNGARTG	4570.8	17	339.2
89	70	GCNTGMSYAARACYTTBTG	4216.6	102	YTRCCNGARTGYTTCTTCC	4562.8	17	346.2

90	70	GCNTGGMSYAARACYTTBTG	4216.6	103	GYTCRCNGARTGYTCTTCC	4563.8	17	347.2
91	66	CBGCONTGGMSYAARACYTT	4213.6	102	YTCRCNGARTGYTCTTCC	4562.8	17	349.2
92	66	CBGCONTGGMSYAARACYTT	4213.6	103	GYTCRCNGARTGYTCTTCC	4563.8	17	350.2
93	57	AARGTBGGNCAGGNATWTC	4195.6	102	YTCRCNGARTGYTCTTCC	4562.8	17	387.2
94	57	AARGTBGGNCAGGNATWTC	4195.6	103	GYTCRCNGARTGYTCTTCC	4563.8	17	388.2
95	54	GYAARGTBGGNCAGGNAT	4192.6	102	YTCRCNGARTGYTCTTCC	4562.8	17	370.2
96	54	GYAARGTBGGNCAGGNAT	4192.6	103	GYTCRCNGARTGYTCTTCC	4563.8	17	371.2
97	63	GGNCAGGNATWTCBGC	4196.6	108	CVGGYTCRCNGARTG	4570.8	17	372.2
98	70	GCNTGGMSYAARACYTTBTG	4216.6	113	YCATTRTCCARAYDGRITCCA	4597.8	17	381.2
99	66	CBGCONTGGMSYAARACYTT	4213.6	113	YCATTRTCCARAYDGRITCCA	4597.8	17	384.2
100	57	AARGTBGGNCAGGNATWTC	4195.6	113	YCATTRTCCARAYDGRITCCA	4597.8	17	402.2

表 17 HEV 共通プライマー検証用ゲノムフラグメント

ID	塩基配列
1	TTTCCAGAAAGATTGTAATAAGTTTACAACCTGGAGAGACCATCGTCCACGGTAAGGTCGGCCAGGGTATATCGGCCCTGGAGTAAAGACCTT TTGCGCTCTGTTTGGCCCGTGGTTCCCGT
150	TTTCCAGAAAGATTGTAATAAAATTTACAACAGGTGAGACCATTGCCACCGCAAGGTGGCCAGGGCATTTCCGCTTGGAGTAAACCTT TTGTGCTTATTGCGGCCCGTGGTTCCCGC
335	CTTTCCAGAAAGATTGTAACAAATTTACAACAGGTGAGACATTGCCACCGCAAGGTGGCCAGGGTATTTCCGCTTGGAGTAAACCTT TTGTGCTCTATTGGACCGTGGTTCCCGT
342	CTTCCAGAAAGATTGTAATAAGTTTACAACCGGGCAGACAAATAGCGCATGGCAAAGTTGGTCAGGGGATATCTGCATGGAGTAAACCTT TTGTGCTTTGTTCCGCCCATGGTTCCCGC
350	CTTCCAGAAAGACTGTAATAAAATTTACAACAGGGCAGACAAATAGCGCACGGTAAAGTTGGCCAGGGGATATCTGCCTGGAGCAAGACCT TTTGTGCCCTGTTTGGCCCATGGTTCCCGC
533	TTTCCAAAAGGATTGTAATAAAATTTACCACAGGTGAGACAAATAGCGCACGGTAAGGTTGGCCAGGGAATATCTGCCTGGAGTAAAGACTTT CTGCGCTGTGTTTGGCCCGTGGTTCCCGC
756	TTTCCAAAAGGATTGCAATAAGTTTACAACCTGGTGGAGACTATAGCCCATGGCAAAGTTGGCCAGGGTATATCGGCCCTGGAGCAAGACCTT CTGCGCCCTGTTCCGCCCGTGGTTCCCGC
888	CTTCCAGAAAGATTGTAATAAGTTTACCACAGGGCAGACCATTTGCCATGGTAAAGTTGGCCAGGGCATTTCCGCTTGGAGCAAGACCT TTTGTGCCCTGTTTGGCCCGTGGTTCCCGT
1142	CTTCCAGAAAGACTGCAATAAAATTTACAACCTGGTGGAGACTATAGCGCACGGTAAAGTTGGCCAGGGGATATCTGCCTGGAGCAAAACCT TCTGCGCTTGTGTTCCGCCCGTGGTTCCCGC
1567	TTTCCAGAAAGACTGCAATAAGTTTACAACCTGGCGAAACAAATAGCGCATGGCAAAGTTGGCCAGGGGATATCTGCATGGAGTAAACCTT TTGCGCCCTGTTTGGCCCGTGGTTCCCGT
1568	TTTCCAAAAGACTGTAACAAATTTACAACCTGGTGGAGACTATAGCCCATGGCAAAGTTGGTCAGGGCATATCGGCCCTGGAGTAAAGACCTT TTGTGCTTTGTTTGGCCCGTGGTTCCCGT
1731	CTTCCAGAAAGATTGTAATAAGTTTACAACAGGTGAGACGATAGCGCACGGTAAAGTTGGCCAGGGTATATCTGCATGGAGTAAACCTT CTGCGCTCTATTGCGGCCCGTGGTTCCCGC
2095	TTTCCAGAAAGATTGCGCCAAATTTACGTTGGACGATCCCGTTGCACATGGTAAAGTTGGACAGGGGATATCTGCCTGGCCAAAACCTT GTGTGCACTTTTTGGCCCGTGGTTCCCGC
2997	CTTCCAGAAAGATTGTAATAAAATTTACAACCGGGTAAACAAATAGCGCACGGTAAAGTTGGCCAGGGGAATATCCGCATGGAGTAAAGACCTT CTGTGCTGTGTTCCGCCCATGGTTCCCGC
3075	TTTCCAAAAGACTGTAACAAATTTACAACCTGGTGGAGACTATAGCCCATGGTAAAGTTGGCCAGGGTATATCGGCCCTGGAGCAAGACTTT CTGCGCCCTGTTTGGCCCGTGGTTCCCGC

表 18 HEV ゲノムフラグメント合成用オリゴマー

ウイルス塩基配列 ID	オリゴマー名	塩基配列
1	oe_hev_g1_p14_01	TTTCCAGAAAGATTGTAATAAGTTTACAACCTGGAGAGACCA
	oe_hev_g1_p14_02	GATATACCTTGGCCGACCTTACCCTGGACGATGGTCTCTCCAGTTGTAACCTATTACA
	oe_hev_g1_p14_03	AGGTCGGCCAGGGTATATCGGCCCTGGAGTAAAGCCTTTTGGCTCTGTTTGGCCCGTGGT
	oe_hev_g1_p14_04	ACGGAACCACGGCCAAAACAGA
50	oe_hev_g150_p14_01	TTTCCAGAAAGATTGTAATAAAATTTACAACAGGTGAGACCA
	oe_hev_g150_p14_02	CGAAATGCCCTGGCCACCTTCCCGTGGGCAATGGTCTCACCTGTTGTAATTTATTACA
	oe_hev_g150_p14_03	TGGGCCAGGGCATTTCCGCTTGGAGTAAACCTTTTGTGCTTATTCCGCCCGTGGTTCC

	oe_hev_g150_p14_04	GCGGAACCACGGGCCGAAT
335	oe_hev_g335_p14_01	CTTTCAGAAAGATTGTAACAAATTCACAACAGGTG
	oe_hev_g335_p14_02	ATACCCCTGGCCACCTTGGCGTGGGCAATAGTCTCACCTGTTGTGAATTTGTTACAATC
	oe_hev_g335_p14_03	AAGGTGGGCCAGGGTATTTTCGGCCTGGAGTAAACCTTTTGTGCTCTATTTGGACCGTGG
	oe_hev_g335_p14_04	ACGGAACCACGGTCCAAATAGAGCAC
342	oe_hev_g342_p14_01	CTTCCAGAAGGATTGTAATAAGTTTACAACGGGCGAGAC
	oe_hev_g342_p14_02	AGATATCCCCTGACCAACTTTGCCATGCGCTATTGTCTCGCCGTTGTAACCTTAT
	oe_hev_g342_p14_03	CAAAGTTGGTCAGGGGATATCTGCATGGAGTAAACCTTTTGTGCTTTGTTCCGGCCCATG
	oe_hev_g342_p14_04	GCGGAACCATGGGCCGAACAAAGC
350	oe_hev_g350_p14_01	CTTCCAGAAGGACTGTAATAAATTCACAACAGGCGAG
	oe_hev_g350_p14_02	GATATCCCCTGCCCAACTTTACCGTGCCTATTGTCTCGCCTGTTGTAATTTATTACA
	oe_hev_g350_p14_03	AAGTTGGGCAGGGGATATCTGCCTGGAGCAAGACCTTTTGTGCCCTGTTGGCCCATGGT
	oe_hev_g350_p14_04	GCGGAACCATGGGCCAAACAGG
533	oe_hev_g533_p14_01	TTTCCAAAAGGATTGTAATAAATTTACCACAGGTGAGACAATAGC
	oe_hev_g533_p14_02	CGCAGATATTCCCTGCCCAACCTTACCGTGCCTATTGTCTCACCTGTTGTAATTTATT
	oe_hev_g533_p14_03	GGCAGGGAATATCTGCCTGGAGTAAAGACTTTCTGCCTCTGTTTGGCCCTGGTTT
	oe_hev_g533_p14_04	GCGGAACCACGGGCCAAACA
756	oe_hev_g756_p14_01	TTTCCAAAAGGATTGCAATAAGTTTACAACGGTGGAGACTATAGC
	oe_hev_g756_p14_02	CGATATACCCTGCCCAACCTTCCATGGGCTATAGTCTCACCAAGTTGTAACCTTATTG
	oe_hev_g756_p14_03	GGTTGGCCAGGGTATATCGGCCTGGAGCAAGACCTTCTGGCCCTGTTGGCCCGTGGTT
	oe_hev_g756_p14_04	GCGGAACCACGGGCCGAACAG
142	oe_hev_g1142_p14_01	CTTCCAGAAGGACTGCAATAAATTCACACTACGG
	oe_hev_g1142_p14_02	ATCCCTGCCCAGCTTACCGTGCCTATCGTCTCACCCGAGTGAATTTATTGAGCTCC
	oe_hev_g1142_p14_03	AAGGTGGGCAGGGGATATCTGCCTGGAGCAAAACCTTCTGCCTTGTTCGGCCCTGG
	oe_hev_g1142_p14_04	GTGGAACCAAGGCCGAACAAAG
567	oe_hev_g1567_p14_01	TTTCCAGAAAGACTGCAATAAGTTTACAACCTGGC
	oe_hev_g1567_p14_02	ATCCCTGCCCACCTTTGCCATGCGCTATTGTTTCCGCGAGTTGTAACCTTATTGAGCTCT
	oe_hev_g1567_p14_03	AAAGTTGGCAGGGGATATCTGCATGGAGTAAACCTTTTGTGCCCTGTTTGGCCCTGG
	oe_hev_g1567_p14_04	ACGGAACCAGGGGCCAAACAGGG
568	oe_hev_g1568_p14_01	TTTCCAAAAGACTGTAACAAGTTTACAACCTGGTGGAGCC
	oe_hev_g1568_p14_02	GATATGCCCTGACCAACCTTCCATGGGCAATGGTCTCACCAAGTTGTAACCTTATTAC
	oe_hev_g1568_p14_03	AAGTTGGTCAGGGCATATCGGCCTGGAGTAAAGACCTTTTGTGCTTTGTTGGCCCGTGG
	oe_hev_g1568_p14_04	ACGGAACCACGGGCCAAACAAAG
731	oe_hev_g1731_p14_01	CTTCCAGAAAGATTGTAATAAGTTTACAACAGGTGAGACGA
	oe_hev_g1731_p14_02	GATATACCCTGCCGACCTTACCGTGCCTATCGTCTCACCTGTTGTAACCTTATTAC
	oe_hev_g1731_p14_03	AGGTGGGCAGGGTATATCTGCATGGAGTAAACCTTCTGCCTCTATTGGCCCGTGGT
	oe_hev_g1731_p14_04	GCGGAACCACGGGCCAAATAGA
2095	oe_hev_g2095_p14_01	TTTCCAGAAGGATTGCGCCAAATTTACGTTG
	oe_hev_g2095_p14_02	GATATCCCCTGTCACCTTTACCATGTGCAACGGGATCGTCAACGTAATTTGGCGCA
	oe_hev_g2095_p14_03	GTAAGTGGGACAGGGGATATCTGCCTGGCCAAAACCTTTGTTGTCACCTTTTGGCCCT
	oe_hev_g2095_p14_04	CCGGAACCAGGGGCCAAAAGTGCA
2297	oe_hev_g2297_p14_01	CTTCCAGAAGGATTGTAATAAATTTACAACGGGTGAAACA
	oe_hev_g2297_p14_02	GGATATCCCTGCCGACTTTACCGTGCCTATTGTTTACCCGTTGTAATTTATTAC
	oe_hev_g2297_p14_03	TCGGGCAGGGAATATCCGCATGGAGTAAAGACCTTCTGTGCTCTGTTGGGCCATGGTTCC
	oe_hev_g2297_p14_04	GCGGAACCATGGGCCGAAC
3075	oe_hev_g3075_p14_01	TTTCCAAAAGGACTGTAACAAGTTTACAACCTGGTGAG

oe_hev_g3075_p14_02	CGATATACCCTGACCGACCTTACCATGGGCGATGGTCTCACAGGTTGTGAACCTGTTACA
oe_hev_g3075_p14_03	AGGTGGTTCAGGTATATCGGCCCTGGAGCAAGACTTTCTGCGCCCTGTTGGCCCGTGGT
oe_hev_g3075_p14_04	ACGGAACCCAGGCGCAACAGG

表 19 Westnile virus 用プライマー設計対象ゲノム塩基配列

ID	Accession	Isolate	Definition	Length
1	FJ483549	15803	West Nile virus strain 15803 complete genome	11030
19	NC_001563	956	West Nile virus (lineage II strain 956) complete genome	10962
34	FJ425721	Reb_VLG_07_H	West Nile virus isolate Reb_VLG_07_H polyprotein gene complete cds	10980
126	FJ159131	B_1-05-Uu	West Nile virus isolate B_1-05-Uu complete genome	10845
127	FJ159130	5_50-05-Uu	West Nile virus isolate 5_50-05-Uu complete genome	10845
1055	DQ256376	804994	West Nile virus strain 804994 complete genome	11014
1063	DQ176636	Madagascar-AnMg798	West Nile virus strain Madagascar-AnMg798 complete genome	10866
1092	AY765264	Rabensburg	West Nile virus strain Rabensburg isolate 97-103 complete genome	10972
1202	AY688948	Sarafend	West Nile virus strain Sarafend complete genome	11057
1240	AY603654	EthAn4766	West Nile virus strain EthAn4766 complete genome	11029

表 20 Westnile virus 用プライマー(上位 100 件のみ表示)

Pair ID	Primer ID (Forward)	塩基配列(Forward)	Primer ID (Reverse)	塩基配列 (Reverse)	プライマーの degeneracy 指数 ¹	予想サイズ
1	81	GGTTCORBGYATHGARAA	105	CRCCNGARTGYTTCTTCCA	13	309.2
3	59	GGYAARGTBGGNCAGGG	105	CRCCNGARTGYTTCTTCCA	13	372.2
8	86	TNTTYGMCNTGGTTCC	105	CRCCNGARTGYTTCTTCCA	14	322.2
9	81	GGTTCORBGYATHGARAA	113	YCATRTCCARAYDGRTRTCCA	14	345.2
13	59	GGYAARGTBGGNCAGGG	113	YCATRTCCARAYDGRTRTCCA	14	408.2
14	50	TYCARAARGAYTYGYRMYAARTTYAG	72	GGAACCCANGGKCCRAA	15	114
15	99	GARAAYGAYTTYTCNGARTTYGA	105	CRCCNGARTGYTTCTTCCA	15	183
16	39	NRRSAARGGYCARGAYGG	72	GGAACCCANGGKCCRAA	15	195
25	86	TNTTYGMCNTGGTTCC	113	YCATRTCCARAYDGRTRTCCA	15	358.2
28	46	GNATHACMTTYTYCARAARGAYTG	72	GGAACCCANGGKCCRAA	16	126
29	136	MVGCSAATGGYGARCC	138	WORTGYTRTTYVCRTRTCTYTG	16	138
30	81	GGTTCORBGYATHGARAA	91	RAAYTCNGARAARTCRTTYTCAAA	16	141.2
35	59	GGYAARGTBGGNCAGGG	91	RAAYTCNGARAARTCRTTYTCAAA	16	204.2
36	99	GARAAYGAYTTYTCNGARTTYGA	113	YCATRTCCARAYDGRTRTCCA	16	219
44	70	GCNTGGMSYAARACYTTBTG	105	CRCCNGARTGYTTCTTCCA	16	345.2
54	50	TYCARAARGAYTYGYRMYAARTTYAG	105	CRCCNGARTGYTTCTTCCA	18	411.2
55	39	NRRSAARGGYCARGAYGG	105	CRCCNGARTGYTTCTTCCA	16	492.2
62	39	NRRSAARGGYCARGAYGG	58	CCGTGNCVCYTYTRCC	17	144
66	86	TNTTYGMCNTGGTTCC	91	RAAYTCNGARAARTCRTTYTCAAA	17	154.2
82	31	ATHCHGHCHMTBGAYTTYGA	33	CCCTGNGCYTCRTGRAC	17	267
98	70	GCNTGGMSYAARACYTTBTG	113	YCATRTCCARAYDGRTRTCCA	17	381.2
104	46	GNATHACMTTYTYCARAARGAYTG	105	CRCCNGARTGYTTCTTCCA	17	423.2
105	50	TYCARAARGAYTYGYRMYAARTTYAG	113	YCATRTCCARAYDGRTRTCCA	17	447.2
112	39	NRRSAARGGYCARGAYGG	113	YCATRTCCARAYDGRTRTCCA	17	528.2
127	122	BKCHTWYTGCCBCGARAC	127	RACNGAVCGCCADCC	18	185
158	46	GNATHACMTTYTYCARAARGAYTG	113	YCATRTCCARAYDGRTRTCCA	18	459.2

160	128	GHTGGCGBTCNGTYGA	138	WCRTGYTRTTYCYRTARTCYTG	18	576
161	50	TYCARAARGAYTYGRMYAARTTYAC	67	GGKCCRAANARDGCRCA	19	105
167	39	NRRSAARGGYCARGAYGG	55	GCVGAWATNCCCTQNC	19	153
175	70	GCNTGMSYAARACYTTBTG	91	RAAYTCNGARAARTCRITTYCAAA	19	177.2
177	39	NRRSAARGGYCARGAYGG	67	GGKCCRAANARDGCRCA	19	186
190	50	TYCARAARGAYTYGRMYAARTTYAC	91	RAAYTCNGARAARTCRITTYCAAA	19	243.2
191	120	SHAAYTAYGCHCARTAYCGBGT	127	RACNGAVGCCADCC	19	249
192	39	NRRSAARGGYCARGAYGG	91	RAAYTCNGARAARTCRITTYCAAA	19	324.2
207	129	HTGGCGBTCNGTYGARAC	138	WCRTGYTRTTYCYRTARTCYTG	19	573
208	40	CYATGSTRNRRSAARGGYCA	44	TRAAATRYKRCARTCYTTYGRAA	20	102
209	46	GNATHACMTTYTYCARAARGAYTG	67	GGKCCRAANARDGCRCA	20	117
238	46	GNATHACMTTYTYCARAARGAYTG	91	RAAYTCNGARAARTCRITTYCAAA	20	255.2
248	126	TBGAYATGAAYTCNATYACNTCBAC	127	RACNGAVGCCADCC	21	120
273	119	RRTGKXYTSYGGGGTG	123	CNGTVGANGTRATNGARTTCATRTC	21	571.487
282	81	GGTTCRBCGYATHGARA	97	AVWMRTTRITTYGDDGDSWRTCRAA	22	162.2
290	59	GGYAARGTBGGNCAGGG	97	AVWMRTTRITTYGDDGDSWRTCRAA	22	225.2
293	130	KSTNATGTYTYRTHCAYGG	138	WCRTGYTRTTYCYRTARTCYTG	22	516
298	128	GHTGGCGBTCNGTYGA	132	SVCCRGTRTARRSHSTRITTDGTRTA	23	117
300	125	CNWSYRTBGAYATGAAYTONATYAC	127	RACNGAVGCCADCC	23	126
302	86	TNTTYGMCNTGGTTCC	97	AVWMRTTRITTYGDDGDSWRTCRAA	23	175.2
313	45	NMGNATHACMTTYTYCARAARGA	58	CAVAARGTYTRSKCCANGC	24	102
314	129	HTGGCGBTCNGTYGARAC	132	SVCCRGTRTARRSHSTRITTDGTRTA	24	114
323	121	VAAHGCBGTHGGYGG	132	SVCCRGTRTARRSHSTRITTDGTRTA	24	291
324	133	SYTAYACHAAYASDSYTYAYCYGG	138	WCRTGYTRTTYCYRTARTCYTG	24	477
329	120	SHAAYTAYGCHCARTAYCGBGT	123	CNGTVGANGTRATNGARTTCATRTC	25	147
330	70	GCNTGMSYAARACYTTBTG	97	AVWMRTTRITTYGDDGDSWRTCRAA	25	198.2
334	122	BKCHTWTYGGCOCBARAC	132	SVCCRGTRTARRSHSTRITTDGTRTA	25	258
336	50	TYCARAARGAYTYGRMYAARTTYAC	97	AVWMRTTRITTYGDDGDSWRTCRAA	25	264.2
337	39	NRRSAARGGYCARGAYGG	97	AVWMRTTRITTYGDDGDSWRTCRAA	25	345.2
346	46	GNATHACMTTYTYCARAARGAYTG	97	AVWMRTTRITTYGDDGDSWRTCRAA	26	276.2
347	120	SHAAYTAYGCHCARTAYCGBGT	132	SVCCRGTRTARRSHSTRITTDGTRTA	26	342
350	126	TBGAYATGAAYTCNATYACNTCBAC	132	SVCCRGTRTARRSHSTRITTDGTRTA	28	213
354	125	CNWSYRTBGAYATGAAYTCHATYAC	132	SVCCRGTRTARRSHSTRITTDGTRTA	30	219

表 21 Human Parvovirus B19 用プライマー設計対象ゲノム塩基配列

ID	Accession	Definition	Length
1	FJ591158	Human parvovirus B19 isolate KU1 complete genome	5412
26	GM703964	Sequence 133 from Patent WO2008089193	5017
28	GM703962	Sequence 131 from Patent WO2008089193	4844
30	GM703960	Sequence 129 from Patent WO2008089193	4846
158	GM703832	Sequence 1 from Patent WO2008089193	4778
393	DQ333427	Human parvovirus B19 isolate BN32.2 non-structural protein NS1 (NS1) minor capsid protein VP1 (VP1) and major capsid protein VP2 (VP2) genes complete cds	4767
561	DQ357065	Human parvovirus B19 isolate Vn115 NS1 (NS1) 7.5 kDa protein (NS1) VP1 (VP1) 9.5 kDa protein (VP1) and VP2 (VP2) genes complete cds	4449

表 22 Human ParvovirusB19 用プライマー(上位 100 件のみ表示)

Pair ID	Primer ID (Forward)	塩基配列(Forward)	Primer ID (Reverse)	塩基配列 (Reverse)	プライマーの degeneracy 指数 ¹⁾	予想サイズ
1	1121	AGTGGTGGTAAAAGCTCTGAA	1286	TCTCCTGAACTGGTCCCG	0	124
2	1862	AAGACTTACACAAGCCTGGGC	1961	AGTCATGAATCCTTGCAGCACT	0	124
3	1121	AGTGGTGGTAAAAGCTCTGAA	1264	GATTCTCCTGAACTGGTCCC	0	125
4	1133	AGTGGTGGTAAAAGCTCTGA	1266	TCTCCTGAACTGGTCCCG	0	125
5	1854	GAAGACTTACACAAGCCTGGG	1961	AGTCATGAATCCTTGCAGCACT	0	125
6	1862	AAGACTTACACAAGCCTGGGC	1946	AGTCATGAATCCTTGCAGCAC	0	125
7	1123	CAGTGGTGGTAAAAGCTCTG	1266	TCTCCTGAACTGGTCCCG	0	126
8	1854	GAAGACTTACACAAGCCTGGG	1946	AGTCATGAATCCTTGCAGCAC	0	126
9	1133	AGTGGTGGTAAAAGCTCTGA	1264	GATTCTCCTGAACTGGTCCC	0	126
10	1862	AAGACTTACACAAGCCTGGGC	1951	AAGTCATGAATCCTTGCAGCA	0	126
11	1854	GAAGACTTACACAAGCCTGGG	1951	AAGTCATGAATCCTTGCAGCA	0	127
12	1862	AAGACTTACACAAGCCTGGGC	1963	CTAAAGTCATGAATCCTTGCAGC	0	127
13	1126	GCAGTGGTGGTAAAAGCTCT	1266	TCTCCTGAACTGGTCCCG	0	127
14	1123	CAGTGGTGGTAAAAGCTCTG	1264	GATTCTCCTGAACTGGTCCC	0	127
15	1113	AGCAGTGGTGGTAAAAGCTC	1266	TCTCCTGAACTGGTCCCG	0	128
16	1854	GAAGACTTACACAAGCCTGGG	1963	CTAAAGTCATGAATCCTTGCAGC	0	128
17	1862	AAGACTTACACAAGCCTGGGC	1969	TACCTAAAGTCATGAATCCTTGCAG	0	128
18	1126	GCAGTGGTGGTAAAAGCTCT	1264	GATTCTCCTGAACTGGTCCC	0	128
19	1862	AAGACTTACACAAGCCTGGGC	1971	ATACCTAAAGTCATGAATCCTTGCAG	0	129
20	1854	GAAGACTTACACAAGCCTGGG	1969	TACCTAAAGTCATGAATCCTTGCAG	0	129
21	1113	AGCAGTGGTGGTAAAAGCTC	1264	GATTCTCCTGAACTGGTCCC	0	129
22	1108	AGCAGTGGTGGTAAAAGCT	1266	TCTCCTGAACTGGTCCCG	0	129
23	1108	AGCAGTGGTGGTAAAAGCT	1264	GATTCTCCTGAACTGGTCCC	0	130
24	1109	CAGCAGTGGTGGTAAAAGC	1266	TCTCCTGAACTGGTCCCG	0	130
25	1862	AAGACTTACACAAGCCTGGGC	1956	TATACCTAAAGTCATGAATCCTTGC	0	130
26	1854	GAAGACTTACACAAGCCTGGG	1971	ATACCTAAAGTCATGAATCCTTGCAG	0	130
27	1862	AAGACTTACACAAGCCTGGGC	1954	CTATACCTAAAGTCATGAATCCTTGC	0	131
28	1854	GAAGACTTACACAAGCCTGGG	1956	TATACCTAAAGTCATGAATCCTTGC	0	131
29	1124	GCAGCAGTGGTGGTAAAAG	1266	TCTCCTGAACTGGTCCCG	0	131
30	1109	CAGCAGTGGTGGTAAAAGC	1264	GATTCTCCTGAACTGGTCCC	0	131
31	1124	GCAGCAGTGGTGGTAAAAG	1264	GATTCTCCTGAACTGGTCCC	0	132
32	1134	AGCAGCAGTGGTGGTAAA	1266	TCTCCTGAACTGGTCCCG	0	132
33	1862	AAGACTTACACAAGCCTGGGC	1967	GCTATACCTAAAGTCATGAATCCTT	0	132
34	1854	GAAGACTTACACAAGCCTGGG	1954	CTATACCTAAAGTCATGAATCCTTGC	0	132
35	1854	GAAGACTTACACAAGCCTGGG	1967	GCTATACCTAAAGTCATGAATCCTT	0	133
36	1130	AGCAGCAGTGGTGGTAAA	1266	TCTCCTGAACTGGTCCCG	0	133
37	1134	AGCAGCAGTGGTGGTAAA	1264	GATTCTCCTGAACTGGTCCC	0	133
38	1862	AAGACTTACACAAGCCTGGGC	1950	GGCTATACCTAAAGTCATGAATCCT	0	133
39	1128	AGCAGCAGTGGTGGTAAA	1266	TCTCCTGAACTGGTCCCG	0	134
40	1854	GAAGACTTACACAAGCCTGGG	1950	GGCTATACCTAAAGTCATGAATCCT	0	134
41	1862	AAGACTTACACAAGCCTGGGC	1944	TGGCTATACCTAAAGTCATGAATCC	0	134
42	1130	AGCAGCAGTGGTGGTAAA	1264	GATTCTCCTGAACTGGTCCC	0	134