

表 25 HIV-1 Genotype 共通プライマー(上位 228 件のみ表示)

Pair ID	Prime r ID (Forward)	塩基配列(Forward)	平均位置 (Forward)	Prime r ID (Reverse)	塩基配列 (Reverse)	平均位置 (Reverse)	プライマーの degeneracy 指数 <sup>1</sup>	予想サイズ
1	1634	CTCTGGAAAGGTGAAGGGG	2381	1667	ACCTGCCATCTGTTTTCCATA	2436	0	109
6	1634	CTCTGGAAAGGTGAAGGGG	2381	1682	AKCACCTGCCATCTGTTTTTC	2452	1	113
8	1634	CTCTGGAAAGGTGAAGGGG	2381	1702	CATCCTGTCTACTYTGCCACAC	2473	1	137
20	1603	GGAAAGGACCAGCMAARCT	2333	1667	ACCTGCCATCTGTTTTCCATA	2436	2	129
27	31	ACTAGCGGAGGCTAGAAGGAGA	93	39	ARCTCYCTGCTTGGCCATAC	154	2	146
30	18	AGGACTGGGCTTGTCTGA	41	39	ARCTCYCTGCTTGGCCATAC	154	2	223.625
32	1987	GGCAGGAAGAAGCGGA	2894	2007	CCACTRTGCTTCTGCTTTCYCT	2918	2	257.125
43	1603	GGAAAGGACCAGCMAARCT	2333	1682	AKCACCTGCCATCTGTTTTTC	2452	3	133
51	1579	GRTACAGTGCASGGGAAAGAATA	2256	1604	TTKGTGGTCCCTTCCAAA	2338	3	141
54	523	ACYCTTTGGCARCGACC	810	576	CCTCCAATTCYCTATCATTT	895	3	147.875
57	31	ACTAGCGGAGGCTAGAAGGAGA	93	44	YARCTCYCTGCTTGCCCA	159	3	149
68	1571	ARATGGCAGTATTATYCACAAATT	2200	1604	TTKGTGGTCCCTTCCAAA	2338	3	188
75	1597	MAACTARAGAAATACAAAAACAAT	2289	1667	ACCTGCCATCTGTTTTCCATA	2436	3	201
79	1928	CRRCAAYAGCAGAATAGGCATT	2819	1977	CCGCTTCTTCCGCCAT	2881	3	202
83	507	RCYAGRCCCAACAGCCC	780	540	CTAATACTGTATCATCTGCTCCTGT	832	3	203.875
96	18	AGGACTGGGCTTGTCTGA	41	44	YARCTCYCTGCTTGCCCA	159	3	226.625
100	1721	TGTGGCARGTAGACAGGATGA	2495	1776	TCCTATCKATGGAGACYCC	2574	3	241
102	568	CAGGAGCAGATGATACAGTATTAGA	868	637	TTACYGGYACAGTKCAATAGGACT	1001	3	243
104	1987	GGCAGGAAGAAGCGGA	2894	2000	CACRTTCTTCTGCTTTCYCTWAT	2911	3	254.125
117	482	RGGVYTTGTGGARATGTGG	727	540	CTAATACTGTATCATCTGCTCCTGT	832	3	326.875
125	530	YTCCTCARATCACYCTTTGG	817	552	TCYCTAATACTGTATCATCTGCTC	845	4	101.875
139	1507	CCTACAAYCCCAAGYCA	2120	1546	ATACTGCCATYTGKACTGCTGTC	2163	4	116
149	806	GCACARGGATGGAAGGATC	1236	836	CTACATAAARTCATCCATRTATTG	1273	4	117.125
181	1947	CCRGRRGYCAGCCT	2847	1977	CCGCTTCTTCCGCCAT	2881	4	125.625
186	1949	ATCCRGRGGYACGCC	2849	1977	CCGCTTCTTCCGCCAT	2881	4	126.625
195	1463	GCAGGMAGRTGGCCAGT	2051	1504	GRCTTTGGGRTTGTAGGG	2116	4	135
213	1217	CAGACTCACARTATGCAWTAGGAAT	1744	1265	TGTTCATTTCCTCCAATYCC	1797	4	147
235	2286	ATAGTGCAACAGCARARCAATYTG	3397	2350	TTCCAGAGCARCCECAA	3484	4	160
236	1056	ACTAATGATGAARRCARTTAACAG	1546	1103	AACTCCCAAYTCAGGAATCCA	1602	4	160
243	2271	TGTGTCTGGHATAGTGCAACAGC	3377	2350	TTCCAGAGCARCCECAA	3484	4	171
245	1507	CCTACAAYCCCAAGYCA	2120	1574	CTTCCSTGGACTGTAYCC	2243	4	174
246	1384	GGACAAGTAGAYTGTAGYCCAGG	1950	1473	CTGGCCAYCTKCTGCTA	2062	4	175
256	507	RCYAGRCCCAACAGCCC	780	548	CTGTATCATCTGCTCCTGTRCTAA	841	4	197.875
284	506	SAGRCYAGRCCCAACAGC	779	540	CTAATACTGTATCATCTGCTCCTGT	832	4	205.875
294	1549	GCTGARCAOYTTARGACAGCAGT	2166	1604	TTKGTGGTCCCTTCCAAA	2338	4	214
297	590	GATAGRRGGAATTGGAGGYTT	921	656	CCATCCATCCCTGGCTT	1028	4	216
304	2018	GAAAGAGCAGAAGAYAGTGGMAA	2930	2067	ACARGCATGTGTRGCCCA	2999	4	239.5
327	507	RCYAGRCCCAACAGCCC	780	576	CCTCCAATTCYCTATCATTT	895	4	261.875
330	1133	GATTCCTGARTGGGAGTTTGT	1633	1193	TGAGTGTGYACTATRTYACTTCT	1717	4	263
341	482	RGGVYTTGTGGARATGTGG	727	548	CTGTATCATCTGCTCCTGTRCTAA	841	4	320.375
361	1987	GGCAGGAAGAAGCGGA	2894	2044	YTGCTTCTYCCACACAGG	2963	4	403.625
363	31	ACTAGCGGAGGCTAGAAGGAGA	93	98	YTGRGTACCATTGYCCYTG	239	4	453.5
366	2304	ACRGTCTGGGGYATYAARCA	3428	2350	TTCCAGAGCARCCECAA	3484	5	101
369	1133	GATTCCTGARTGGGAGTTTGT	1633	1149	CTGCYCATCTACATAGWARGTYTC	1653	5	102
371	1507	CCTACAAYCCCAAGYCA	2120	1539	ACTGTGTCYTAAGRTGYTCAGC	2156	5	102
377	198	GGRCACCCCAACAAGA	348	224	ATTCWGCAGCYTMTCAATGA	394	5	106
379	2311	MRCTCAORGTCTGGGGYAT	3435	2350	TTCCAGAGCARCCECAA	3484	5	107
383	107	CARGGRCAAAATGGTACAYCA	249	156	ATAATGCTGWRAACATGGGTATTAC	299	5	108
389	1133	GATTCCTGARTGGGAGTTTGT	1633	1152	CTRYTWGCTGCYCCATCATACAG	1656	5	110
396	1571	ARATGGCAGTATTATYCACAAATT	2200	1587	TTGTTTTGTARTTCTYTAGTTKGT	2275	5	111
469	107	CARGGRCAAAATGGTACAYCA	249	182	GGCYCCTCTGATAATGCTG	329	5	124
478	172	ATACCCATGTTYWCAGCATTATCAG	316	224	ATTCWGCAGCYTMTCAATGA	394	5	125
488	1217	CAGACTCACARTATGCAWTAGGAAT	1744	1251	YTRTYGCTGGTACCCTATG	1783	5	127
491	507	RCYAGRCCCAACAGCCC	780	513	CCAAAGRTGATYTGAGGGA	800	5	127
529	1228	GCAWTAGGAATYATTCARGCACA	1755	1265	TGTTTCATTYCCCTCCAATYCC	1797	5	135
538	107	CARGGRCAAAATGGTACAYCA	249	191	TCTTGTGRRGTGGYCC	338	5	138
598	1579	GRTACAGTGCASGGGAAAGAATA	2256	1622	CCTTCACTTCCAGAGDAGYTT	2360	5	158
610	1489	HGCMGTGTTGGTGGG	2094	1546	ATACTGCCATYTGKACTGCTGTC	2163	5	161
628	18	AGGACTGGGCTTGTCTGA	41	34	CKYAACCKRATTTTTYCCCA	133	5	166.625
636	568	CAGGAGCAGATGATACAGTATTAGA	868	621	ATTATRTTGYAGGNGTAGGCTCTA	963	5	169
639	2253	GCAGGAAGYACKATGGGC	3346	2305	AGGACTCTTGYCYGGAGYTG	3429	5	170
645	848	AATAYATGGATGAYTTRTATGTAGG	1286	927	ACTGTCCATYTRCAGGATGGAG	1372	5	171
649	1056	ACTAATGATGAARRCARTTAACAG	1546	1115	GGGGTRTRACAACTCCCA	1614	5	172
658	2253	GCAGGAAGYACKATGGGC	3346	2325	TATCTTTCYASAGCYAGGACTCTTG	3450	5	180
667	590	GATAGRRGGAATTGGAGGYTT	921	637	TTACYGGYACAGTKCAATAGGACT	1001	5	186
668	198	GGRGCCACYCCACAAGA	348	266	AGTAGYTCWGGTATRTCACTTCCC	451	5	188
683	506	SAGRCYAGRCCCAACAGC	779	548	CTGTATCATCTGCTCCTGTRCTAA	841	5	199.875
684	25	RCWRCGAAGGCGGAG	58	39	ARCTCYCTGCTTGGCCATAC	154	5	201.625
687	421	ATGACAGCATGYCARGGAGT	655	462	CCAACARCCCTTTTTYCTAGG	700	5	202.875
690	1038	AAAATCTRAARACAGGRAARTATGC	1528	1103	AACTCCCAAYTCAGGAATCCA	1602	5	204
693	1571	ARATGGCAGTATTATYCACAAATT	2200	1622	CCTTCACTTCCAGAGDAGYTT	2360	5	205
698	1278	TTGGAGGRAATGAACAAGTRGATAA	1815	1364	CATGCARWGTTCYCTTTT	1917	5	206
727	1463	GCAGGMAGRTGGCCAGT	2051	1539	ACTGCTGTCYTAAGRTGYTCAGC	2156	5	216

734	1592	ATAKCAWAGAYATACMAACTARAG	2282	1667	ACCTGCCATCTGTTTTCCATA	2436	5	217
739	1489	HGCMGTGTTGGTGGG	2094	1574	CTTTCCSTGCACTGTAYCC	2243	5	219
742	1507	CCTACAAAYCCCCAAAGYCA	2120	1587	TTGTTTTGTARTTCTYTAGTKGT	2275	5	221
745	1920	TYRYHCATTTCAGAATTGGGTG	2802	1977	CGCTTCTTCTGCCAT	2881	5	224
748	1924	GTTYRYHCATTTCAGAATTGGG	2806	1977	CGCTTCTTCTGCCAT	2881	5	226
749	928	CTCCATCTGAYARATGGACAGT	1373	995	TAGAATYTCOCTRTTYTCTGCCA	1462	5	226
764	1842	ARGAYAGATGGAACRAGCCC	2686	1906	YGRACCCAAATTCTGAAATG	2779	5	238
781	1701	GMTGATWGTGTGGCARGTAGACA	2472	1776	CTCCATTCKATGGAGACYCC	2574	5	247
793	482	RGGGYTGTGGARATGTGG	727	513	CCAAARGGTGATYTGAGGGA	800	5	249.5
812	1976	ATYTMCYATGGCAGGAAGAAGC	2880	2007	CCACTRTCTTCTGCTTTTCYCT	2918	5	260.125
820	506	SAGRCYAGRGCCAACAGC	779	576	CCTCCAATTCYCTATCATT	895	5	263.875
830	1133	GATTCCTGARTGGGAGTTTGT	1633	1194	AYTGTGAGTCTGYACTATRTTYAC	1720	5	267
844	2476	GGARCTGTGGCTYTTTCAG	3637	2503	AGCCCTGTCTKATTCTTSTRGGTAT	3676	5	277.5
845	1899	GGGATACYTGGRRMGGRT	2769	1977	CGCTTCTTCTGCCAT	2881	5	281
847	483	RGARGMCAAYCARATGAAAGA	728	540	CTAATACTGTATCATCTGCTCCTGT	832	5	302.375
863	2355	GGGGYTGCTCTGGAAA	3489	2421	GTGARTAKCCCTKCTRACTCTATT	3578	5	353
875	1987	GGCAGGAAGAAGCGGA	2894	2037	YCCACACAGGHACYCCATA	2955	5	394.625
882	2355	GGGGYTGCTCTGGAAA	3489	2443	KCTCKCACCTYCTTCTCKAT	3600	5	434
885	1928	CRRCAYAGCAGAAATAGGCATT	2819	2007	CCACTRTCTTCTGCTTTTCYCT	2918	5	436.125
895	236	AKGARGCTGCWGAATGGG	406	255	CTAGTAGYTCWGWCTATRTCACTTC	440	6	101
899	175	GARGTAATCCCATGTTYWAGCA	319	211	AACATTTGCATDGTGCTG	377	6	101
900	1542	GCTGARCACTTARGACAGCAG	2159	1578	ATTATRTCTAYTATTCTTTCCSTG	2253	6	101
910	199	GRGCCACYCCACAAGAYTT	350	224	ATTCWGCAGCYTGMTCAATTGA	394	6	103
919	143	CTAGRACYTTRAAAYGCATGGGT	286	191	TCTTGTGGRTGGYCY	338	6	105
928	1592	ATAKCAWAGAYATACMAACTARAG	2282	1604	TTKCTGGCTCTTCCAAA	2338	6	107
931	813	GAAAGGATCMCCRCGART	1243	836	CTACATAAARTGATCCARTATTG	1273	6	107.125
932	2286	ATAGTGCAACAGCARARCAATYTG	3397	2325	TATCTTTCYASAGCYAGGACTCTTG	3450	6	108
935	1597	MAACTARAGAYTACAAAACAAAT	2289	1622	CCCTCACCTTCCAGAGDAGYTT	2360	6	108
943	2271	RTTGCTGGHATAGTGCAACAGC	3377	2305	AGGACTCTTGYCYGGAGYTG	3429	6	109
946	2450	RAATMGAAGAAGRAGTGGMGA	3608	2463	GGTARCTGAARAGGCACAGG	3624	6	110
967	928	CTCCATCTGAYARATGGACAGT	1373	975	SRTAAATYTRGCTTGCCCA	1438	6	114
971	1228	GCAWTAGGAATYATTCARGCACA	1755	1251	YTRTYGCTGGTACCCATG	1783	6	115
976	1316	ATTGGARARCAATGGYYAGTGA	1867	1369	GRCTACARTACTTGTCCATGCA	1926	6	115
1012	2271	RTTGCTGGHATAGTGCAACAGC	3377	2325	TATCTTTCYASAGCYAGGACTCTTG	3450	6	119
1045	1278	TTGGAGGRAATGAACAAGTRGATAA	1815	1310	CACTRRCCATTGYTYTCCAATT	1860	6	123
1101	506	SAGRCYAGRGCCAACAGC	779	513	CCAAARGGTGATYTGAGGGA	800	6	129
1115	1384	GGACAAGTAGAYTGTAGYCCAGG	1950	1444	TGYCCTGYTCTGYTGGRT	2024	6	129
1161	1380	GCATGGCAAGTAGAYTGTAGYCC	1946	1444	TGYCCTGYTCTGYTGGRT	2024	6	132
1183	1579	GRTACAGTGCASGGGAAAGAATA	2256	1602	GGTCTTTCAAAABWGGRTC	2326	6	134
1203	203	CARGCAGHATGCAAAATGT	365	266	AGTAGYTCWGWCTATRTCACTTCCC	451	6	135
1212	806	CCACARGGATGGAAAGGATC	1236	841	CTATTCTAARTCWGANCCACATA	1278	6	135.125
1235	1549	GCTGARCACTTARGACAGCAGT	2166	1587	TTGTTTTGTARTTCTYTAGTKGT	2275	6	137
1271	848	AATAYATGGATGAYTTRTATGTAGG	1286	892	CATCCAAAGRAATGGDGGTTC	1336	6	141
1297	1721	TGTGGCARGTAGACAGGATGA	2495	1742	CTAVTGGTRATRTACTTCTGARCT	2526	6	145
1306	848	AATAYATGGATGAYTTRTATGTAGG	1286	897	ATAHCCCATCCAAAGRAATGG	1341	6	147
1307	1489	HGCMGTGTTGGTGGG	2094	1539	ACTGTGTCTYTAAGRTGYTCAGC	2156	6	147
1313	2253	GCAAGGAAGYACKATGGGG	3346	2300	YTRATRCCCCAGACGYGTGAG	3424	6	149
1322	1402	ATATGGCAAYTRGATTYACMCA	1971	1473	CTGGCCAYCTKCCCTGCTA	2062	6	151
1338	1248	CATGGGTACCAGRCRAYAA	1779	1310	CACTRRCCATTGYTYTCCAATT	1860	6	153
1343	1278	TTGGAGGRAATGAACAAGTRGATAA	1815	1328	YTTTGTACAYRGGTGGCA	1879	6	154
1351	750	AAARRTCAGTAWCAGTAYTRGATGT	1165	809	GATCCTTCCATCCYGTGG	1239	6	155.125
1391	2018	GAAAGAGCAAGAYAGTGGMAA	2930	2044	YTGOWTCTYCCACACAGG	2963	6	161.5
1401	421	ATGACAGCATGYCARGGAGT	655	453	GYCCTKCYTGCCACA	690	6	163.875
1419	1278	TTGGAGGRAATGAACAAGTRGATAA	1815	1337	CAGYTRGCTACTTTCTYTTGCTA	1888	6	166
1450	1696	AAAACAGATGGCAGGTGMTG	2467	1742	CTAVTGGTRATRTACTTCTGARCT	2526	6	170
1479	1687	AYTATGGAAAACAGATGGCAGGT	2458	1742	CTAVTGGTRATRTACTTCTGARCT	2526	6	174
1493	1448	CARCAGARACAGGRCARGA	2028	1504	GRTCTTGGGGRTGTAGGG	2116	6	177
1504	198	GGRGCCACYCCACAAGA	348	264	CTATRTCACTTCCSTWGGKTC	449	6	180
1509	1571	ARATGGCAGTATTCATYCACAAATT	2200	1602	GGTCTTTCAAAABWGGRTC	2326	6	181
1522	1248	CATGGGTACCAGRCRAYAA	1779	1328	YTTTGTACAYRGGTGGCA	1879	6	184
1525	2431	ATAGAGTYAGMAGGGMATYTCACC	3588	2463	GGTARCTGAARAGGCACAGG	3624	6	185
1529	199	GRGCCACYCCACAAGAYTT	350	266	AGTAGYTCWGWCTATRTCACTTCCC	451	6	185
1531	1928	CRRCAYAGCAGAATTAGGCATT	2819	1953	CCATRGKARATGCCTAAGCC	2857	6	186
1533	1601	CAAAAACAATYWYAWAWATTCRAA	2299	1667	ACCTGCCATCTGTTTTCCATA	2436	6	187
1545	1001	GGCAGARAAAYAGGARATTTCTAAA	1468	1049	TTAAYTTGYTTACATCATTAGTGTG	1539	6	189
1569	1158	ARACYTWTATGTAGATGGRGCAGC	1663	1210	TTCTAWTGCATAYTGTGAGTCTGT	1736	6	192
1572	1783	GGRGCTCCATMGAATGGAG	2586	1812	CCAARTAYTGTARRGATCCTACCTT	2646	6	192
1607	1248	CATGGGTACCAGRCRAYAA	1779	1337	CAGYTRGCTACTTTCTYTTGCTA	1888	6	196
1615	1851	AGRGARCOMYCAATGAAATGG	2709	1906	YGRACCCAAATTCTGAAATG	2779	6	197
1617	2253	GCAAGGAAGYACKATGGGG	3346	2330	RCTKTTGATCCYKTAGGTATCTTTC	3455	6	197
1621	590	GATAGGRGAATTTGGAGGYTT	921	641	GGCTTYAATKTACYGGYACAGT	1009	6	198
1623	1156	GAGYAGARACYTWTATGTAGATGG	1661	1210	TTCTAWTGCATAYTGTGAGTCTGT	1736	6	198
1628	331	GACATAARACARAGGRCCAAARGA	540	391	GRCATGCTGTCATCATTTCYCT	624	6	198
1632	172	ATACCATGTTWCAAGCATTATCAG	316	264	CTATRTCACTTCCSTWGGKTC	449	6	199
1679	25	ROWCRGCAAGAGGGGAG	58	44	YARCTCYCTGCTGGCCCA	159	6	204.625
1684	198	GRRGCCACYCCACAAGA	348	269	TGTTCTYGMAGGSTACTAGTAYTC	454	6	205
1713	568	CAGGAGCAGATGATACAGTATTAGA	868	628	RGTRCARCOMAKYTGAGTCAA	981	6	207
1722	806	CCACARGGATGAAAAGGATC	1236	876	RTCTGGTGRKWRRAATCCCA	1317	6	207.125
1764	407	CAHTAGARGAAATGATGACAGCATG	641	462	CCAACARCCCYTTTYCTAGG	700	6	211.875

1786	421	ATGACAGCATGYCARGGAGT	655	466	KYCCACATYTCCAACARCC	706	6	214.875
1791	1038	AAAATCTRAARACAGGRAARTATGC	1528	1115	GGGTRTRTRACAAACTCCCA	1614	6	216
1798	732	AGRACTOARGAYTYTGGGARGT	1143	809	GATCCTTTCCATCCYGTGG	1239	6	218.25
1812	2227	TRARRRACAATTGGGAAGTGAATT	3280	2266	GCTGTTGCACTATDCCAGACAA	3389	6	225
1815	1721	TGTGGCARGTAGACAGGATGA	2495	1774	CMTGMCCCARDTGCCA	2571	6	226
1830	1549	GCTGARCAVCTTARGACAGCAGT	2166	1622	CCTTCCACTTTCCAGAGDAGYTT	2360	6	231
1845	933	GGGDTATGARCTCCATCCTGA	1378	995	TAGAATYTCCTRTITYTCTGCCA	1462	6	238
1850	573	TRYMAGGAARATGGAACCAAAA	879	656	CCATCCATBCCTGGCTT	1028	6	239
1875	2016	GRATWAGRGAAGAGCAGAAGAYAG	2928	2067	ACARGCATGTGTRGCCCA	2999	6	245.5
1885	713	GAGRAAATRTGRAYTTCAGRGA	1119	809	GATCCTTTCCATCCYGTGG	1239	6	251.25
1890	1124	ARTGGGAGTTTGTYYAAYACCCC	1624	1193	TGAGTCTGYACTATRTTYACTTCT	1717	6	254
1898	1976	ATYTMCOYATGGCAGGAAGAAGC	2880	2000	CACRTCTTCTGCTCTTTCYCTWAT	2911	6	257.125
1912	1124	ARTGGGAGTTTGTYYAAYACCCC	1624	1195	WTGCATAYTGTGAGTCTGYACTAT	1721	6	264
1950	2478	GTCCTYTTTCAGYTACRCRC	3639	2503	AGCCCTGTCTKATCTTSTRGGTAT	3676	6	269.5
1960	1721	TGTGGCARGTAGACAGGATGA	2495	1790	GGYCWGRRCTAYTTGTGTRCTATA	2599	6	271
1993	1896	TCTATRAHAMYTATGGGGATACYTG	2765	1977	CGCTCTTCTCCTGCCAT	2881	6	290
1996	483	RGARGMCAVCARATGAAAGA	728	548	CTGTATCATCTGCTCCTGTRTCTAA	841	6	296.375
2001	455	GTGGCARRMGAGGRCA	692	513	CCAAARGRTGATYTGAGGGA	800	6	300.5
2012	481	ATGTGRRMRARGGMCA	725	540	CTAATACTGTATCATCTGCTCCTGT	832	6	314.375
2021	1783	GGRTCTCCATMGAATGGAG	2586	1859	CCATTCATTGTRKGGYTCYCT	2719	6	323
2022	1842	ARGAYAGTGGAAACRAGCCC	2686	1937	CGTCCAAATCCYCTCATTT	2834	6	323.375
2044	2511	CCYASAGAATMAGACAGGGGCTT	3697	2544	AAAYTARCCWTTCCAGTCCCC	3763	6	350.875
2050	1947	CCRRGRRGYCAGCCT	2847	2007	CGACTRTCTTCTGCTCTTTCYCT	2918	6	359.75
2051	483	RGARGMCAVCARATGAAAGA	728	576	CTCCAAATCCYCTCATTT	895	6	360.375
2052	1949	ATCCRRGRRGYCAGCC	2849	2007	CGACTRTCTTCTGCTCTTTCYCT	2918	6	360.75
2055	442	AGRGTWTRGCTGARCAATGAG	677	513	CCAAARGRTGATYTGAGGGA	800	6	395.375
2068	1928	CRRCAYAGCAGAATAGGCATT	2819	2000	CACRTCTTCTGCTCTTTCYCTWAT	2911	6	433.125
2077	2355	GGGGYTGCTTGAAAA	3489	2449	GYCTYKCTCKCCACTYCT	3607	6	442
2083	2188	AGRRGARTTTTTCTAYTYAATAACA	3202	2266	GCTGTTGCACTATDCCAGACAA	3389	6	497
2085	1323	GYAGTGAKTTTAAAYTGCCACC	1874	1370	GGRTACARTCTACTTTGCCATGC	1928	7	101
2086	900	CHCCATTYCTTTGGATGGG	1344	955	YTTYTGATRTCATTRACAGTCCAG	1415	7	101
2090	1571	ARATGGCAGTATTCATYCACAAAT	2200	1586	ARTTCYTAGTGTGATRTCTGWG	2274	7	101
2091	362	GAMACCYTYTTRTCCAAAATG	593	399	COYTGRCATGCTGCATCA	633	7	101
2092	1589	GTMAACTARAGAAYTACAAAAACA	2277	1612	CAGAGDAGYTTKCGTGGTCT	2349	7	101
2096	542	GARGCYTWTAGAYACAGGAGCA	835	585	TTACYTTRATAAARCCCTCCAATTC	914	7	101
2097	136	ACCTAGRACYTTRAAAYGCATGG	279	194	GRGTGGCYCCYCTGTA	341	7	101
2098	1124	ARTGGGAGTTTGTYYAAYACCCC	1624	1152	CTRYTWGCTGCVCCATCTACATAG	1656	7	101
2102	936	CTCGATCCTGAYARATGGACA	1381	965	TGCCARTTYARTTYCCYAC	1427	7	101
2111	2050	GTDCCGTGTGGRRAGAWGC	2970	2067	ACARGCATGTGTRGCCCA	2999	7	102
2113	2319	TCCRGRCAAGAGTCCTRGC	3444	2368	GCACABYAGTGGTGCARAT	3504	7	102
2122	2445	RAGGTGGMGAGMRAGRCA	3603	2463	GGTARCTGAARAGGCACAGG	3624	7	102
2161	2324	CARCTCCRRCAAGAGTCCCT	3449	2368	GCACABYAGTGGTGCARAT	3504	7	105
2168	1078	TARTVATATGGGGAARAYYCCCTAA	1574	1103	AAACTCCGAYTCAGGAATCCA	1602	7	105
2187	2450	RAATMGAAGAAGRAGGTGGMGA	3608	2472	GTARCTGAARAGGCACAGGYTC	3633	7	107
2188	353	RYTGGATGACMGAMACCYTG	584	391	GRCATGCTGCATCATTTTCYTC	624	7	107
2209	1947	CCRRGRRGYCAGCCT	2847	1953	CCATRGKARATGCCTAAGCC	2857	7	109.625
2219	1949	ATCCRRGRRGYCAGCC	2849	1953	CCATRGKARATGCCTAAGCC	2857	7	110.625
2232	1783	GGRTCTCCATMGAATGGAG	2586	1805	TYCTTARCGAWKCTGMAAAAACA	2623	7	111
2241	590	GATAGRRGAATGGAGGYTT	921	621	ATTARTTGAAYGNGTAGGTCCTA	963	7	112
2249	237	GARGCTCGWGAATGGGAYAG	412	269	TGTTCTYGMAGGSTACTAGTAGYTC	454	7	112
2259	1752	AAGYTCAGAAGTACAYATYCCABTA	2538	1776	CTCCATTCCKATGGAGACYCC	2574	7	113
2277	2476	GGARCCCTGTGCCTYTTCCAG	3637	2485	TRAKRSCYTCACCACCCC	3650	7	114.5
2290	1384	GGACAAGTAGAYTGTAGYCCAGG	1950	1440	GYTGRATMACYTCYCTTCT	2020	7	116
2320	1380	GGATGGACAAGTAGAYTGTAGYCC	1946	1440	GYTGRATMACYTCYCTTCT	2020	7	119
2367	1493	TTTGGVRYCCCTACAAYCC	2102	1546	ATACTGCCATYTGKACTGCTGTC	2163	7	125
2370	2286	ATAGTGCAAGCAGARARCAATYTG	3397	2330	RCTKTTGATCCYKTAGGTATCTTTC	3455	7	125
2377	933	GGGDTATGARCTCCATCCTGA	1378	975	SRTAAAYTGRCTTGCCCA	1438	7	126
2390	203	CARGCAGCHATGCAAAATGT	365	264	CTATRTCACTTCCSTWGGKTC	449	7	127
2440	762	GDGRTGCATAYTTCAGTYCC	1183	809	GATCCTTTCCATCCYGTGG	1239	7	131.125
2455	375	CAAAATGCRAAYCCAGAYTG	606	432	CTCATTGCYTCAGCYAAWACYOT	667	7	132
2468	1278	TTGGAGGRAATGAACAAGTRGATAA	1815	1318	GCARRTTAAAMTCACTRRCCATTG	1869	7	133
2483	763	GTRGGDRTGCATAYTTCAGT	1184	809	GATCCTTTCCATCCYGTGG	1239	7	134.125
2493	1448	CARCAGARACAGRCARGA	2028	1486	CCACCAACAKGCDGC	2080	7	135
2496	2271	RTTGTCTGGHATAGTGCAACAGC	3377	2330	RCTKTTGATCCYKTAGGTATCTTTC	3455	7	136
2499	331	GACATAARACARGRCCAAARGA	540	369	RTOTGRRTYGCAATTTTGA	600	7	136
2584	900	CHCCATTYCTTTGGATGGG	1344	975	SRTAAAYTGRCTTGCCCA	1438	7	144
2588	865	CWYGATYTAGAAATAGRCARCAYAG	1306	927	ACTGTCCATYTRTCCAGTGGAG	1372	7	144
2600	1463	GCAGGMAGRTGGCCAGT	2051	1516	CYACYACYCCYTGCTTTGG	2131	7	146
2608	1934	GTAGAYCTARMHWAGASCCTGG	2830	1977	CCGCTTTCTCCTGCCAT	2881	7	146.625
2610	662	RAAGCCAGGVATGGATGG	1036	685	CAAAATYTGAGATRTTATGGRTT	1087	7	147
2645	18	AGGACTCGGCTTCTGTA	41	32	TCCCADKYATCTARWYTCCCC	130	7	149.625
2663	2286	ATAGTGCAACAGCAGARARCAATYTG	3397	2345	CARCCCAAAKYCCYAG	3475	7	152
2665	203	CARGCAGCHATGCAAAATGT	365	269	TGTTCTYGMAGGSTACTAGTAGYTC	454	7	152
2669	2018	GAAAGAGCAGAAAGAYAGTGGMAA	2930	2037	YYCCACACAGGHACYCCATA	2955	7	152.5
2673	855	ATGTAGNTQWGYATTTAGAAATAGG	1295	927	ACTGTCCATYTRTCCAGTGGAG	1372	7	153
2702	143	CTAGRACYTTRAAAYGCATGGGT	286	211	AACATTTGCATDGGTGCYTG	377	7	156

表 26 HIV-1 共通プライマー検証用ゲノムフラグメント

Genotype	Sequence
A	TTATAGGYTCTGATTTAGAAATAGGGCAGCATAGAAAMGAAAATAGAGGAGYTAAGASCCCATCTATTGAGSTGGGGATTTACYACA CCAGACAAAAGCATCAGAAAGAACCTCCATTCTTTGGATGGGGATATGAACTCCATCCTGACAAAATGGACAGTCCAG
B	TTATAGGATCTGATTTAGAAATAGGGCAGCATAGAAACAAAATAGAGGAACTGAGACAACATTGTTGAGGTGGGGATTTTACACA CCAGACAAAACATCAGAAAGAACCTCCATTCTTTGGATGGGGTATGAACTCCATCCTGATAAAATGGACAGTACAG
F	TTATAGGGTCTGACTTAGAAAATAGGGCAGCATAGAAACAAAAGTAGAGGAGTTAAGAGAACATCTACTGAAATGGGGATTTACTACA CCAGACAAAACATCAGAAAGAACCCCATCTCTTTGGATGGGGTATGAACTCCATCCTGATAAAATGGACAGTGCAG
D	TTATAGGATCTGACTTAGAAAATAGGGCAGCATAGAAATAAAAATAGAGGAATTAAGGGGACACCTATTGAAAGTGGGGATTTACCACA CCAGACAAAAGCATCAGAAAGAACCCCATTTCTTTGGATGGGGTATGAACTCCATCCTGATAAAATGGACAGTACAG
H	TTATAGGATCTGACTTAGAAAATAGGACAACATAGAGAAAAAATAGAAGAGTTAAGAGCTCATTGTTGAGGTGGGGATTCACCACA CCAGACAAAACATCAGAAAGAACCCCATTTCTTTGGATGGGGATATGAACTCCATCCTGACAAAATGGACAGTACAG
C	TTATAGGATCTGATTTAGAAAATAGGGCAGCACAATAAAAATAGAGGAGCTAAGAGCTCATCTATTGAGCTGGGGATTTACTACA CCAGACAAAAGCATCAGAAAGAACCCCATTTCTTTGGATGGGGTATGAACTCCATCCTGATAAAATGGACAGTACAG
E	TTATAGGATCTGATTTAGAAAATAGGGCAGCACAATAAAAATAGAGGAGCTAAGAGCTCATCTATTGAGCTGGGGATTTACTACA CCAGACAAAAGCATCAGAAAGAACCTCCATTCTTTGGATGGGGATATGAACTCCATCCTGACAGATGGACAGTCCAG
G	TTATAGGATCAGACTTAGAAAATAGGGCAGCATAGAACAAAATAGAAGAGTTAAGAGAACATCTACTGAGATGGGGATTTACCACA CCAGATAAGAACATCAGAAAGAACCTCCATTCTTTGGATGGGGATATGAGCTCCATCCTGACAAAATGGACAGTACAA

表 27 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	TTGTATGTAGGTCTGATTTAGAAATAGGGCAGCATAGAAG	40
	HIV-1A_T2	TCAATAGATGGGTCTTACTCCTCTATTTCTTCTATGCTGCCCTATTTCTAAATCAGA	58
	HIV-1A_T3	AAAATAGAGGAGTAAGACCCATCTATTGATGGGGATTACACACCAGAC	50
	HIV-1A_T4	ATGGAGTTCTTTCTGATGCTTTTGTCTGGTGTGTAATCCCCAC	46
	HIV-1A_T5	AAAAAGCATCAGAAAGAACCTCCATTCTTTGGATGGGATATGAACTCCAT	50
	HIV-1A_T6	GGCTGGACTGTCCATTGTCCAGGATGGAGTTCATATCCCATCCAAGA	48
B	HIV-1B_T1	TTGTATGTAGGATCTGATTTAGAAATAGGGCAGCATAGA	39
	HIV-1B_T2	CAAATGTTGCTCAGTTCCCTCTATTTTGTCTATGCTGCCCTATTTCTAAATCAGATC	59
	HIV-1B_T3	ACAAAAATAGAGGAACTGAGACAACATTTGTTGAGGTGGGGATTTACACACC	53
	HIV-1B_T4	ATGGAGTTCTTTCTGATGTTTTTGTCTGGTGTGTAATCCCCACTCAA	52
	HIV-1B_T5	AGACAAAACATCAGAAAGAACCTCCATTCTTTGGATGGGTTATGAACTCCA	54
	HIV-1B_T6	GGCTGTACTGTCCATTTATCAGGATGGAGTTCATAACCCATCCAAGGA	49
C	HIV-1C_T1	TTGTATGTAGGATCTGATTTAGAAATAGGGCAGCATAGA	39
	HIV-1C_T2	ACTTTAATAGATGGTTTCTTAATTCCTCTATTTTGTCTATGTTGCCCTATTTCTAAATCAGATC	66
	HIV-1C_T3	GCAAAAATAGAGGAATTAAGAAACCATCTATTAAGTGGGGATTTACCACACCAGACA	58
	HIV-1C_T4	AATGGGGTTCTTTCTGATGTTTTCTTGTCTGGTGTGGTAAATCCCC	46
	HIV-1C_T5	AGAAACATCAGAAAGAACCCCATTTCTTTGGATGGGGTATGAACTCC	48
	HIV-1C_T6	GGCTGTACTGTCCATTTATCAGGATGGAGTTCATAACCCATCCAAGGA	48
D	HIV-1D_T1	TTGTATGTAGGATCTGACTTAGAAATAGGGCAGCAT	36
	HIV-1D_T2	TAGGTGTGCCCTTAATTCCTCTATTTTATTCTATGCTGCCCTATTTCTAAGTCAGAT	58
	HIV-1D_T3	AGATAAAAATAGAGGAATTAAGGGGACACCTATTGAAGTGGGGATTTACCACACC	56
	HIV-1D_T4	GTGGTTCTTTCTGATGCTTTTTGTCTGGTGTGGTAAATCCCCACTCAA	49
	HIV-1D_T5	AGACAAAAGCATCAGAAAGAACCCCATTTCTTTGGATGGGTTATGAACTCCAT	55
	HIV-1D_T6	GGCTGTACTGTCCATTTATCAGGATGGAGTTCATAACCCATCCAAGAAATG	52
F	HIV-1F_T1	TTGTATGTAGGTCTGACTTAGAAATAGGGCAGCATAGA	39
	HIV-1F_T2	AGATGTTCTCTTAACCTCCTACTTTTGTCTATGCTGCCCTATTTCTAAGTCA	54
	HIV-1F_T3	ACAAAAGTAGAGGAGTTAAGAGAACATCTACTGAAATGGGGATTTACTACACCA	54
	HIV-1F_T4	GGGGTTCTTTTTGATGTTTTTGTCTGGTGTAGTAAATCCCCATTTCACT	51
	HIV-1F_T5	GACAAAAACATCAAAAAGAACCCCATCTCTTTGGATGGGGTATGAACTC	51
	HIV-1F_T6	GGCTGCACTGTCCATTTATCAGGATGGAGTTCATAACCCATCCAAGGAAT	51
G	HIV-1G_T1	TTATATGTAGGATCAGACTTAGAAATAGGGCAGCATAGA	39
	HIV-1G_T2	CAGTAGATGTTCTCTTAACCTCTTCTATTTTGTCTATGCTGCCCTATTTCTAAGTCT	58
	HIV-1G_T3	GCAAAAATAGAAGAGTTAAGAGAACATCTACTGAGATGGGGATTTACCACACCA	54
	HIV-1G_T4	AATGGAGTTCTTTCTGATGTTTTCTTATCTGGTGTGGTAAATCCCCATCT	50
	HIV-1G_T5	GATAAGAAACATCAGAAAGAACCTCCATTTCTTTGGATGGGATATGAGCTCC	52
	HIV-1G_T6	GGTTGTACTGTCCATTTGTCCAGGATGGAGTTCATATCCCATCCAAGGA	48
H	HIV-1H_T1	TTGTATGTAGGATCTGACTTAGAAATAGGACAACATAGA	39
	HIV-1H_T2	TCAACAAATGAGCTCTTAACCTCTCTATTTTCTCTATGTTGTCTATTTCTAAGTCAGATCCTAC	67
	HIV-1H_T3	GAAAAATAGAAGAGTTAAGAGCTCATTGTTGAGGTGGGGATTCACCACACC	53
	HIV-1H_T4	GGGGTTCTTTCTGATGTTTTTGTCTGGTGTGGTAAATCCCCACC	45
	HIV-1H_T5	AGACAAAACATCAGAAAGAACCCCATTTCTTTGGATGGGATATGAACTCCAT	55
	HIV-1H_T6	GGCTGTACTGTCCATTTGTCCAGGATGGAGTTCATATCCCATCCAAGAAATG	52

表 28 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 29 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 <sup>1</sup>	予想サイズ
1	81	GGTTCRGGCYATHGARAA	4252.6	105	CRCCNGARTGYTTCCTCCA	4561.8	13	309.2
2	83	CCNTGGTTCRGGCYAT	4246.6	105	CRCCNGARTGYTTCCTCCA	4561.8	13	315.2
3	59	GGYAARGTBGGNCAGGG	4189.6	105	CRCCNGARTGYTTCCTCCA	4561.8	13	372.2
4	81	GGTTCRGGCYATHGARAA	4252.6	102	YTCRCCNGARTGYTTCCTCC	4562.8	14	310.2
5	81	GGTTCRGGCYATHGARAA	4252.6	103	GYTCRCCNGARTGYTTCCTCC	4563.8	14	311.2
6	83	CCNTGGTTCRGGCYAT	4246.6	102	YTCRCCNGARTGYTTCCTCC	4562.8	14	316.2
7	83	CCNTGGTTCRGGCYAT	4246.6	103	GYTCRCCNGARTGYTTCCTCC	4563.8	14	317.2
8	86	TNTTYGMCNTGGTTCC	4239.6	105	CRCCNGARTGYTTCCTCCA	4561.8	14	322.2
9	81	GGTTCRGGCYATHGARAA	4252.6	113	YCARTTCCARAYDGRTRTCCA	4597.8	14	345.2
10	83	CCNTGGTTCRGGCYAT	4246.6	113	YCARTTCCARAYDGRTRTCCA	4597.8	14	351.2
11	59	GGYAARGTBGGNCAGGG	4189.6	102	YTCRCCNGARTGYTTCCTCC	4562.8	14	373.2
12	59	GGYAARGTBGGNCAGGG	4189.6	103	GYTCRCCNGARTGYTTCCTCC	4563.8	14	374.2
13	59	GGYAARGTBGGNCAGGG	4189.6	113	YCARTTCCARAYDGRTRTCCA	4597.8	14	408.2
14	50	TYCARAARGAYTYQRYMYAARTTYAC	4150.6	72	GGAACCAANGGKCCRAA	4264.6	15	114
15	99	GARAAYGAYTTYTCNGARTTYGA	4378.8	105	CRCCNGARTGYTTCCTCCA	4561.8	15	183
16	39	NRRSAARGGYCARGAYGG	4069.6	72	GGAACCAANGGKCCRAA	4264.6	15	195
17	38	ATGSTNRRSAARGGYCARGA	4066.6	72	GGAACCAANGGKCCRAA	4264.6	15	198
18	40	CYATGSTNRRSAARGGYCA	4063.6	72	GGAACCAANGGKCCRAA	4264.6	15	201
19	79	NTGGTTCRGGCYATHGA	4249.6	105	CRCCNGARTGYTTCCTCCA	4561.8	15	312.2
20	81	GGTTCRGGCYATHGARAA	4252.6	108	CVGGYTCRCCNGARTG	4570.8	15	318.2
21	86	TNTTYGMCNTGGTTCC	4239.6	102	YTCRCCNGARTGYTTCCTCC	4562.8	15	323.2
22	83	CCNTGGTTCRGGCYAT	4246.6	108	CVGGYTCRCCNGARTG	4570.8	15	324.2
23	86	TNTTYGMCNTGGTTCC	4239.6	103	GYTCRCCNGARTGYTTCCTCC	4563.8	15	324.2
24	73	TGYGCHYNTTYGGMCC	4231.6	105	CRCCNGARTGYTTCCTCCA	4561.8	15	330.2
25	86	TNTTYGMCNTGGTTCC	4239.6	113	YCARTTCCARAYDGRTRTCCA	4597.8	15	358.2
26	63	GGNCAAGGNATWTCBGC	4198.6	105	CRCCNGARTGYTTCCTCCA	4561.8	15	363.2
27	59	GGYAARGTBGGNCAGGG	4189.6	108	CVGGYTCRCCNGARTG	4570.8	15	381.2
28	46	GNATHACMTTYTYGARAARGAYTG	4138.6	72	GGAACCAANGGKCCRAA	4264.6	16	126
29	136	MVGC SAATGGYGARCC	6317.73	138	WCRTGYTGRITVYCRARTCYTG	6455.73	16	138
30	81	GGTTCRGGCYATHGARAA	4252.6	91	RAAYTCNGARAARTCRITTYCAAAA	4393.8	16	141.2
31	83	CCNTGGTTCRGGCYAT	4246.6	91	RAAYTCNGARAARTCRITTYCAAAA	4393.8	16	147.2
32	99	GARAAYGAYTTYTCNGARTTYGA	4378.8	102	YTCRCCNGARTGYTTCCTCC	4562.8	16	184
33	99	GARAAYGAYTTYTCNGARTTYGA	4378.8	103	GYTCRCCNGARTGYTTCCTCC	4563.8	16	185
34	98	KGTDTTTCGARAAYGAYTTYTCNGA	4372.8	105	CRCCNGARTGYTTCCTCCA	4561.8	16	189
35	59	GGYAARGTBGGNCAGGG	4189.6	91	RAAYTCNGARAARTCRITTYCAAAA	4393.8	16	204.2
36	99	GARAAYGAYTTYTCNGARTTYGA	4378.8	113	YCARTTCCARAYDGRTRTCCA	4597.8	16	219
37	79	NTGGTTCRGGCYATHGA	4249.6	102	YTCRCCNGARTGYTTCCTCC	4562.8	16	313.2
38	79	NTGGTTCRGGCYATHGA	4249.6	103	GYTCRCCNGARTGYTTCCTCC	4563.8	16	314.2
39	81	GGTTCRGGCYATHGARAA	4252.6	104	VGGYTCRCCNGARTGYTT	4567.8	16	315.2
40	83	CCNTGGTTCRGGCYAT	4246.6	104	VGGYTCRCCNGARTGYTT	4567.8	16	321.2

41	86	TNTTYGGMCCNTGGTTCC	4239.6	108	CVGGYTCRCCNGARTG	4570.8	16	331.2
42	73	TGYGCHYNTNTYGGMCC	4231.6	102	YTCRCCNGARTGYTCTTCC	4562.8	16	331.2
43	73	TGYGCHYNTNTYGGMCC	4231.6	103	GYTCRCCNGARTGYTCTTCC	4563.8	16	332.2
44	70	GCNTGGMSYAARACYTTBTG	4216.6	105	CRCCNGARTGYTCTTCCA	4561.8	16	345.2
45	66	CBGCNTGGMSYAARACYTT	4213.6	105	CRCCNGARTGYTCTTCCA	4561.8	16	348.2
46	79	NTGGTTCCRBGCYATHGA	4249.6	113	YCATRITCCARAYDGRITCCA	4597.8	16	348.2
47	63	GGNCAGGNATWTCBGC	4198.6	102	YTCRCCNGARTGYTCTTCC	4562.8	16	364.2
48	63	GGNCAGGNATWTCBGC	4198.6	103	GYTCRCCNGARTGYTCTTCC	4563.8	16	365.2
49	57	AARGTBGGNCAGGNATWTC	4195.6	105	CRCCNGARTGYTCTTCCA	4561.8	16	366.2
51	54	GAAARGTBGGNCAGGNAT	4192.6	105	CRCCNGARTGYTCTTCCA	4561.8	16	369.2
52	59	GGYAAARGTBGGNCAGGG	4189.6	104	VGGYTCRCCNGARTGYTT	4567.8	16	378.2
53	63	GGNCAGGNATWTCBGC	4198.6	113	YCATRITCCARAYDGRITCCA	4597.8	16	399.2
54	50	TYCARAARGAYTYGRMYAARTTYAC	4150.6	105	CRCCNGARTGYTCTTCCA	4561.8	16	411.2
55	39	NRRSAARGGYCARAYGG	4069.6	105	CRCCNGARTGYTCTTCCA	4561.8	16	492.2
56	38	ATGSTNRRSAARGGYCARGA	4066.6	105	CRCCNGARTGYTCTTCCA	4561.8	16	495.2
57	40	CYATGSTNRRSAARGGYCA	4063.6	105	CRCCNGARTGYTCTTCCA	4561.8	16	498.2
58	50	TYCARAARGAYTYGRMYAARTTYAC	4150.6	74	VYGGAAACCANGGKCC	4267.6	17	117
59	50	TYCARAARGAYTYGRMYAARTTYAC	4150.6	71	ATRCGVYGGAAACCANGG	4270.6	17	120
60	50	TYCARAARGAYTYGRMYAARTTYAC	4150.6	78	YTCDATRGCYVYGGAAACCA	4273.6	17	123
61	81	GGTTCCRBGCYATHGARA	4252.6	88	AYTCNGARAARTCRITTYCAAHAC	4390.8	17	138.2
62	39	NRRSAARGGYCARAYGG	4069.6	56	CCCTGNCCVACYTTRCC	4213.6	17	144
63	83	CCNTGGTTCORBGCYAT	4246.6	88	AYTCNGARAARTCRITTYCAAHAC	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	TNTTYGGMCCNTGGTTCC	4239.6	91	RAAYTCNGARAARTCRITTYCAAAA	4393.8	17	154.2
67	98	KGTDITTGARAAYGAYTTYCNGA	4372.8	102	YTCRCCNGARTGYTCTTCC	4562.8	17	190
68	98	KGTDITTGARAAYGAYTTYCNGA	4372.8	103	GYTCRCCNGARTGYTCTTCC	4563.8	17	191
69	99	GARAAYGAYTTYCNGARTTYGA	4378.8	108	CVGGYTCRCCNGARTG	4570.8	17	192
70	39	NRRSAARGGYCARAYGG	4069.6	74	VYGGAAACCANGGKCC	4267.6	17	198
72	39	NRRSAARGGYCARAYGG	4069.6	71	ATRCGVYGGAAACCANGG	4270.6	17	201
73	38	ATGSTNRRSAARGGYCARGA	4066.6	74	VYGGAAACCANGGKCC	4267.6	17	201
74	59	GGYAAARGTBGGNCAGGG	4189.6	88	AYTCNGARAARTCRITTYCAAHAC	4390.8	17	201.2
75	40	CYATGSTNRRSAARGGYCA	4063.6	74	VYGGAAACCANGGKCC	4267.6	17	204
76	38	ATGSTNRRSAARGGYCARGA	4066.6	71	ATRCGVYGGAAACCANGG	4270.6	17	204
77	39	NRRSAARGGYCARAYGG	4069.6	78	YTCDATRGCYVYGGAAACCA	4273.6	17	204
78	40	CYATGSTNRRSAARGGYCA	4063.6	71	ATRCGVYGGAAACCANGG	4270.6	17	207
79	38	ATGSTNRRSAARGGYCARGA	4066.6	78	YTCDATRGCYVYGGAAACCA	4273.6	17	207
80	40	CYATGSTNRRSAARGGYCA	4063.6	78	YTCDATRGCYVYGGAAACCA	4273.6	17	210
81	98	KGTDITTGARAAYGAYTTYCNGA	4372.8	113	YCATRITCCARAYDGRITCCA	4597.8	17	225
82	31	ATHCCHGCHMTBGAYTTYGA	3176	33	CCCTGNCCVACYTTRCC	3443	17	267
83	79	NTGGTTCCRBGCYATHGA	4249.6	108	CVGGYTCRCCNGARTG	4570.8	17	321.2
84	75	HYTNTTYGGMCCNTGGTTC	4238.6	105	CRCCNGARTGYTCTTCCA	4561.8	17	323.2
85	76	CHYNTNTTYGGMCCNTGGTT	4237.6	105	CRCCNGARTGYTCTTCCA	4561.8	17	324.2
86	86	TNTTYGGMCCNTGGTTCC	4239.6	104	VGGYTCRCCNGARTGYTT	4567.8	17	328.2
87	77	ACYTTBTGYGCHYNTNTYGG	4228.6	105	CRCCNGARTGYTCTTCCA	4561.8	17	333.2
88	73	TGYGCHYNTNTYGGMCC	4231.6	108	CVGGYTCRCCNGARTG	4570.8	17	339.2
89	70	GCNTGGMSYAARACYTTBTG	4216.6	102	YTCRCCNGARTGYTCTTCC	4562.8	17	346.2
90	70	GCNTGGMSYAARACYTTBTG	4216.6	103	GYTCRCCNGARTGYTCTTCC	4563.8	17	347.2
91	66	CBGCNTGGMSYAARACYTT	4213.6	102	YTCRCCNGARTGYTCTTCC	4562.8	17	349.2
92	66	CBGCNTGGMSYAARACYTT	4213.6	103	GYTCRCCNGARTGYTCTTCC	4563.8	17	350.2
93	57	AARGTBGGNCAGGNATWTC	4195.6	102	YTCRCCNGARTGYTCTTCC	4562.8	17	367.2
94	57	AARGTBGGNCAGGNATWTC	4195.6	103	GYTCRCCNGARTGYTCTTCC	4563.8	17	368.2
95	54	GAAARGTBGGNCAGGNAT	4192.6	102	YTCRCCNGARTGYTCTTCC	4562.8	17	370.2
96	54	GAAARGTBGGNCAGGNAT	4192.6	103	GYTCRCCNGARTGYTCTTCC	4563.8	17	371.2
97	63	GGNCAGGNATWTCBGC	4198.6	108	CVGGYTCRCCNGARTG	4570.8	17	372.2
98	70	GCNTGGMSYAARACYTTBTG	4216.6	113	YCATRITCCARAYDGRITCCA	4597.8	17	381.2
99	66	CBGCNTGGMSYAARACYTT	4213.6	113	YCATRITCCARAYDGRITCCA	4597.8	17	384.2
100	57	AARGTBGGNCAGGNATWTC	4195.6	113	YCATRITCCARAYDGRITCCA	4597.8	17	402.2

表 30 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	TTTCCAGAAAGATTGTAATAAGTTTACAACCTGGAGAGACCATCGTCCACGGTAAGGTCGGCCAGGGTATATCGGCCTGGAGTAAGA CCTTTTGGCGCTCTGTTTGGCCCCGTGGTTCCGT
150	TTTCCAGAAGGATTGTAATAAATTTACAACAGGTGAGACCATTGCCACGGCAAGGTGGGCCAGGGCATTTCCGGCTTGAGTAAAA CCTTTTGTGCTTTATTCGGCCCCGTGGTTCCGC
335	CTTCCAGAAAGATTGTAACAAATTCACAACAGGTGAGACTATTGCCACGGCAAGGTGGGCCAGGGTATTTCCGGCTTGAGTAAAA CCTTTTGTGCTCTATTTGGACCGTGGTTCCGT
342	CTTCCAGAAGGATTGTAATAAGTTTACAACGGGCGAGACAATAGCGCATGGCAAAGTTGGTCAGGGGATATCTGCATGGAGTAAAA CCTTTTGTGCTTTGTTCCGGCCCATGGTTCCGC
350	CTTCCAGAAGGACTGTAATAAATTCACAACAGGCGAGACAATAGCGCACGGTAAAGTTGGGCAGGGGATATCTGCGTGGAGCAAGA CCTTTTGTGCCCTGTTTGGCCCCATGGTTCCGC
533	TTTCCAAAAGGATTGTAATAAATTTACCACAGGTGAGACAATAGCGCACGGTAAGGTTGGCCAGGGAATATCTGCGTGGAGTAAGA CCTTCTGCGCTCTGTTTGGCCCCGTGGTTCCGC
756	TTTCCAAAAGGATTGCAATAAGTTTACAACCTGGTGAGACTATAGCCCATGGCAAGGTTGGCCAGGGTATATCGGCCTGGAGCAAGA CCTTTTGGCGCCCTGTTCCGGCCCCGTGGTTCCGC
888	CTTCCAGAAAGATTGTAATAAGTTTACCACGGGCGAGACCATTGCCCATGGTAAGGTTGGGCCAGGGCATTTCCGGCTTGAGCAAGA CCTTTTGGCGCCCTCTTGGCCCCGTGGTTCCGT
1142	CTTCCAGAAGGACTGCAATAAATTCACTACGGGTGAGACGATAGCGCACGGTAAAGTTCGGCCAGGGGATATCTGCGTGGAGCAAAA CCTTCTGCGCTTTGTTCCGGCCCCGTGGTTCCAC
1567	TTTCCAGAAAGACTGCAATAAGTTTACAACCTGGCGAAACAATAGCGCATGGCAAAGTTGGCCAGGGGATATCTGCATGGAGTAAAA CCTTTTGGCGCCCTGTTTGGCCCCGTGGTTCCGT
1568	TTTCCAAAAGACTGTAACAAGTTTACAACCTGGTGAGACCATTGCCCATGGCAAGGTTGGTCAGGGCATATCGGCCTGGAGTAAGAC CCTTTTGTGCTTTGTTTGGCCCCGTGGTTCCGT
1731	CTTCCAGAAAGATTGTAATAAGTTTACAACAGGTGAGACGATAGCGCACGGTAAAGTTCGGCCAGGGTATATCTGCATGGAGTAAAA CCTTCTGCGCTCTATTTGGCCCCGTGGTTCCGC
2095	TTTCCAGAAGGATTGCGCCAAATTTACGTTGGACGATCCCGTTGCACATGGTAAAGTGGGACAGGGGATATCTGCGTGGCCAAAA CCTTGTGTGCACCTTTTGGCCCCGTGGTTCCGC
2997	CTTCCAGAAGGATTGTAATAAATTTACAACGGGTGAAACAATAGCGCACGGTAAAGTTCGGCCAGGGGATATCCGCATGGAGTAAGA CCTTCTGTGCTCTGTTCCGGCCCCATGGTTCCGC
3075	TTTCCAAAAGACTGTAACAAGTTTACAACCTGGTGAGACCATGCCCATGGTAAGGTTGGTCAGGGTATATCGGCCTGGAGCAAGA CCTTCTGCGCCCTGTTTGGCCCCGTGGTTCCGT

表 31 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	GATATACCCTGGCCGACCTTACCGTGGACGATGGTCTCTCCAGTTGTAACCTTATTACA
	oe_hev_g1_p14_03	AGGTGGCCAGGGTATATCGGCCTGGAGTAAGACCTTTTGGCGCTCTGTTTGGCCCCGTGGT
	oe_hev_g1_p14_04	ACGGAACCCAGGGCCAAACAGA
50	oe_hev_g150_p14_01	TTTCCAGAAGGATTGTAATAAATTTACAACAGGTGAGACCA
	oe_hev_g150_p14_02	CGAAATGCCCTGGCCACCTTGCCGTGGGCAATGGTCTCACCTGTTGTAATTTATTACA
	oe_hev_g150_p14_03	TGGGCCAGGGCATTTCGGCTGGAGTAAACCTTTTGTGCTTTATTCGGCCCCGTGGTTCC
oe_hev_g150_p14_04	GCGGAACCCAGGGCCGAAT	
335	oe_hev_g335_p14_01	CTTCCAGAAAGATTGTAACAAATTCACAACAGGTG
	oe_hev_g335_p14_02	ATACCCTGGCCACCTTCCGTGGCAATAGTCTCACCTGTTGTAATTTGTTACAATC
	oe_hev_g335_p14_03	AAGGTGGCCAGGGTATTTCGGCCTGGAGTAAACCTTTTGTGCTCTATTTGGACCGTGG
	oe_hev_g335_p14_04	ACGGAACCCAGGTCCAAATAGAGCAC
342	oe_hev_g342_p14_01	CTTCCAGAAGGATTGTAATAAGTTTACAACGGGCGAGAC
	oe_hev_g342_p14_02	AGATATCCCCTGACCAACTTGGCCATGCGCTATTGTCTGCGCCGTTGTAACCTTAT
	oe_hev_g342_p14_03	CAAAGTTGGTCAGGGGATATCTGCATGGAGTAAACCTTTTGTGCTTTGTTCCGGCCCATG
	oe_hev_g342_p14_04	GCGGAACCCATGGCCGAACAAGC
350	oe_hev_g350_p14_01	CTTCCAGAAGGACTGTAATAAATTCACAACAGGCGAG
	oe_hev_g350_p14_02	GATATCCCCTGCCCACTTTACCGTGCCTATTGTCTCGCCTGTTGTAATTTATTACA
	oe_hev_g350_p14_03	AAGTTGGGCAGGGGATATCTGCGTGGAGCAAGACCTTTTGTGCCCTGTTTGGCCCCATGGT
	oe_hev_g350_p14_04	GCGGAACCCATGGCCAAACAGG
533	oe_hev_g533_p14_01	TTTCCAAAAGGATTGTAATAAATTTACCACAGGTGAGACAATAGC
	oe_hev_g533_p14_02	CGCAGATATCCCTGCCCACTTACCGTGCCTATTGTCTCACCTGTTGTAATTT
	oe_hev_g533_p14_03	GGCAGGGAATATCTGCGTGGAGTAAAGACTTTTCTGCGCTCTGTTTGGCCCCGTGGTTC
	oe_hev_g533_p14_04	GCGGAACCCAGGGCCAAACA
756	oe_hev_g756_p14_01	TTTCCAAAAGGATTGCAATAAGTTTACAACCTGGTGAGACTATAGC
	oe_hev_g756_p14_02	CGATATACCCTGGCCACCTTGCATGGGCTATAGTCTCACCAAGTTGTAACCTTATTG
	oe_hev_g756_p14_03	GGTTGGCCAGGGTATATCGGCCTGGAGCAAGACCTTCTGCGCCCTGTTCCGGCCCCGTGGT
	oe_hev_g756_p14_04	GCGGAACCCAGGGCCGAACAG
142	oe_hev_g1142_p14_01	CTTCCAGAAGGACTGCAATAAATTCACTACGG
	oe_hev_g1142_p14_02	ATCCCCTGCCGACCTTACCGTGCCTATCGTCTCACCCGTAGTGAATTTATTGAGTCC

	oe_hev_g1142_p14_03	AAGGTCGGGCAGGGGATATCTGCGTGGAGCAAAACCTTCTGCGCTTTGTTGGGCCCTTGG
	oe_hev_g1142_p14_04	GTGGAACCAAGGGCCGAACAAAG
567	oe_hev_g1567_p14_01	TTTCCAGAAAGACTGCAATAAGTTTACAACCTGGC
	oe_hev_g1567_p14_02	ATCCCTGCCCCAACTTTGCCATGCGCTATTGTTTCCAGTTGTAACTTATTGCAGTCT
	oe_hev_g1567_p14_03	AAAGTTGGGCAGGGGATATCTGCATGGAGTAAACCTTTTGGCCCTGTTGGCCCTGG
	oe_hev_g1567_p14_04	ACGGAACCAGGGGCCAAACAGGG
568	oe_hev_g1568_p14_01	TTTCCAAAAAGACTGTAACAAGTTTACAACCTGGTGAGACC
	oe_hev_g1568_p14_02	GATATGCCCTGACCAACCTTGCCATGGCAATGGTCTCACCAGTTGTAACCTTGTAC
	oe_hev_g1568_p14_03	AAGGTTGGTCAGGGCATATCGGCCTGGAGTAAGACCTTTTGTGCTTTGTTGGCCCGTGG
	oe_hev_g1568_p14_04	ACGGAACCAGGGGCCAAACAAAG
731	oe_hev_g1731_p14_01	CTTCCAGAAAGATTGTAATAAGTTTACAACAGGTGAGACGA
	oe_hev_g1731_p14_02	GATATACCCTGCCGACCTTACCCTGCGCTATCGTCTCACCTGTTGTAACCTTATTAC
	oe_hev_g1731_p14_03	AGGTCGGGCAGGGTATATCTGCATGGAGTAAACCTTCTGCGCTCTATTGGCCCGTGGT
	oe_hev_g1731_p14_04	GCGGAACCAGGGGCCAAATAGA
2095	oe_hev_g2095_p14_01	TTTCCAGAAAGATTGCGCCAAATTTACGTTG
	oe_hev_g2095_p14_02	GATATCCCTGCCCACCTTTACCATGTGCAACGGGATCGTCCAACGTAAATTTGGCCCA
	oe_hev_g2095_p14_03	GTAAGTGGGACAGGGGATATCTGCGTGGCCCAAACTTTGTGTGCACTTTTGGCCCT
	oe_hev_g2095_p14_04	CCGGAACCAGGGGCCAAAAAGTGA
2297	oe_hev_g2297_p14_01	CTTCCAGAAAGATTGTAATAAATTTACAACGGGTGAAACA
	oe_hev_g2297_p14_02	GGATATCCCTGCCGACTTTACCCTGCGCTATTGTTTACCCGTTGTAATTTATTAC
	oe_hev_g2297_p14_03	TCCGGCAGGGAATATCCGCATGGAGTAAGACCTTCTGTGCTCTGTTCCGCCCATGGTTCC
	oe_hev_g2297_p14_04	GCGGAACCATGGGCCGAAAC
3075	oe_hev_g3075_p14_01	TTTCCAAAAAGACTGTAACAAGTTTACAACCTGGTGAG
	oe_hev_g3075_p14_02	CGATATACCCTGACCGACCTTACCATGGGCGATGGTCTCACCAGTTGTGAACCTTGTACA
	oe_hev_g3075_p14_03	AGGTCGGTCAGGGTATATCGGCCTGGAGCAAGACTTCTGCGCCTGTTGGCCCGTGGT
	oe_hev_g3075_p14_04	ACGGAACCAGGGGCCAAACAGG

表 32 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	8_1-05-Uu	West Nile virus isolate 8_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 33 Westnile virus 用プライマー(上位 100 件のみ表示)

Pair I D	Primer I D (Forwa rd)	塩基配列(Forward)	Primer I D (Rever se)	塩基配列 (Reverse)	プライマー の degenera cy 指数 <sup>1</sup>	予想サイズ
1	81	GGTTCRBCGYATHGARAA	105	CRCCNGARTGYTTCTTCCA	13	309.2
3	59	GGYAARGTBGGNCAGGG	105	CRCCNGARTGYTTCTTCCA	13	372.2
8	86	TNTTYGMCNCGTTCC	105	CRCCNGARTGYTTCTTCCA	14	322.2
9	81	GGTTCRBCGYATHGARAA	113	YCATRTTCCARAYDGRTRTCCA	14	345.2
13	59	GGYAARGTBGGNCAGGG	113	YCATRTTCCARAYDGRTRTCCA	14	408.2
14	50	TYCARAARGAYTYRMYAARTTYAC	72	GGAACCANGGKCCRAA	15	114
15	99	GARAAYGAYTTYCNGARTTYGA	105	CRCCNGARTGYTTCTTCCA	15	183
16	39	NRRSAARGGYCARGAYGG	72	GGAACCANGGKCCRAA	15	195
25	86	TNTTYGMCNCGTTCC	113	YCATRTTCCARAYDGRTRTCCA	15	358.2
28	46	GNATHACMTTYTYCARAARGAYTG	72	GGAACCANGGKCCRAA	16	126
29	136	MVGCSAATGGYGARCC	138	WCRTGYTGRTTVYCRTARTCYTG	16	138
30	81	GGTTCRBCGYATHGARAA	91	RAAYTCNGARAARTCRTTYTCAAA	16	141.2
35	59	GGYAARGTBGGNCAGGG	91	RAAYTCNGARAARTCRTTYTCAAA	16	204.2
36	99	GARAAYGAYTTYCNGARTTYGA	113	YCATRTTCCARAYDGRTRTCCA	16	219
44	70	GCNTGGMSYAARACYTTBTG	105	CRCCNGARTGYTTCTTCCA	16	345.2
54	50	TYCARAARGAYTYRMYAARTTYAC	105	CRCCNGARTGYTTCTTCCA	16	411.2
55	39	NRRSAARGGYCARGAYGG	105	CRCCNGARTGYTTCTTCCA	16	492.2
62	39	NRRSAARGGYCARGAYGG	56	CCCTGNCCVACYTTRCC	17	144
66	86	TNTTYGMCNCGTTCC	91	RAAYTCNGARAARTCRTTYTCAAA	17	154.2
82	31	ATHCCHGHMTBGAYTTYGA	33	CCCTGNCCVACYTTRCC	17	267
98	70	GCNTGGMSYAARACYTTBTG	113	YCATRTTCCARAYDGRTRTCCA	17	381.2
104	46	GNATHACMTTYTYCARAARGAYTG	105	CRCCNGARTGYTTCTTCCA	17	423.2
105	50	TYCARAARGAYTYRMYAARTTYAC	113	YCATRTTCCARAYDGRTRTCCA	17	447.2
112	39	NRRSAARGGYCARGAYGG	113	YCATRTTCCARAYDGRTRTCCA	17	528.2
127	122	BKCHTWYTGCCBCARAC	127	RACNGAVGCCADCC	18	165
156	46	GNATHACMTTYTYCARAARGAYTG	113	YCATRTTCCARAYDGRTRTCCA	18	459.2
160	128	GHTGGCBTCNGTYGA	138	WCRTGYTGRTTVYCRTARTCYTG	18	576
161	50	TYCARAARGAYTYRMYAARTTYAC	67	GGKCCRAANARDGCRCA	19	105
167	39	NRRSAARGGYCARGAYGG	55	GCVGAWATNCCCTGNCC	19	153
175	70	GCNTGGMSYAARACYTTBTG	91	RAAYTCNGARAARTCRTTYTCAAA	19	177.2
177	39	NRRSAARGGYCARGAYGG	67	GGKCCRAANARDGCRCA	19	186
190	50	TYCARAARGAYTYRMYAARTTYAC	91	RAAYTCNGARAARTCRTTYTCAAA	19	243.2
191	120	SHAAYTAYGCHCARTAYCGBGT	127	RACNGAVGCCADCC	19	249
192	39	NRRSAARGGYCARGAYGG	91	RAAYTCNGARAARTCRTTYTCAAA	19	324.2
207	129	HTGGGCBTCNGTYGARAC	138	WCRTGYTGRTTVYCRTARTCYTG	19	573
208	40	CYATGSTNRRSAARGGYCA	44	TRAAAYTRKYRCARTCYTTYTGRAA	20	102
209	46	GNATHACMTTYTYCARAARGAYTG	67	GGKCCRAANARDGCRCA	20	117
238	46	GNATHACMTTYTYCARAARGAYTG	91	RAAYTCNGARAARTCRTTYTCAAA	20	255.2
248	126	TBGAYATGAAYTCNATYACNTCBAC	127	RACNGAVGCCADCC	21	120
273	119	RRTGKKYTSYGGGGTG	123	CNGTVGANGTRATNGARTTCATRTC	21	571.467
282	81	GGTTCRBCGYATHGARAA	97	AVWMRTTRTTYTGDDTDSWRTCRAA	22	162.2
290	59	GGYAARGTBGGNCAGGG	97	AVWMRTTRTTYTGDDTDSWRTCRAA	22	225.2
293	130	KSTNATGSTYTYRTHCAYGG	138	WCRTGYTGRTTVYCRTARTCYTG	22	516
298	128	GHTGGGCBTCNGTYGA	132	SVCCRGTRTARRSHSTRITDGTRTA	23	117
300	125	CNWSYRTBGAYATGAAYTCNATYAC	127	RACNGAVGCCADCC	23	126
302	86	TNTTYGMCNCGTTCC	97	AVWMRTTRTTYTGDDTDSWRTCRAA	23	175.2
313	45	NMGNATHACMTTYTYCARAARGA	58	CAVAARGTYTTRSKCCANGC	24	102
314	129	HTGGGCBTCNGTYGARAC	132	SVCCRGTRTARRSHSTRITDGTRTA	24	114
323	121	VAAHGCBGTHGGYGG	132	SVCCRGTRTARRSHSTRITDGTRTA	24	291
324	133	SYTAYACHAAYASDSYTYAYACYGG	138	WCRTGYTGRTTVYCRTARTCYTG	24	477
329	120	SHAAYTAYGCHCARTAYCGBGT	123	CNGTVGANGTRATNGARTTCATRTC	25	147
330	70	GCNTGGMSYAARACYTTBTG	97	AVWMRTTRTTYTGDDTDSWRTCRAA	25	198.2
334	122	BKCHTWYTGCCBCARAC	132	SVCCRGTRTARRSHSTRITDGTRTA	25	258
336	50	TYCARAARGAYTYRMYAARTTYAC	97	AVWMRTTRTTYTGDDTDSWRTCRAA	25	264.2
337	39	NRRSAARGGYCARGAYGG	97	AVWMRTTRTTYTGDDTDSWRTCRAA	25	345.2
346	46	GNATHACMTTYTYCARAARGAYTG	97	AVWMRTTRTTYTGDDTDSWRTCRAA	26	276.2
347	120	SHAAYTAYGCHCARTAYCGBGT	132	SVCCRGTRTARRSHSTRITDGTRTA	26	342
350	126	TBGAYATGAAYTCNATYACNTCBAC	132	SVCCRGTRTARRSHSTRITDGTRTA	28	213
354	125	CNWSYRTBGAYATGAAYTCNATYAC	132	SVCCRGTRTARRSHSTRITDGTRTA	30	219

表 34 Human ParvovirusB19 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 35 Human ParvovirusB19 用プライマー(上位 100 件のみ表示)

Pair ID	Primer I D (Forward)	塩基配列(Forward)	Primer I D (Reverse)	塩基配列 (Reverse)	プライマーの degeneracy 指数 <sup>1</sup>	予想サイズ
1	1121	AGTGGTGGTGAAAGCTCTGAA	1266	TCTCCTGAACTGGTCCCG	0	124
2	1862	AAGACTTACACAAGCCTGGGC	1961	AGTCATGAATCCTTGCAGCACT	0	124
3	1121	AGTGGTGGTGAAAGCTCTGAA	1264	GATTCTCCTGAACTGGTCCC	0	125
4	1133	AGTGGTGGTGAAAGCTCTGAA	1266	TCTCCTGAACTGGTCCCG	0	125
5	1854	GAAGACTTACACAAGCCTGGG	1961	AGTCATGAATCCTTGCAGCACT	0	125
6	1862	AAGACTTACACAAGCCTGGGC	1946	AGTCATGAATCCTTGCAGCAC	0	125
7	1123	CAGTGGTGGTGAAAGCTCTG	1266	TCTCCTGAACTGGTCCCG	0	126
8	1854	GAAGACTTACACAAGCCTGGG	1946	AGTCATGAATCCTTGCAGCAC	0	126
9	1133	AGTGGTGGTGAAAGCTCTGAA	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	GCAGTGGTGGTGAAAGCTCT	1266	TCTCCTGAACTGGTCCCG	0	127
14	1123	CAGTGGTGGTGAAAGCTCTG	1264	GATTCTCCTGAACTGGTCCC	0	127
15	1113	AGCAGTGGTGGTGAAAGCTC	1266	TCTCCTGAACTGGTCCCG	0	128
16	1854	GAAGACTTACACAAGCCTGGG	1963	CTAAAGTCATGAATCCTTGCAGC	0	128
17	1862	AAGACTTACACAAGCCTGGGC	1969	TACCTAAAGTCATGAATCCTGCAG	0	128
18	1126	GCAGTGGTGGTGAAAGCTCT	1264	GATTCTCCTGAACTGGTCCC	0	128
19	1862	AAGACTTACACAAGCCTGGGC	1971	ATACCTAAAGTCATGAATCCTTGA	0	129
20	1854	GAAGACTTACACAAGCCTGGG	1969	TACCTAAAGTCATGAATCCTGCAG	0	129
21	1113	AGCAGTGGTGGTGAAAGCTC	1264	GATTCTCCTGAACTGGTCCC	0	129
22	1108	AGCAGTGGTGGTGAAAGCT	1266	TCTCCTGAACTGGTCCCG	0	129
23	1108	AGCAGTGGTGGTGAAAGCT	1264	GATTCTCCTGAACTGGTCCC	0	130
24	1109	CAGCAGTGGTGGTGAAAGC	1266	TCTCCTGAACTGGTCCCG	0	130
25	1862	AAGACTTACACAAGCCTGGGC	1956	TATACCTAAAGTCATGAATCCTTG	0	130
26	1854	GAAGACTTACACAAGCCTGGG	1971	ATACCTAAAGTCATGAATCCTTGA	0	130
27	1862	AAGACTTACACAAGCCTGGGC	1954	CTAACCTAAAGTCATGAATCCTTG	0	131
28	1854	GAAGACTTACACAAGCCTGGG	1956	TATACCTAAAGTCATGAATCCTTG	0	131
29	1124	GCAGCAGTGGTGGTGAAAG	1266	TCTCCTGAACTGGTCCCG	0	131
30	1109	CAGCAGTGGTGGTGAAAGC	1264	GATTCTCCTGAACTGGTCCC	0	131
31	1124	GCAGCAGTGGTGGTGAAAG	1264	GATTCTCCTGAACTGGTCCC	0	132
32	1134	AGCAGCAGTGGTGGTGAAA	1266	TCTCCTGAACTGGTCCCG	0	132
33	1862	AAGACTTACACAAGCCTGGGC	1967	GCTATACCTAAAGTCATGAATCCTT	0	132
34	1854	GAAGACTTACACAAGCCTGGG	1954	CTAACCTAAAGTCATGAATCCTTG	0	132
35	1854	GAAGACTTACACAAGCCTGGG	1967	GCTATACCTAAAGTCATGAATCCTT	0	133
36	1130	AGCAGCAGTGGTGGTGAA	1266	TCTCCTGAACTGGTCCCG	0	133
37	1134	AGCAGCAGTGGTGGTGAAA	1264	GATTCTCCTGAACTGGTCCC	0	133
38	1862	AAGACTTACACAAGCCTGGGC	1950	GGCTATACCTAAAGTCATGAATCCTT	0	133
39	1128	AGCAGCAGTGGTGGTGAA	1266	TCTCCTGAACTGGTCCCG	0	134
40	1854	GAAGACTTACACAAGCCTGGG	1950	GGCTATACCTAAAGTCATGAATCCTT	0	134
41	1862	AAGACTTACACAAGCCTGGGC	1944	TGGCTATACCTAAAGTCATGAATCCTT	0	134
42	1130	AGCAGCAGTGGTGGTGAA	1264	GATTCTCCTGAACTGGTCCC	0	134
43	1128	AGCAGCAGTGGTGGTGAA	1264	GATTCTCCTGAACTGGTCCC	0	135
44	1854	GAAGACTTACACAAGCCTGGG	1944	TGGCTATACCTAAAGTCATGAATCCTT	0	135
45	1862	AAGACTTACACAAGCCTGGGC	1959	TGGCTATACCTAAAGTCATGAATCCTT	0	135
46	1854	GAAGACTTACACAAGCCTGGG	1959	TGGCTATACCTAAAGTCATGAATCCTT	0	136
47	1730	GGACAGTTATYTGACCACCCC	1829	CCAGGCTTGTGTAAGTCTTCA	1	103
48	1172	GAASAACTCAGTGAAAGCAGCTTT	1266	TCTCCTGAACTGGTCCCG	1	103
49	1172	GAASAACTCAGTGAAAGCAGCTTT	1264	GATTCTCCTGAACTGGTCCC	1	104
50	1735	ATGGACAGTTATYTGACCACCCC	1829	CCAGGCTTGTGTAAGTCTTCA	1	104
51	1730	GGACAGTTATYTGACCACCCC	1839	CCAGGCTTGTGTAAGTCTTCA	1	104
52	1166	GAASAACTCAGTGAAAGCAGCTT	1266	TCTCCTGAACTGGTCCCG	1	104
53	1738	CATGGACAGTTATYTGACCACCCC	1829	CCAGGCTTGTGTAAGTCTTCA	1	105
54	1167	TGAASAACTCAGTGAAAGCAGCTT	1266	TCTCCTGAACTGGTCCCG	1	105
55	1166	GAASAACTCAGTGAAAGCAGCTT	1264	GATTCTCCTGAACTGGTCCC	1	105

56	1735	ATGGACAGTTATYTGACCACCC	1839	CCCAGGCTTGTGAAGTCTTC	1	105
57	1730	GGACAGTTATYTGACCACCC	1836	GCCCAGGCTTGTGAAGTCTT	1	105
58	1735	ATGGACAGTTATYTGACCACCC	1836	GCCCAGGCTTGTGAAGTCTT	1	106
59	1730	GGACAGTTATYTGACCACCC	1824	GCCCAGGCTTGTGAAGTCT	1	106
60	1738	CATGGACAGTTATYTGACCACC	1839	CCCAGGCTTGTGAAGTCTTC	1	106
61	1167	TGAASAACTCAGTAAAAGCAGGT	1264	GATTCTCCTGAACTGGTCCC	1	106
62	1170	CTGAASAACTCAGTAAAAGCAGC	1266	TCTCCTGAACTGGTCCCG	1	106
63	1170	CTGAASAACTCAGTAAAAGCAGC	1264	GATTCTCCTGAACTGGTCCC	1	107
64	1735	ATGGACAGTTATYTGACCACCC	1824	GCCCAGGCTTGTGAAGTCT	1	107
65	1738	CATGGACAGTTATYTGACCACC	1836	GCCCAGGCTTGTGAAGTCTT	1	107
66	1164	CTCTGAASAACTCAGTAAAAGCAG	1266	TCTCCTGAACTGGTCCCG	1	107
67	1730	GGACAGTTATYTGACCACCC	1819	GCCCAGGCTTGTGAAGTC	1	107
68	1164	CTCTGAASAACTCAGTAAAAGCAG	1264	GATTCTCCTGAACTGGTCCC	1	108
69	1735	ATGGACAGTTATYTGACCACCC	1819	GCCCAGGCTTGTGAAGTC	1	108
70	1738	CATGGACAGTTATYTGACCACC	1824	GCCCAGGCTTGTGAAGTCT	1	108
71	1159	CTCTGAASAACTCAGTAAAAGCA	1266	TCTCCTGAACTGGTCCCG	1	108
72	1139	AGCTCTGAASAACTCAGTAAAAGC	1266	TCTCCTGAACTGGTCCCG	1	109
73	1738	CATGGACAGTTATYTGACCACC	1819	GCCCAGGCTTGTGAAGTC	1	109
74	1159	CTCTGAASAACTCAGTAAAAGCA	1264	GATTCTCCTGAACTGGTCCC	1	109
75	1139	AGCTCTGAASAACTCAGTAAAAGC	1264	GATTCTCCTGAACTGGTCCC	1	110
76	1150	AAAGCTCTGAASAACTCAGTAAAAG	1266	TCTCCTGAACTGGTCCCG	1	110
77	1150	AAAGCTCTGAASAACTCAGTAAAAG	1264	GATTCTCCTGAACTGGTCCC	1	111
78	1156	GAAAGCTCTGAASAACTCAGTGAAA	1266	TCTCCTGAACTGGTCCCG	1	111
79	1152	GAAAGCTCTGAASAACTCAGTGAA	1266	TCTCCTGAACTGGTCCCG	1	112
80	1156	GAAAGCTCTGAASAACTCAGTGAAA	1264	GATTCTCCTGAACTGGTCCC	1	112
81	1143	TGAAAGCTCTGAASAACTCAGTGA	1266	TCTCCTGAACTGGTCCCG	1	113
82	1152	GAAAGCTCTGAASAACTCAGTGAA	1264	GATTCTCCTGAACTGGTCCC	1	113
83	1143	TGAAAGCTCTGAASAACTCAGTGA	1264	GATTCTCCTGAACTGGTCCC	1	114
84	1146	GTGAAAGCTCTGAASAACTCAGTG	1266	TCTCCTGAACTGGTCCCG	1	114
85	1155	GGTAAAAGCTCTGAASAACTCAGT	1266	TCTCCTGAACTGGTCCCG	1	115
86	1146	GTGAAAGCTCTGAASAACTCAGTG	1264	GATTCTCCTGAACTGGTCCC	1	115
87	1148	GGTAAAAGCTCTGAASAACTCAG	1266	TCTCCTGAACTGGTCCCG	1	116
88	1863	AAGCCTGGGCRAGTTAGC	1961	AGTCATGAATCCTTGCAGCAC	1	116
89	1155	GGTAAAAGCTCTGAASAACTCAGT	1264	GATTCTCCTGAACTGGTCCC	1	116
90	1863	AAGCCTGGGCRAGTTAGC	1946	AGTCATGAATCCTTGCAGCAC	1	117
91	1860	ACAAGCCTGGGCRAGTTAG	1961	AGTCATGAATCCTTGCAGCAC	1	117
92	1141	GGTAAAAGCTCTGAASAACTCA	1266	TCTCCTGAACTGGTCCCG	1	117
93	1148	GGTAAAAGCTCTGAASAACTCAG	1264	GATTCTCCTGAACTGGTCCC	1	117
94	1847	CACAAGCCTGGGCRAGTTA	1961	AGTCATGAATCCTTGCAGCAC	1	118
95	1863	AAGCCTGGGCRAGTTAGC	1951	AAGTCATGAATCCTTGCAGCA	1	118
96	1860	ACAAGCCTGGGCRAGTTAG	1946	AGTCATGAATCCTTGCAGCAC	1	118
97	1140	GTGGTAAAAGCTCTGAASAACTC	1266	TCTCCTGAACTGGTCCCG	1	118
98	1141	GGTAAAAGCTCTGAASAACTCA	1264	GATTCTCCTGAACTGGTCCC	1	118
99	1863	AAGCCTGGGCRAGTTAGC	1963	CTAAAGTCATGAATCCTTGCAGC	1	119
100	1140	GTGGTAAAAGCTCTGAASAACTC	1264	GATTCTCCTGAACTGGTCCC	1	119

表 36 HHV-5, HHV-6 および HHV-7 共通検出プライマー設計対象とした遺伝子群

Cluster No	ID	Organism	Product	Nucleotide length	Amino Acid length
1	14	Human herpesvirus 5	DNA packaging terminase subunit 2	2553	850
	282	Human herpesvirus 6A	DNA packaging terminase subunit 2	2181	726
	283	Human herpesvirus 6B	transport/capsid assembly	2181	726
	284	Human herpesvirus 6B	transport protein	2181	726
	285	Human herpesvirus 6	U40	2181	726
	586	Human herpesvirus 7	DNA packaging terminase subunit 2	2166	721
	587	Human herpesvirus 7	U40	2166	721
2	4	Human herpesvirus 5	single-stranded DNA-binding protein	3708	1235
	234	Human herpesvirus 6	U41 major DNA binding protein	3399	1132
	232	Human herpesvirus 6A	single-stranded DNA-binding protein	3399	1132
	235	Human herpesvirus 6B	U41	3399	1132
	233	Human herpesvirus 6B	major DNA binding protein	3399	1132
	557	Human herpesvirus 7	U41	3396	1131
	558	Human herpesvirus 7	major DNA binding protein	3396	1131
3	556	Human herpesvirus 7	single-stranded DNA-binding protein	3396	1131
	3	Human herpesvirus 5	DNA polymerase catalytic subunit	3729	1242
	244	Human herpesvirus 6	U38 DNA polymerase	3039	1012
	242	Human herpesvirus 6A	DNA polymerase catalytic subunit	3039	1012
	243	Human herpesvirus 6B	DNA polymerase	3039	1012
	245	Human herpesvirus 6B	U38	3039	1012
	559	Human herpesvirus 7	DNA polymerase catalytic subunit	3042	1013
4	560	Human herpesvirus 7	U38	3042	1013
	561	Human herpesvirus 7	DNA polymerase	3039	1012
	7	Human herpesvirus 5	helicase-primase helicase subunit	2871	956
	264	Human herpesvirus 6A	helicase-primase helicase subunit	2475	824
	265	Human herpesvirus 6B	helicase	2475	824
	266	Human herpesvirus 6B	U77	2475	824
	572	Human herpesvirus 7	helicase-primase helicase subunit	2463	820
5	573	Human herpesvirus 7	U77	2463	820
	574	Human herpesvirus 7	helicase	2463	820
	64	Human herpesvirus 5	nuclear egress lamina protein	1131	376
	445	Human herpesvirus 6	U37	795	264
	444	Human herpesvirus 6A	nuclear egress lamina protein	795	264
6	688	Human herpesvirus 7	nuclear egress lamina protein	780	259
	689	Human herpesvirus 7	U37	780	259
	2	Human herpesvirus 5	major capsid protein	4113	1370
	227	Human herpesvirus 6	U57 major capsid protein	4038	1345
	226	Human herpesvirus 6A	major capsid protein	4038	1345
	228	Human herpesvirus 6B	U57	4038	1345
	548	Human herpesvirus 7	major capsid protein	4038	1345
	549	Human herpesvirus 7	U57	4038	1345

表 37 プライマー設計対象クラスターごとの CoCoMo プログラムによる設計プライマー数

Cluster No	Main Product	No. of Predicted Primers	Degeneracy in predicted primers
1	DNA packaging terminase subunit 2	21	13~27
2	Single-stranded DNA-binding protein	52	14~26
3	DNA polymerase catalytic subunit	45	13~24
4	Helicase-primase helicase subunit	110	12~27
5	Nuclear egress lamina protein	29	13~25
6	Major capsid protein	177	8~27

表 38 HHV-5, HHV-6 および HHV-7 遺伝子群の第 6 クラスターから予測された最適プライマー

Pair ID	Forward primer	Average location of forward primer	Reverse primer	Average location of reverse primer	Total degeneracy in primer pair	Average size of PCR product
1	GACGGYGGTTTTCKCT	142	GCRAADCCMGGRTGRAT	152	8	198

表 39 ヒトアデノウイルスプライマー設計用の DNA polymerase 遺伝子を選択したゲノムデータ

ID	Accession	Annotation	Subgenus/Serotype	Nucleotide length	Amino acid length
1	AF534906	Human adenovirus type 1 subgroup C complete genome	1	3171	1056
2	AF532578	Human adenovirus type 11 strain Slobitski complete genome	11	3369	1122
3	X73487	Adenovirus type 12 DNA complete genome	12	3186	1061
4	AY803294	Human adenovirus type 14 strain de Wit complete genome	14	3582	1193
5	FJ822614	Human adenovirus 14 isolate Ad14-303600 complete genome	14	3369	1122
6	AY601636	Human adenovirus type 16 strain ch. 79 complete genome	16	3582	1193
7	AF108105	Human adenovirus type 17 complete genome	17	3276	1091
8	GU191019	Human adenovirus 18 complete genome	18	3576	1191
9	EF121005	Human adenovirus 19 strain C complete genome	19	3276	1091
10	J01917	Adenovirus type 2 complete genome	2	3171	1056
11	AY601633	Human adenovirus type 21 strain AV-1645 complete genome	21	3582	1193
12	FJ404771	Human adenovirus 22 isolate AV-2711 complete genome	22	3531	1176
13	EF153474	Human adenovirus type 26 complete genome	26	3276	1091
14	FJ824826	Human adenovirus 28 strain BP-5 complete genome	28	3531	1176
15	AY599834	Human adenovirus type 3 strain GB complete genome	3	3582	1193
16	AY599836	Human adenovirus type 3 strain NHRC 1276 complete genome	3	3573	1190
17	AM749299	Human adenovirus type 31 complete genome serotype 31	31	3555	1184
18	AY737797	Human adenovirus type 34 strain Compton complete genome	34	3582	1193
19	AY128640	Human adenovirus type 35 strain Holden complete genome	35	3369	1122
20	AY271307	Human adenovirus type 35 strain 35p complete genome	35	3369	1122
21	AY458656	Human adenovirus type 4 strain CL68578 complete genome	4	3066	1021
22	AY594253	Human adenovirus type 4 strain RI-67 complete genome	4	3582	1193

23	AY594254	Human adenovirus type 4 vaccine strain complete genome	4	3582	1193
24	AY599835	Human adenovirus type 4 strain NHRC 42606 complete genome	4	3582	1193
25	AY599837	Human adenovirus type 4 strain NHRC 3 complete genome	4	3582	1193
26	EF153473	Human adenovirus type 48 complete genome	48	3276	1091
27	DQ393829	Human adenovirus type 49 complete genome	49	3276	1091
28	AY601635	Human adenovirus type 5 strain NHRC Ad5FS 7151 complete genome	5	3597	1198
29	AY737798	Human adenovirus type 50 strain Wan complete genome	50	3582	1193
30	FJ169625	Human adenovirus 53 complete genome	53	3498	1165
31	AY495969	Human adenovirus type 7 vaccine strain complete genome	7	3369	1122
32	AY594255	Human adenovirus type 7 strain Gomen complete genome	7	3582	1193
33	AY594256	Human adenovirus type 7 vaccine strain complete genome	7	3582	1193
34	AY601634	Human adenovirus type 7 strain NHRC 1315 complete genome	7	3582	1193
35	GQ478341	Human adenovirus 7 strain GZ08 complete genome	7	3582	1193
36	NC_001460	Human adenovirus A complete genome	A	3570	1189
37	DQ099432	Human adenovirus B strain Guangzhou01 complete genome	B	3501	1166
38	DQ105654	Human adenovirus B strain Guangzhou02 complete genome	B	3501	1166
39	NC_011202	Human adenovirus B2 complete genome	B	3582	1193
40	NC_011203	Human adenovirus B1 complete genome	B	3582	1193
41	NC_001405	Human adenovirus C complete genome	C	3597	1198
42	NC_010956	Human adenovirus D complete genome	D	3531	1176
43	NC_003266	Human adenovirus E complete genome	E	3582	1193
44	NC_001454	Human adenovirus F complete genome	F	3567	1188

表 40 ヒトアデノウイルスの各亜属に含まれる血清型

亜属	血清型
A	12, 18, 31
B1	3, 7, 16, 21, 50
B2	11, 14, 34, 35
C	1, 2, 5, 6
D	8-10, 13, 15, 17, 19, 20, 22-30, 32, 33, 36-39, 42-49, 51
E	4,
F	40, 41

表 41 ヒトアデノウイルス A, B1, B2, D および E 各亜種から予測された亜種共通プライマーセット

Pair ID	Forward primer	Average location of forward primer	Reverse primer	Average location of reverse primer	Total degeneracy in primer pair	Average size of PCR product
1	GGCATGTAYGCMTCBGC	101	IGGRGGGTCNGCRTC*	286	12	185

I: Inosine 酸塩基ヌクレオチド、全ての塩基と二重鎖が形成される

表 42 ヒトアデノウイルス亜種共通プライマーセットのうち、適用範囲の最大だったプライマーによって増幅されるヒトアデノウイルス血清型

ウイルス種	cc-1	ウイルス種	cc-1
HAdV 1	○	HAdV4	○
HAdV 11	○	HAdV4/NHRC42606	○
HAdV 12	○	HAdV4 /NHRC3	○
HAdV 14	○	HAdV 48	○
HAdV 14/Ad14	○	HAdV49	○
HAdV 16	○	HAdV5	○
HAdV 17	○	HAdV 50	○
HAdV 18	○	HAdV53	○
HAdV 19	○	HAdV 7	○
HAdV 2	○	HAdV7	○
HAdV 21	○	HAdV 7/Gome	○
HAdV 22	○	HAdV 7/NHRC1315	○
HAdV 26	○	HAdV 7 /GZ08	○
HAdV 28	○	HAdV A	◎
HAdV 3	○	HAdV B/Gua01	○
HAdV 3/NHRC1276	○	HAdV B/Gua02	○
HAdV 31	○	HAdVB2	◎
HAdV 34	○	HAdV B1	◎
HAdV 35	○	HAdV C	◎
HAdV 35/35p	○	HAdV D	◎
HAdV 4/CL68578	○	HAdV E	◎
HAdV 4/RI67	○	HAdV F	◎

表 43 ヒトアデノウイルス共通プライマーの PCR 試験用鋳型合成用オリゴマー

Oligomer name	Sequence	Oligomer length
HAdV_o_dp2_141_t36_1	GCGGCATGTATGCATC	16
HAdV_o_dp2_141_t36_2	GGGGTTAAGGGGAGGACCCCAAGGCATGGGGTGTGTGAGGGCCGATGCATACATGCCG	58
HAdV_o_dp2_141_t36_3	CCTCCCCTTAACCCCTATGAGCGGGCATTGGCCGTGCGGCAATGGCAGGTGGCGCTGG	58
HAdV_o_dp2_141_t36_4	ACAAAGATTTTGTCAAAAATAATCAATTTGCAAGTGTAATTTCCAGCGCCACCTGCC	59
HAdV_o_dp2_141_t36_5	TTATTTTGACAAAAATCTTTGTCTCTGGCATTTTACTATAGATGCCGACCCCCAGA	57
HAdV_o_dp2_141_t36_6	TCTGGGGGGTCCGCA	15
HAdV_o_dp2_141_t39_1	GTGGCATGTATGCCTCTG	18
HAdV_o_dp2_141_t39_2	GGGTTAAGGGGACTGCCCATGGCATGGGATGGGTGAGTGCAGAGGCATACATGCC	56
HAdV_o_dp2_141_t39_3	CAGTCCCCTTAACCCATATGAGCGCGCACTGGCAGCTCGAGAATGCCAAATGGCCT	56
HAdV_o_dp2_141_t39_4	TAAATCCTTATCAAAATAGCTGATGGGAGTGGGGTCATCTAAGGCCATTTGCCATT	56
HAdV_o_dp2_141_t39_5	AGCTATTTTGATAAGGATTTACTTCCGGGAATCTTACCATGGATGCAGACCCCTCCGA	59
HAdV_o_dp2_141_t39_6	TCGGGAGGGTCTGCA	15
HAdV_o_dp2_141_t40_1	GTGGCATGTATGCCTCC	17
HAdV_o_dp2_141_t40_2	GGTTAAGAGGGGTGCCCCAGGGCATGGGGTGGGTGAGCGGGAGGCATACATGCCA	56
HAdV_o_dp2_141_t40_3	GCACCCTCTTAACCCCTATGAGCGCGCGCTGGCAGTTCGAGAATGGCAGATGACCTT	58
HAdV_o_dp2_141_t40_4	AGCAAATCTTTGTCAAAATAGCTGATGGTGGCGGGATCATCCAAGGTCATCTGCCATTC	59
HAdV_o_dp2_141_t40_5	TATTTTGACAAAGATTTGCTACCGGAATATTTACCATAGATGCCGACCCCCCTGA	56
HAdV_o_dp2_141_t40_6	TCAGGGGGGTCCGCA	15
HAdV_o_dp2_141_t41_1	GCGGCATGTACGCCTC	16
HAdV_o_dp2_141_t41_2	GGTTGAGTGGGGGACCCCATGGCATGGGGTGGGTGAGCGGGAGGCGTACATGCCG	56
HAdV_o_dp2_141_t41_3	GTCCCCACTCAACCCATACGAGCGCGCGCTGCCGCCGCGCATGGCAGCAGGCG	56
HAdV_o_dp2_141_t41_4	CGCGCGTCAAGTAGTCTATCTTGCATCCTTGCAAGTCTAGCGCTGCTGCCATGC	56
HAdV_o_dp2_141_t41_5	CTACTTCGACGCGCGCTGCTGCCGGGGTCTTTACCGTGGACGAGACCCCCCGGA	57
HAdV_o_dp2_141_t41_6	TCCGGGGGGTCTGCG	15
HAdV_o_dp2_141_t42_1	GCGGCATGTACGCCTC	16
HAdV_o_dp2_141_t42_2	GGTTGAGGGGCGGACCCAGGGCATGGGATGAGTGAAGGGCGGAGGCGTACATGCCG	56
HAdV_o_dp2_141_t42_3	GTCCGCCCTCAACCCCTACGAGCGAGCGCTGGCCGCCGCGAGTGGCAGATGGCC	56
HAdV_o_dp2_141_t42_4	GTTCTTGTCAAAATAATCGATTTTGGAGGATGCATCATCAAGGCCATCTGCCACTC	58
HAdV_o_dp2_141_t42_5	GATTATTTTGACAAGGAACTCTGTCCGGGCATCTTACCATCGATGCCGACCCCCCTGA	59
HAdV_o_dp2_141_t42_6	TCAGGGGGGTCCGCA	15
HAdV_o_dp2_141_t43_1	GCGGCATGTACGCCTC	16
HAdV_o_dp2_141_t43_2	GACTAAGGGGCGTGCCCCAGGGCATGGGGTGGGTGAGCGGGAGGCGTACATGCCG	56
HAdV_o_dp2_141_t43_3	GCACGCCCTTAGTCCCACGAGCGCGCGCTGGCCGTGCGGCAATGGCAAGCTTCT	56
HAdV_o_dp2_141_t43_4	TCGGGGTCAAGTAGCTTATGCAGGTGCCAGATCGTCCAGAGAAGCTTGCCATTC	56
HAdV_o_dp2_141_t43_5	CTACTTCGACCCGACCTCCTGCCAGGCATCTTACCATCGATGCTGACCCCCCGGA	57
HAdV_o_dp2_141_t43_6	TCGGGGGGGTACGCA	15
HAdV_o_dp2_141_t44_1	GTGGCATGTACGCCTC	16
HAdV_o_dp2_141_t44_2	GATTGAGTGGGAAGCCCCACGGCATGGGATGGGTAAGTGCAGAGGCGTACATGCCA	56
HAdV_o_dp2_141_t44_3	GCTTCCCCTCAATCCCTACGAGCGCGCCCTAGCGGTCCGAGATTGGGAACACGCTC	57
HAdV_o_dp2_141_t44_4	CAGGGTGCAGATTGAAATAATCAATGGGGGTACCAACTTGCAAAAGAGCGTGTCCCAAT	59
HAdV_o_dp2_141_t44_5	TTCAATCGCACCTGCTGCCTGGCATTTTTACCATCGACGCGGACCCCCACC	53
HAdV_o_dp2_141_t44_6	GGTGGGGGGTCCGCG	15



図 1 CoCoMo における PCR 位置モチーフ選定アルゴリズムの流れ図

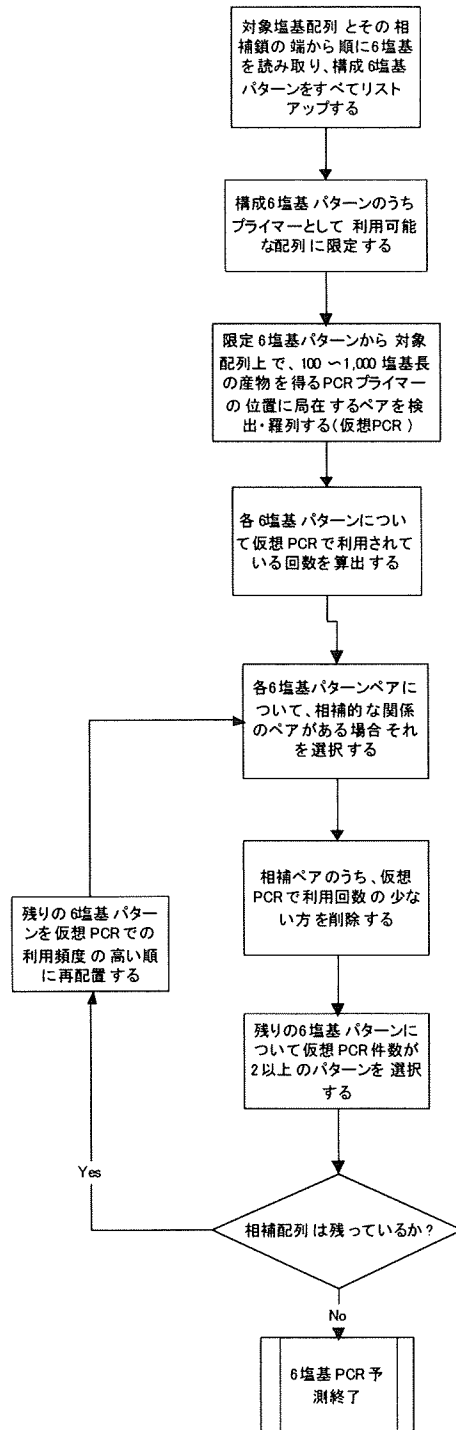


図 2 CoCoMo プログラムの模式図

A: 対象配列の整列

A 株	ATGGCGGCCGTATGTGCC
B 株	ATGGGGCGTATGAGCC
C 株	ACCGCGGCTGTGCG
↓	
A 株	ATGGCGGCCGTATGAGCC
B 株	ATGGC-GCCGTATGACCC
C 株	ATCGCGG-C---TGAGCG

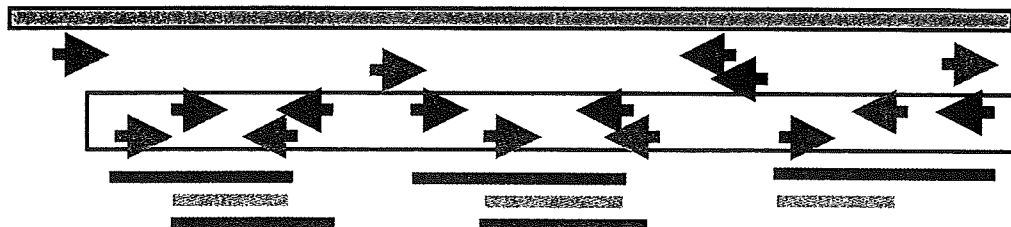
B: ギャップ motif 検索の概念図

A	株
GCCAGATGGCGGCCGTATGAGCGAATGCG	
B	株
ギャップ motif ATYGC                      GASC	

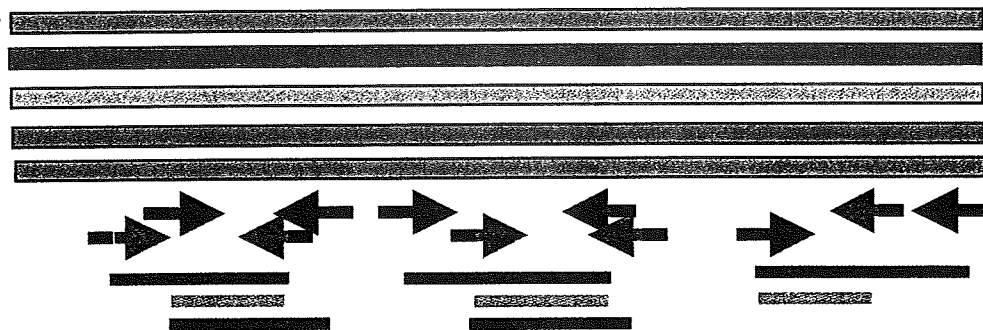
C: motif flanking 配列の抽出と degenerate 配列の決定

A	株
GCCAGATGGCGGCCGTATGAGCGAATGCG	
B	株
CCGGGATGGC-GCCGTATGACCGATACCC	
C	株
GCCAG	AATGCC
CGGGG	ATACCC
SSSRGATYGC	
GASCGAWWCS	

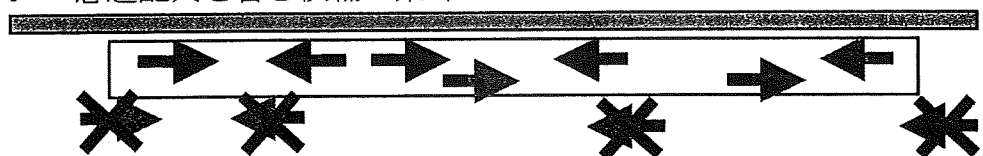
D: プライマー候補 1 の仮想 PCR



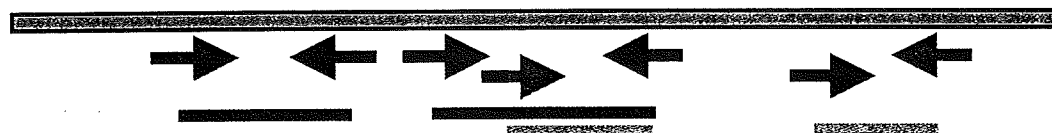
E: プライマー候補1の伸長



F: 忌避配列を含む候補の棄却



G: プライマー候補2による仮想PCR



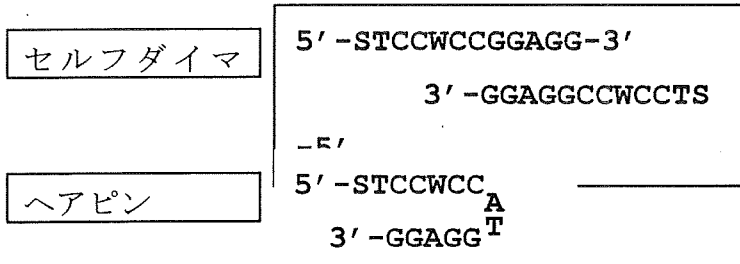
H: プライマー候補2の塩基長の調整

GSSSSTCCWGCCAGG

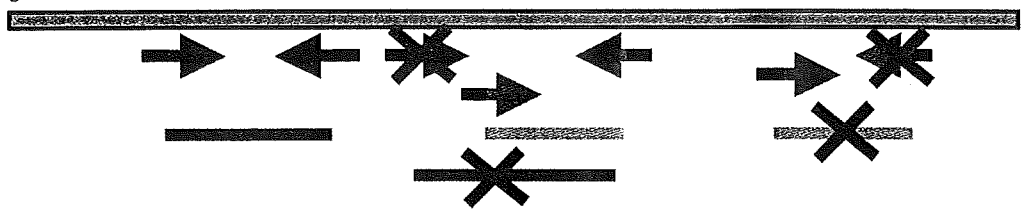
→ STCCWGCCAGG

ATACWWTWSCWWWAT

I: プライマー候補 3 の評価



J: プライマー候補 3 の評価



K: プライマーペア候補 2 の評価

