

Appendix A: Results of MS32 (Locus D1S8) typing

Sex	EP No.	Race	Allele	Dimp1	HF	Dimp2	1/1	1/2
1	1127	F	1	G	+	C	0	0
			2	G	+	F	0	0
2	1128	F	1	C	+	C	0	0
			2	C	+	G	0	0
3	1129	M	1	C	+	C	0	0
			2	C	-	F	0	0
4	1131	F	1	G	+	C	0	0
			2	C	+	C	0	0
5	1133	M	1	G	+	C	0	0
			2	C	+	F	0	0
6	1137	C	1	G	+	G	0	0
			2	C	+	C	0	0
7	1138	M	1	G	+	C	0	0
			2	G	-	C	0	0
8	1140	C	1	G	+	C	0	0
			2	G	+	F	0	0
9	1142	F	1	G	+	C	0	0
			2	G	-	F	0	0
10	1143	F	1	G	+	C	0	0
			2	C	+	C	0	0
11	1129	F	1	G	+	G	0	0
			2	C	+	F	0	0
12	1144	F	1	G	+	C	0	0
			2	G	+	C	0	0
13	1121	M	1	G	+	C	0	0
			2	G	-	F	0	0
14	1127	C	1	G	+	C	0	0
			2	G	+	F	0	0
15	1135	C	1	G	+	C	0	0
			2	G	+	C	0	0
16	1161	C	1	G	+	C	0	0
			2	C	+	C	0	0
17	1142	M	1	C	+	C	0	0
			2	G	-	F	0	0
18	1147	C	1	G	+	C	0	0
			2	C	+	F	0	0
19	1124	C	1	G	-	C	0	0
			2	G	-	F	0	0
20	1144	M	1	G	-	F	0	0
			2	G	-	F	0	0

Appendixes

Appendix A: Results of MS32 (Locus D1S8) typing

No.	UH No.	Race	Allele	Hump1	Hfl	Hump2	O1	O2
1	1120	I	1	G	+	C	G	G
			2	G	-	T	G	G
2	1130	I	1	C	+	C	G	G
			2	C	+	C	G	G
3	1110	M	1	C	+	C	G	G
			2	C	+	C	G	G
4	1111	I	1	G	+	C	G	G
			2	C	+	C	G	G
5	1113	M	1	G	+	C	G	G
			2	C	+	T	G	G
6	1117	C	1	G	+	C	G	G
			2	C	+	C	G	G
7	1131	M	1	G	+	C	G	G
			2	G	-	C	G	G
8	1146	C	1	G	+	C	G	G
			2	G	+	T	G	G
9	1112	I	1	G	+	C	G	G
			2	G	-	T	G	G
10	1115	M	1	G	+	C	G	G
			2	G	+	C	G	G
11	1129	I	1	G	+	C	G	G
			2	C	+	C	G	G
12	1144	I	1	G	+	C	G	G
			2	G	+	C	G	G
13	1123	M	1	G	+	C	G	G
			2	G	-	T	G	G
14	1127	C	1	G	+	C	G	G
			2	G	-	T	G	G
15	1135	C	1	G	+	C	G	G
			2	G	+	C	G	G
16	1162	C	1	G	+	C	G	G
			2	C	+	C	G	G
17	1142	M	1	C	+	C	G	G
			2	G	-	T	G	G
18	1167	C	1	G	+	C	G	G
			2	C	+	C	G	G
19	1114	C	1	G	-	C	G	G
			2	G	-	T	G	G
20	1134	M	1	G	-	T	G	G
			2	G	-	T	G	G

Appendix A : Results of MS32 (Locus D1S8) typing

No.	UH No.	Race	Allele	Hump1	Hfl	Hump2	O1	O2
21	1139	I	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
22	1138	I	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>G</i>	+	<i>C</i>	G	G
23	1116	C	1	<i>G</i>	+	<i>T</i>	G	G
			2	<i>G</i>	-	<i>C</i>	G	G
24	1119	C	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>G</i>	+	<i>C</i>	G	G
25	1136	C	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
26	1141	I	1	<i>C</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
27	1160	C	1	<i>C</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
28	1166	C	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>G</i>	+	<i>C</i>	G	G
29	1122	C	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>G</i>	+	<i>C</i>	G	G
30	1125	I	1	<i>G</i>	+	<i>T</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
31	1133	C	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>G</i>	-	<i>C</i>	G	G
32	1145	C	1	<i>G</i>	+	<i>T</i>	G	G
			2	<i>G</i>	-	<i>C</i>	G	G
33	1154	C	1	<i>C</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
34	1164	I	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>G</i>	+	<i>C</i>	G	G
35	1121	M	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>G</i>	+	<i>T</i>	G	G
36	1147	M	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
37	1151	M	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>G</i>	-	<i>C</i>	G	G
38	1153	C	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
39	1155	C	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>G</i>	-	<i>T</i>	G	G
40	1170	C	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>G</i>	+	<i>C</i>	G	G

Appendix A : Results of MS32 (Locus D1S8) typing

No.	UH No.	Race	Allele	Hump1	HFI	Hump2	O1	O2
41	1128	M	1	G	+	C	G	G
			2	G	-	T	G	G
42	1140	C	1	G	+	C	G	G
			2	G	-	T	G	G
43	1143	C	1	G	+	C	G	G
			2	G	+	C	G	G
44	1148	C	1	G	+	C	G	G
			2	C	+	C	G	G
45	1150	C	1	G	+	C	G	G
			2	G	+	C	G	G
46	1168	I	1	G	+	C	G	G
			2	G	-	T	G	G
47	1118	C	1	G	+	C	G	G
			2	C	+	C	G	G
48	1124	C	1	C	+	C	G	G
			2	G	-	C	G	G
49	1126	M	1	G	+	C	G	G
			2	C	+	C	G	G
50	1157	C	1	G	+	C	G	G
			2	G	+	T	G	G
51	1161	C	1	G	+	C	G	G
			2	G	+	T	G	G
52	1165	I	1	C	+	C	G	G
			2	G	-	C	G	G
53	1132	C	1	G	+	C	G	G
			2	G	-	C	G	G
54	1137	I	1	G	+	C	G	G
			2	G	+	C	G	G
55	1149	M	1	G	+	C	G	G
			2	G	+	C	G	G
56	1156	C	1	C	+	C	G	G
			2	C	+	C	G	G
57	1158	C	1	G	+	C	G	G
			2	G	-	T	G	G
58	1159	C	1	G	+	C	G	G
			2	C	+	C	G	G
59	1163	M	1	G	+	C	G	G
			2	G	+	T	G	G
60	1169	I	1	G	+	C	G	G
			2	C	+	C	G	G

Appendix A : Results of MS32 (Locus DIS8) typing

No.	UH No.	Race	Allele	Hump1	HPI	Hump2	O1	O2
61	1234	I	1	C	+	C	G	G
			2	C	+	T	G	G
62	1247	C	1	G	+	C	G	G
			2	C	+	C	G	G
63	1264	I	1	C	+	C	G	G
			2	G	-	T	G	G
64	1267	M	1	G	+	C	G	G
			2	G	-	C	G	G
65	1268	M	1	G	+	C	G	G
			2	G	+	C	G	G
66	1276	M	1	G	+	T	G	G
			2	C	+	C	G	G
67	1281	C	1	G	-	C	G	G
			2	G	-	T	G	G
68	1282	C	1	G	+	C	G	G
			2	C	+	C	G	G
69	1283	I	1	G	+	C	G	G
			2	G	-	T	G	G
70	1286	C	1	G	+	C	G	G
			2	G	-	T	G	G
71	1287	C	1	C	+	C	G	G
			2	C	+	C	G	G
72	1288	M	1	G	+	C	G	G
			2	C	+	C	G	G
73	1222	C	1	G	+	C	G	G
			2	G	-	C	G	G
74	1223	I	1	G	+	C	G	G
			2	G	-	C	G	G
75	1225	M	1	C	+	C	G	G
			2	G	-	T	G	G
76	1237	C	1	G	+	C	G	G
			2	C	+	C	G	G
77	1238	C	1	G	+	C	G	G
			2	C	+	C	G	G
78	1239	I	1	G	+	C	G	G
			2	C	+	C	G	G
79	1243	M	1	G	+	C	G	G
			2	C	+	C	G	G
80	1250	I	1	G	+	C	G	G
			2	G	-	T	G	G

Appendix A : Results of MS32 (Locus D1S8) typing

No.	UH No.	Race	Allele	Hump1	Hfl	Hump2	O1	O2
81	1251	I	1	G	+	<i>T</i>	G	G
			2	G	-	<i>C</i>	G	G
82	1269	M	1	G	+	<i>C</i>	G	G
			2	G	+	<i>C</i>	G	G
83	1278	C	1	G	+	<i>C</i>	G	G
			2	G	+	<i>C</i>	G	G
84	1279	C	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
85	1236	C	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
86	1254	C	1	G	+	<i>C</i>	G	G
			2	G	-	<i>T</i>	G	G
87	1261	I	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>T</i>	G	G
88	1262	C	1	<i>C</i>	+	<i>C</i>	G	G
			2	<i>G</i>	-	<i>T</i>	G	G
89	1265	C	1	G	+	<i>C</i>	G	G
			2	G	+	<i>C</i>	G	G
90	1277	C	1	G	-	<i>C</i>	G	G
			2	G	-	<i>C</i>	G	G
91	1224	M	1	G	+	<i>C</i>	G	G
			2	G	-	<i>T</i>	G	G
92	1226	C	1	G	+	<i>C</i>	G	G
			2	G	-	<i>C</i>	G	G
93	1227	C	1	G	+	<i>C</i>	G	G
			2	G	+	<i>C</i>	G	G
94	1245	M	1	<i>C</i>	+	<i>C</i>	G	G
			2	<i>G</i>	-	<i>C</i>	G	G
95	1255	C	1	G	+	<i>C</i>	G	G
			2	G	+	<i>C</i>	G	G
96	1256	C	1	G	+	<i>C</i>	G	G
			2	G	+	<i>C</i>	G	G
97	1257	C	1	G	+	<i>C</i>	G	G
			2	G	+	<i>T</i>	G	G
98	1258	C	1	G	+	<i>C</i>	G	G
			2	G	+	<i>C</i>	G	G
99	1270	M	1	G	+	<i>C</i>	G	G
			2	G	+	<i>C</i>	G	G
100	1271	M	1	G	-	<i>C</i>	G	G
			2	G	-	<i>T</i>	G	G

Appendix A : Results of MS32 (Locus D1S8) typing

No.	UH No.	Race	Allele	Hump1	Hfl	Hump2	O1	O2
101	1274	C	1	G	+	C	G	G
			2	G	-	C	G	G
102	1280	C	1	<i>G</i>	+	<i>T</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
103	1229	I	1	G	+	<i>T</i>	G	G
			2	G	-	<i>C</i>	G	G
104	1235	C	1	G	+	C	G	G
			2	G	+	C	G	G
105	1240	C	1	G	-	<i>C</i>	G	G
			2	<i>G</i>	-	<i>T</i>	G	G
106	1242	I	1	G	-	C	G	G
			2	G	-	C	G	G
107	1244	M	1	G	+	C	G	G
			2	G	+	C	G	G
108	1249	C	1	C	+	C	G	G
			2	C	+	C	G	G
109	1260	I	1	G	-	T	G	G
			2	G	-	T	G	G
110	1263	C	1	G	+	C	G	G
			2	G	+	C	G	G
111	1266	M	1	G	+	C	G	G
			2	G	+	C	G	G
112	1275	C	1	<i>G</i>	+	<i>T</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
113	1285	C	1	G	+	C	G	G
			2	G	+	C	G	G
114	1290	C	1	G	+	C	G	G
			2	G	-	C	G	G
115	1228	M	1	G	+	C	G	G
			2	G	+	C	G	G
116	1230	I	1	G	+	<i>T</i>	G	G
			2	G	-	<i>C</i>	G	G
117	1231	I	1	G	+	C	G	G
			2	G	-	C	G	G
118	1241	M	1	G	+	T	G	G
			2	G	-	T	G	G
119	1362	I	1	<i>C</i>	+	<i>C</i>	G	G
			2	<i>G</i>	-	<i>T</i>	G	G
120	1284	C	1	<i>C</i>	+	C	G	G
			2	<i>G</i>	-	C	G	G

Appendix A : Results of MS32 (Locus D1S8) typing

No.	UH No.	Race	Allele	Hump1	Hfl	Hump2	O1	O2
121	1329	I	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>T</i>	G	G
122	1339	C	1	G	+	C	G	G
			2	G	+	C	G	G
123	1340	C	1	G	-	<i>C</i>	G	G
			2	G	-	<i>T</i>	G	G
124	1345	M	1	G	+	C	G	G
			2	G	+	C	G	G
125	1346	M	1	G	-	<i>C</i>	G	G
			2	G	-	<i>T</i>	G	G
126	1375	I	1	<i>G</i>	+	C	G	G
			2	<i>C</i>	+	C	G	G
127	1298	I	1	G	+	C	G	G
			2	G	+	C	G	G
128	1302	M	1	C	+	C	G	G
			2	C	+	C	G	G
129	1317	I	1	G	+	C	G	G
			2	G	+	C	G	G
130	1318	I	1	G	+	C	G	G
			2	G	+	C	G	G
131	1319	M	1	<i>G</i>	+	<i>T</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
132	1327	M	1	G	+	C	G	G
			2	G	+	C	G	G
133	1332	I	1	<i>G</i>	+	C	G	G
			2	<i>C</i>	+	C	G	G
134	1342	M	1	<i>G</i>	+	C	G	G
			2	<i>C</i>	+	C	G	G
135	1369	I	1	G	+	C	G	G
			2	G	+	C	G	G
136	1370	I	1	<i>G</i>	+	<i>T</i>	G	G
			2	<i>C</i>	+	<i>T</i>	G	G
137	1372	I	1	G	+	<i>C</i>	G	G
			2	G	-	<i>T</i>	G	G
138	1385	I	1	G	+	C	G	G
			2	G	+	C	G	G
139	405	I	1	G	+	C	G	G
			2	G	-	C	G	G
140	410	M	1	G	+	C	G	G
			2	G	+	C	G	G

Appendix A : Results of MS32 (Locus D1S8) typing

No.	UH No.	Race	Allele	Hump1	Hfl	Hump2	O1	O2
141	1306	M	1	G	+	C	G	G
			2	G	-	C	G	G
142	1309	I	1	G	+	C	G	G
			2	C	+	C	G	G
143	1316	I	1	G	+	C	G	G
			2	G	+	C	G	G
144	1349	M	1	C	+	T	G	G
			2	G	-	C	G	G
145	1354	M	1	G	+	C	G	G
			2	G	+	C	G	G
146	1356	M	1	G	+	C	G	G
			2	G	-	T	G	G
147	1367	I	1	G	+	C	G	G
			2	G	-	C	G	G
148	1374	I	1	G	+	C	G	G
			2	C	+	C	G	G
149	1376	I	1	G	+	C	G	G
			2	C	+	C	G	G
150	1378	I	1	G	+	C	G	G
			2	C	+	C	G	G
151	1391	I	1	G	+	C	G	G
			2	G	-	C	G	G
152	1396	I	1	G	+	C	G	G
			2	G	+	C	G	G
153	1295	M	1	G	+	C	G	G
			2	G	+	C	G	G
154	1301	M	1	G	+	C	G	G
			2	G	-	C	G	G
155	1308	M	1	G	-	C	G	G
			2	G	-	T	G	G
156	1328	M	1	G	+	C	G	G
			2	G	+	C	G	G
157	1341	I	1	G	+	C	G	G
			2	G	-	T	G	G
158	1343	M	1	G	+	C	G	G
			2	C	+	C	G	G
159	1352	M	1	G	+	C	G	G
			2	C	+	C	G	G
160	1360	I	1	G	+	T	G	G
			2	C	+	T	G	G

Appendix A : Results of MS32 (Locus D1S8) typing

No.	UH No.	Race	Allele	Hump1	HPI	Hump2	O1	O2
161	1363	I	1	G	+	C	G	G
			2	G	-	C	G	G
162	1371	I	1	G	+	C	G	G
			2	G	+	C	G	G
163	1379	I	1	G	+	C	G	G
			2	G	+	C	G	G
164	1389	I	1	G	+	C	G	G
			2	G	-	T	G	G
165	1292	M	1	G	+	C	G	G
			2	G	+	T	G	G
166	1297	M	1	C	+	C	G	G
			2	C	+	T	G	G
167	1312	I	1	G	+	C	G	G
			2	G	+	C	G	G
168	1313	I	1	C	+	T	G	G
			2	C	+	T	G	G
169	1364	I	1	G	+	C	G	G
			2	G	-	C	G	G
170	1384	I	1	G	+	C	G	G
			2	G	+	C	G	G
171	1386	I	1	G	+	C	G	G
			2	G	-	C	G	G
172	1387	M	1	G	+	C	G	G
			2	G	+	C	G	G
173	1390	I	1	G	+	T	G	G
			2	G	-	C	G	G
174	1393	I	1	C	+	C	G	G
			2	C	+	T	G	G
175	1394	I	1	G	+	C	G	G
			2	C	+	C	G	G
176	1395	I	1	G	+	C	G	G
			2	G	+	C	G	G
177	1057	M	1	G	+	C	G	G
			2	G	-	C	G	G
178	1071	M	1	G	-	C	G	G
			2	G	-	T	G	G
179	1072	M	1	G	+	C	G	G
			2	G	+	T	G	G
180	1073	M	1	G	+	C	G	G
			2	C	+	C	G	G

Appendix A : Results of MS32 (Locus D1S8) typing

No.	UH No.	Race	Allele	Hump1	Hfl	Hump2	O1	O2
181	1075	M	1	G	+	C	G	G
			2	G	-	T	G	G
182	1076	M	1	G	+	T	G	G
			2	C	+	C	G	G
183	1077	M	1	G	+	C	G	G
			2	G	-	T	G	G
184	1084	M	1	G	+	C	G	G
			2	G	-	T	G	G
185	1095	M	1	C	+	C	G	G
			2	G	-	T	G	G
186	1098	M	1	G	+	C	G	G
			2	G	+	C	G	G
187	1102	M	1	G	+	C	G	G
			2	C	+	C	G	G
188	1105	M	1	G	+	C	G	G
			2	G	-	C	G	G
189	1296	M	1	G	+	C	G	G
			2	G	+	C	G	G
190	1355	M	1	C	+	C	G	G
			2	G	-	T	G	G
191	1015	I	1	G	+	C	G	G
			2	G	+	T	G	G
192	1023	I	1	C	+	C	G	G
			2	C	+	C	G	G
193	1028	M	1	G	+	C	G	G
			2	G	+	C	G	G
194	1035	M	1	G	+	C	G	G
			2	G	+	C	G	G
195	1039	I	1	G	+	C	G	G
			2	G	+	T	G	G
196	1040	I	1	G	+	C	G	G
			2	G	-	C	G	G
197	1041	I	1	C	+	C	G	G
			2	G	-	T	G	G
198	1049	M	1	G	+	T	G	G
			2	G	-	T	G	G
199	1065	M	1	G	+	C	G	G
			2	G	+	C	G	G
200	1074	M	1	G	+	C	G	G
			2	G	+	C	G	G

Appendix A : Results of MS32 (Locus D1S8) typing

No.	UH No.	Race	Allele	Hump1	HП	Hump2	O1	O2
201	1085	M	1	G	+	C	G	G
			2	G	-	C	G	G
202	1087	I	1	G	+	T	G	G
			2	G	-	T	G	G
203	1094	I	1	G	+	C	G	G
			2	C	+	C	G	G
204	1096	M	1	G	+	C	G	G
			2	G	+	C	G	G
205	541	C	1	G	+	C	G	G
			2	G	+	T	G	G
206	556	C	1	C	+	C	G	G
			2	G	-	C	G	G
207	561	C	1	G	+	C	G	G
			2	G	+	T	G	G
208	562	C	1	G	+	C	G	G
			2	G	-	C	G	G
209	592	C	1	C	+	C	G	G
			2	G	-	C	G	G
210	593	C	1	G	+	C	G	G
			2	G	+	T	G	G

Note :

C : Chinese

I : Indian

M : Malay

UH : University Hospital

Appendix B: Methods of calculation for polymorphic site assays

The calculations of the data of MS32 *Hinf*I assay in the Malaysia Chinese population as an example are illustrated as below:

(i) χ^2 test

- (a) Null hypothesis: The numbers observed for the genotypes in the MS32 *Hinf*I site are according to the Hardy-Weinberg equilibrium.
- (b) Alternative hypothesis: The numbers observed for the genotypes in the MS32 *Hinf*I site are not according to the Hardy-Weinberg equilibrium.
- (c) Level of significance: $\alpha = 0.05$
- (d) Criterion: Reject the null hypothesis if $\chi^2 > 3.841$, the value of $\chi^2_{0.05}$ for 1 degree of freedom, which

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$

or otherwise accept it.

(e) Expected numbers:

$$\begin{aligned} \text{For } +/+ (C/C), E &= p^2 \times 70 \\ &= (0.786)^2 \times 70 \\ &= 43.246 \\ \text{For } +/- (C/T), E &= 2pq \times 70 \\ &= 2 \times (0.786) \times (0.214) \times 70 \\ &= 23.549 \\ \text{For } -/- (T/T), E &= q^2 \times 70 \\ &= (0.214)^2 \times 70 \\ &= 3.206 \end{aligned}$$

(f) Calculation:

$$\begin{aligned} \chi^2 &= \sum \frac{(O-E)^2}{E} \\ &= 0.701 + 0.535 + 1.004 \\ &= 1.610 \end{aligned}$$

- (g) Decision: Since $\chi^2 = 1.610$ does not exceed 3.841, the null hypothesis is accepted.

(ii) **Power of discrimination (Pd)**

$$\begin{aligned} Pd &= 1 - \Sigma f^2 \\ &= 1 - (0.500) \\ &= 0.500 \end{aligned}$$

(iii) Heterozygosity (h)

$$\begin{aligned}h &= [1 - (p^2 + q^2)] \times [n/(n-1)] \\&= [1 - \{(0.786)^2 + (0.214)^2\}] \times 1.007 \\&= 0.339\end{aligned}$$

Appendix C: (i) Results of *Hinf*I-Hump1 assay

No.	UH No.	Race	Allele	Hump1	HfI	Hump2	O1	O2
1	1142	M	1	C	+	C	G	G
			2	G	-	T	G	G
2	1124	C	1	C	+	C	G	G
			2	G	-	C	G	G
3	1165	I	1	C	+	C	G	G
			2	G	-	C	G	G
4	1264	I	1	C	+	C	G	G
			2	G	-	T	G	G
5	1225	M	1	C	+	C	G	G
			2	G	-	T	G	G
6	1262	C	1	C	+	C	G	G
			2	G	-	T	G	G
7	1245	M	1	C	+	C	G	G
			2	G	-	C	G	G
8	1362	I	1	C	+	C	G	G
			2	G	-	T	G	G
9	1284	C	1	C	+	C	G	G
			2	G	-	C	G	G
10	1349	M	1	C	+	T	G	G
			2	G	-	C	G	G
11	1095	M	1	C	+	C	G	G
			2	G	-	T	G	G
12	1355	M	1	C	+	C	G	G
			2	G	-	T	G	G
13	1041	I	1	C	+	C	G	G
			2	G	-	T	G	G
14	556	C	1	C	+	C	G	G
			2	G	-	C	G	G
15	592	C	1	C	+	C	G	G
			2	G	-	C	G	G

Appendix C: (ii) Results of *Hinf*I-Hump2 assay

No.	UH No.	Race	Allele	Hump1	HfI	Hump2	O1	O2
1	1120	I	1	G	+	C	G	G
			2	G	-	T	G	G
2	1112	I	1	G	+	C	G	G
			2	G	-	T	G	G
3	1123	M	1	G	+	C	G	G
			2	G	-	T	G	G

No.	UH No.	Race	Allele	Hump1	HП	Hump2	O1	O2
4	1127	C	1	G	+	C	G	G
			2	G	-	T	G	G
5	1142	M	1	C	+	C	G	G
			2	G	-	T	G	G
6	1116	C	1	G	+	T	G	G
			2	G	-	C	G	G
7	1145	C	1	G	+	T	G	G
			2	G	-	C	G	G
8	1155	C	1	G	+	C	G	G
			2	G	-	T	G	G
9	1128	M	-1	G	+	C	G	G
			2	G	-	T	G	G
10	1140	C	1	G	+	C	G	G
			2	G	-	T	G	G
11	1168	I	1	G	+	C	G	G
			2	G	-	T	G	G
12	1158	C	1	G	+	C	G	G
			2	G	-	T	G	G
13	1264	I	1	C	+	C	G	G
			2	G	-	T	G	G
14	1283	I	1	G	+	C	G	G
			2	G	-	T	G	G
15	1286	C	1	G	+	C	G	G
			2	G	-	T	G	G
16	1225	M	1	C	+	C	G	G
			2	G	-	T	G	G
17	1250	I	1	G	+	C	G	G
			2	G	-	T	G	G
18	1251	I	1	G	+	T	G	G
			2	G	-	C	G	G
19	1254	C	1	G	+	C	G	G
			2	G	-	T	G	G
20	1262	C	1	C	+	C	G	G
			2	G	-	T	G	G
21	1224	M	1	G	+	C	G	G
			2	G	-	T	G	G
22	1229	I	1	G	+	T	G	G
			2	G	-	C	G	G
23	1230	I	1	G	+	T	G	G
			2	G	-	C	G	G

No.	UH No.	Race	Allele	Hump1	Hfl	Hump2	O1	O2
24	1362	I	1	C	+	C	G	G
			2	G	-	T	G	G
25	1372	I	1	G	+	C	G	G
			2	G	-	T	G	G
26	1349	M	1	C	+	T	G	G
			2	G	-	C	G	G
27	1356	M	1	G	+	C	G	G
			2	G	-	T	G	G
28	1341	I	1	G	+	C	G	G
			2	G	-	T	G	G
29	1389	I	1	G	+	C	G	G
			2	G	-	T	G	G
30	1390	I	1	G	+	T	G	G
			2	G	-	C	G	G
31	1075	M	1	G	+	C	G	G
			2	G	-	T	G	G
32	1077	M	1	G	+	C	G	G
			2	G	-	T	G	G
33	1084	M	1	G	+	C	G	G
			2	G	-	T	G	G
34	1095	M	1	C	+	C	G	G
			2	G	-	T	G	G
35	1355	M	1	C	+	C	G	G
			2	G	-	T	G	G
36	1041	I	1	C	+	C	G	G
			2	G	-	T	G	G

Appendix C: (iii) Results of Hump1-Hump2 assay

No.	UH No.	Race	Allele	Hump1	Hfl	Hump2	O1	O2
1	1113	M	1	G	+	C	G	G
			2	C	+	T	G	G
2	1142	M	1	C	+	C	G	G
			2	G	-	T	G	G
3	1125	I	1	G	+	T	G	G
			2	C	+	C	G	G
4	1264	I	1	C	+	C	G	G
			2	G	-	T	G	G
5	1276	M	1	G	+	T	G	G
			2	C	+	C	G	G
6	1225	M	1	C	+	C	G	G
			2	G	-	T	G	G

No.	UH No.	Race	Allele	Hump1	Hfl	Hump2	O1	O2
7	1261	I	1	<i>G</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>T</i>	G	G
8	1262	C	1	<i>C</i>	+	<i>C</i>	G	G
			2	<i>G</i>	-	<i>T</i>	G	G
9	1280	C	1	<i>G</i>	+	<i>T</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
10	1275	C	1	<i>G</i>	+	<i>T</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
11	1362	I	1	<i>C</i>	+	<i>C</i>	G	G
			2	<i>G</i>	-	<i>T</i>	G	G
12	1329	I	1*	<i>G</i>	+	<i>C</i>	G	G
			2	<i>C</i>	+	<i>T</i>	G	G
13	1319	M	1	<i>G</i>	+	<i>T</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
14	1349	M	1	<i>C</i>	+	<i>T</i>	G	G
			2	<i>G</i>	-	<i>C</i>	G	G
15	1076	M	1	<i>G</i>	+	<i>T</i>	G	G
			2	<i>C</i>	+	<i>C</i>	G	G
16	1095	M	1	<i>C</i>	+	<i>C</i>	G	G
			2	<i>G</i>	-	<i>T</i>	G	G
17	1355	M	1	<i>C</i>	+	<i>C</i>	G	G
			2	<i>G</i>	-	<i>T</i>	G	G
18	1041	I	1	<i>C</i>	+	<i>C</i>	G	G
			2	<i>G</i>	-	<i>T</i>	G	G

Note :

C : Chinese

I : Indian

M : Malay

UH : University Hospital

Appendix D: Method of calculation for haplotype assays

The calculation of the Malaysian haplotypes as an example is illustrated as below:

(i) χ^2 test

- (a) Null hypothesis: All the three polymorphic sites (Hump1, *Hinf*I, and Hump2) are not associated together.
- (b) Alternative hypothesis: All the three polymorphic sites (Hump1, *Hinf*I, and Hump2) are associated together.
- (c) Level of significance: $\alpha = 0.05$
- (d) Criterion: Reject the null hypothesis if $\chi^2 > 14.067$, the value of $\chi^2_{0.05}$ for 7 degree of freedom, which

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$

or otherwise accept it.

(e) Expected number:

e.g. : in C - T,

$$\begin{aligned} \text{the expected number } E &= (0.214) \times (0.221) \times (0.202) \times 420 \\ &= 4.012 \end{aligned}$$

(f) Calculation:

$$\begin{aligned} \chi^2 &= \sum \frac{(O-E)^2}{E} \\ &= 98.989 \end{aligned}$$

- (g) Decision: Since $\chi^2 = 98.989$ exceeds 14.067, the null hypothesis is rejected.

Appendix E: Method of calculation for each pair of polymorphic sites

The calculation of the data of *Hinf*I-Hump1 polymorphic sites as an example is illustrated as below:

(i) χ^2 test

(a) Null hypothesis: Association is not existed in *Hinf*I-Hump1 polymorphic sites.

(b) Alternative hypothesis: Association is existed in *Hinf*I-Hump1 polymorphic sites.

(c) Level of significance: $\alpha = 0.05$

(d) Criterion: Reject the null hypothesis if $\chi^2 > 3.841$, the value of $\chi^2_{0.05}$ for 1 degree of freedom, which

$$\chi^2 = (f-F)^2 \Sigma (1/F)$$

or otherwise accept it.

(e) Expected number:

e.g. : in G/+,

$$\begin{aligned} \text{the expected number } F &= (327)(330)/420 \\ &= 256.93 \end{aligned}$$

(f) Calculation:

$$\begin{aligned} \chi^2 &= (f-F)^2 \Sigma (1/F) \\ &= (397.2049) (1/256.93 + 1/73.07 + 1/70.07 + 1/19.93) \\ &= 32.58 \end{aligned}$$

(g) Decision: Since $\chi^2 = 32.58$ exceeds 3.841, the null hypothesis is rejected.

Appendix F: Samples for DNA sequencing

Sample	Race	Number of heterozygous polymorphic sites
UH 1041	I	3 (Hump1, <i>Hinf</i> I, and Hump2)
UH 1355	M	3 (Hump1, <i>Hinf</i> I, and Hump2)
UH 1262	C	3 (Hump1, <i>Hinf</i> I, and Hump2)
UH 1095	M	3 (Hump1, <i>Hinf</i> I, and Hump2)
UH 1362	I	3 (Hump1, <i>Hinf</i> I, and Hump2)
UH 1225	M	3 (Hump1, <i>Hinf</i> I, and Hump2)
UH 1076	M	2 (Hump1 and Hump2)
UH 1284	C	2 (Hump1 and <i>Hinf</i> I)
UH 1329	I	2 (Hump1 and Hump2)
UH 1094	I	1 (Hump1)
UH 1102	M	1 (Hump1)
UH 1236	C	1 (Hump1)

Note :

C : Chinese

I : Indian

M : Malay

UH : University Hospital

Appendix G: Pairwise comparisons by the heterogeneity G-test of the distributions of *HinfI* + and - , Hump1 C and G, and Hump2 C and T alleles between different population samples.

(i) G_H test

The calculation of the pairwise comparison by the heterogeneity G-test of the distributions of *HinfI* + and - alleles between the Chinese and Indians as an example is illustrated as below:

- (a) Null hypothesis: The distributions of *HinfI* + and - alleles between the Chinese and Indians are similar.
- (b) Alternative hypothesis: The distributions of *HinfI* + and - alleles between the Chinese and Indians are different.
- (c) Level of significance: $\alpha = 0.05$
- (d) Criterion: Reject the null hypothesis if $G_H > 3.841$, the value of $G_{H, 0.05}$ for 1 degree of freedom (df), which

$$G_H = 2 \times (j + k - m - n + s)$$

or otherwise accept it.

(e) Calculation:

	<i>HinfI</i> (+)	<i>HinfI</i> (-)	Total
Chinese	110	30	140
Indians	110	30	140
Total	220	60	280

$$\begin{aligned} j &= [110 \times \ln(110) + 30 \times \ln(30)] = 619.089 \\ k &= [110 \times \ln(110) + 30 \times \ln(30)] = 619.089 \\ m &= [220 \times \ln(220) + 60 \times \ln(60)] = 1432.259 \\ n &= [140 \times \ln(140) + 140 \times \ln(140)] = 1383.660 \\ s &= [280 \times \ln(280)] = 1577.741 \end{aligned}$$

$$\begin{aligned} G_H &= 2 \times (j + k - m - n + s) \\ &= 2 \times (619.089 + 619.089 - 1432.259 - 1383.660 + 1577.741) \\ &= 0 \\ df &= (2-1)(2-1) = 1 \end{aligned}$$

- (f) Decision: Since $G_H = 0$ does not exceed 3.841, the null hypothesis is accepted.

(ii) The results of pairwise comparisons of the distributions of *Hinf*I + and - alleles:

Chinese/Indians				
	<i>Hinf</i> I (+)	<i>Hinf</i> I (-)	Total	
Chinese	110	30	140	$j = 619.089$ $k = 619.089$
Indians	110	30	140	$m = 1432.259$
Total	220	60	280	$n = 1383.660$
				$s = 1577.741$
				$G_H = 0.000$
				$df = 1$

Chinese/Malays				
	<i>Hinf</i> I (+)	<i>Hinf</i> I (-)	Total	
Chinese	110	30	140	$j = 619.089$ $k = 615.377$
Malays	107	33	140	$m = 1428.455$
Total	217	63	280	$n = 1383.660$
				$s = 1577.741$
				$G_H = 0.184$
				$df = 1$

Chinese/Caucasians				
	<i>Hinf</i> I (+)	<i>Hinf</i> I (-)	Total	
Chinese	110	30	140	$j = 619.089$ $k = 733.369$
Caucasians	129	31	160	$m = 1559.638$
Total	239	61	300	$n = 1503.858$
				$s = 1711.135$
				$G_H = 0.194$
				$df = 1$

Chinese/Japanese				
	<i>Hinf</i> I (+)	<i>Hinf</i> I (-)	Total	
Chinese	110	30	140	$j = 619.089$ $k = 973.160$
Japanese	163	39	202	$m = 1823.539$

Total	273	69	342	$n = 1764.100$
				$s = 1995.505$
				$G_H = 0.230$
				$df = 1$

Indians/Malays				
	<i>Hinf</i> l (+)	<i>Hinf</i> l (-)	Total	
				$j = 619.089$
Indians	110	30	140	$k = 615.377$
Malays	107	33	140	$m = 1428.455$
Total	217	63	280	$n = 1383.660$
				$s = 1577.741$
				$G_H = 0.184$
				$df = 1$

Indians/Caucasians				
	<i>Hinf</i> l (+)	<i>Hinf</i> l (-)	Total	
				$j = 619.089$
Indians	110	30	140	$k = 733.369$
Caucasians	129	31	160	$m = 1559.638$
Total	239	61	300	$n = 1503.858$
				$s = 1711.135$
				$G_H = 0.194$
				$df = 1$

Indians/Japanese				
	<i>Hinf</i> l (+)	<i>Hinf</i> l (-)	Total	
				$j = 619.089$
Indians	110	30	140	$k = 973.160$
Japanese	163	39	202	$m = 1823.539$
Total	273	69	342	$n = 1764.100$
				$s = 1995.505$
				$G_H = 0.230$
				$df = 1$

Malays/Caucasians				
	<i>Hinf</i> l (+)	<i>Hinf</i> l (-)	Total	
				$j = 615.377$

Malays	107	33	140	$k = 733.369$
Caucasians	129	31	160	$m = 1555.633$
Total	236	64	300	$n = 1503.858$
				$s = 1711.135$
				$G_H = 0.782$
				$df = 1$

Malays/Japanese				
	<i>Hinf</i> I (+)	<i>Hinf</i> I (-)	Total	
Malays	107	33	140	$j = 615.377$
Japanese	163	39	202	$k = 973.160$
Total	270	72	342	$m = 1819.494$
				$n = 1764.100$
				$s = 1995.505$
				$G_H = 0.898$
				$df = 1$

Caucasians/Japanese				
	<i>Hinf</i> I (+)	<i>Hinf</i> I (-)	Total	
Caucasians	129	31	160	$j = 733.369$
Japanese	163	39	202	$k = 973.160$
Total	292	70	362	$m = 1955.007$
				$n = 1884.298$
				$s = 2132.775$
				$G_H = 0.000$
				$df = 1$

(iii) The results of pairwise comparisons of the distributions of Hump1 C and G alleles:

Chinese/Indians				
	Hump1 (G)	Hump1 (C)	Total	
Chinese	109	31	140	$j = 617.811$
Indians	106	34	140	$k = 614.221$
Total	215	65	280	$m = 1426.022$
				$n = 1383.660$
				$s = 1577.741$

$G_H = 0.180$
df = 1

Chinese/Malays				
	Hump1 (G)	Hump1 (C)	Total	
Chinese	109	31	140	j = 617.811 k = 626.139
Malays	115	25	140	m = 1437.628
Total	224	56	280	n = 1383.660
				s = 1577.741
				$G_H = 0.805$
				df = 1

Chinese/Caucasians				
	Hump1 (G)	Hump1 (C)	Total	
Chinese	109	31	140	j = 617.811 k = 300.875
Caucasians	55	25	80	m = 1061.798
Total	164	56	220	n = 1042.392
				s = 1186.598
				$G_H = 2.188$
				df = 1

Chinese/Japanese				
	Hump1 (G)	Hump1 (C)	Total	
Chinese	109	31	140	j = 617.811 k = 958.212
Japanese	159	41	200	m = 1806.304
Total	268	72	340	n = 1751.493
				s = 1981.842
				$G_H = 0.133$
				df = 1

Indians/Malays				
	Hump1 (G)	Hump1 (C)	Total	
Indians	106	34	140	j = 614.221 k = 626.139
Malays	115	25	140	m = 1433.569

Total	221	59	280	$n = 1383.660$
				$s = 1577.741$
				$G_H = 1.745$
				$df = 1$

Indians/Caucasians				
	Hump1 (G)	Hump1 (C)	Total	
Indians	106	34	140	$j = 614.221$
Caucasians	55	25	80	$k = 300.875$
Total	161	59	220	$m = 1058.681$
				$n = 1042.392$
				$s = 1186.598$
				$G_H = 1.242$
				$df = 1$

Indians/Japanese				
	Hump1 (G)	Hump1 (C)	Total	
Indians	106	34	140	$j = 614.221$
Japanese	159	41	200	$k = 958.212$
Total	265	75	340	$m = 1802.440$
				$n = 1751.493$
				$s = 1981.842$
				$G_H = 0.682$
				$df = 1$

Malays/Caucasians				
	Hump1 (G)	Hump1 (C)	Total	
Malays	115	25	140	$j = 626.139$
Caucasians	55	25	80	$k = 300.875$
Total	170	50	220	$m = 1068.687$
				$n = 1042.392$
				$s = 1186.598$
				$G_H = 5.067$
				$df = 1$

Malays/Japanese				
	Hump1 (G)	Hump1 (C)	Total	
				$j = 626.139$

Malays	115	25	140	$k = 958.212$
Japanese	159	41	200	$m = 1814.514$
Total	274	66	340	$n = 1751.493$
				$s = 1981.842$
				$G_H = 0.370$
				$df = 1$

Caucasians/Japanese				
	Hump1 (G)	Hump1 (C)	Total	$j = 300.875$
Caucasians	55	25	80	$k = 958.212$
Japanese	159	41	200	$m = 1424.836$
Total	214	66	280	$n = 1410.226$
				$s = 1577.741$
				$G_H = 3.534$
				$df = 1$

(iv) The results of pairwise comparisons of the distributions of Hump2 C and T alleles:

Chinese/Indians				
	Hump2 (C)	Hump2 (T)	Total	$j = 630.944$
Chinese	118	22	140	$k = 616.574$
Indians	108	32	140	$m = 1440.446$
Total	226	54	280	$n = 1383.660$
				$s = 1577.741$
				$G_H = 2.305$
				$df = 1$

Chinese/Malays				
	Hump2 (C)	Hump2 (T)	Total	$j = 630.944$
Chinese	118	22	140	$k = 617.811$
Malays	109	31	140	$m = 1441.889$
Total	227	53	280	$n = 1383.660$
				$s = 1577.741$

$G_H = 1.893$
$df = 1$

Chinese/Caucasians				
	Hump2 (C)	Hump2 (T)	Total	
Chinese	118	22	140	$j = 630.944$
Caucasians	94	66	160	$k = 703.587$
Total	212	88	300	$m = 1529.602$
				$n = 1503.858$
				$s = 1711.135$
				$G_H = 24.411$
				$df = 1$

Chinese/Japanese				
	Hump2 (C)	Hump2 (T)	Total	
Chinese	118	22	140	$j = 630.944$
Japanese	184	18	202	$k = 1011.575$
Total	302	40	342	$m = 1872.104$
				$n = 1764.100$
				$s = 1995.505$
				$G_H = 3.639$
				$df = 1$

Indians/Malays				
	Hump2 (C)	Hump2 (T)	Total	
Indians	108	32	140	$j = 616.574$
Malays	109	31	140	$k = 617.811$
Total	217	63	280	$m = 1428.455$
				$n = 1383.660$
				$s = 1577.741$
				$G_H = 0.022$
				$df = 1$

Indians/Caucasians				
	Hump2 (C)	Hump2 (T)	Total	
Indians	108	32	140	$j = 616.574$
Caucasians	94	66	160	$k = 703.587$
				$m = 1521.597$

Total	202	98	300	$n = 1503.858$
				$s = 1711.135$
				$G_H = 11.681$
				$df = 1$

Indians/Japanese				
	Hump2 (C)	Hump2 (T)	Total	
Indians	108	32	140	$j = 616.574$
Japanese	184	18	202	$k = 1011.575$
Total	292	50	342	$m = 1853.213$
				$n = 1764.100$
				$s = 1995.505$
				$G_H = 12.681$
				$df = 1$

Malays/Caucasians				
	Hump2 (C)	Hump2 (T)	Total	
Malays	109	31	140	$j = 617.811$
Caucasians	94	66	160	$k = 703.587$
Total	203	97	300	$m = 1522.328$
				$n = 1503.858$
				$s = 1711.135$
				$G_H = 12.693$
				$df = 1$

Malays/Japanese				
	Hump2 (C)	Hump2 (T)	Total	
Malays	109	31	140	$j = 617.811$
Japanese	184	18	202	$k = 1011.575$
Total	293	49	342	$m = 1854.990$
				$n = 1764.100$
				$s = 1995.505$
				$G_H = 11.602$
				$df = 1$

Caucasians/Japanese				
	Hump2 (C)	Hump2 (T)	Total	
				$j = 703.587$

Caucasians	94	66	160	$k = 1011.575$
Japanese	184	18	202	$m = 1936.667$
Total	278	84	362	$n = 1884.298$
				$s = 2132.775$
				$G_H = 53.944$
				$df = 1$

Appendix H: Pairwise comparisons by the heterogeneity G-test of the distributions of 8 haplotypes between different population samples.

(i) G_H test

The calculation of the pairwise comparison by the heterogeneity G-test of the distributions of 8 haplotypes between the Chinese and Indians as an example is illustrated as below:

(a) Null hypothesis: The distributions of 8 haplotypes between the Chinese and Indians are similar.

(b) Alternative hypothesis: The distributions of 8 haplotypes between the Chinese and Indians are different.

(c) Level of significance: $\alpha = 0.05$

(d) Criterion: Reject the null hypothesis if $G_H > 14.067$, the value of $G_{H, 0.05}$ for 7 degrees of freedom (df), which

$$G_H = 2 \times (j + k - m - n + s)$$

or otherwise accept it.

(e) Calculation:

	C-T	C-C	G-T	G-C	C+T	C+C	G+T	G+C	Total
Chinese	0	0	11	19	0	31	11	68	140
Indians	0	0	14	16	8	26	10	66	140
Total	0	0	25	35	8	57	21	134	280

$$j = [0 \times \ln(0) + 0 \times \ln(0) + 11 \times \ln(11) + 19 \times \ln(19) + 0 \times \ln(0) + 31 \times \ln(31) + 11 \times \ln(11) + 68 \times \ln(68)] = 502.078$$

$$k = [0 \times \ln(0) + 0 \times \ln(0) + 14 \times \ln(14) + 16 \times \ln(16) + 8 \times \ln(8) + 26 \times \ln(26) + 10 \times \ln(10) + 66 \times \ln(66)] = 482.197$$

$$m = [0 \times \ln(0) + 0 \times \ln(0) + 25 \times \ln(25) + 35 \times \ln(35) + 8 \times \ln(8) + 57 \times \ln(57) + 21 \times \ln(21) + 134 \times \ln(134)] = 1172.244$$

$$n = [140 \times \ln(140) + 140 \times \ln(140)] = 1383.660$$

$$s = [280 \times \ln(280)] = 1577.741$$

$$\begin{aligned} G_H &= 2 \times (j + k - m - n + s) \\ &= 2 \times (502.078 + 482.197 - 1172.244 - 1383.660 + 1577.741) \\ &= 12.224 \end{aligned}$$

$$df = (8-1)(2-1) = 7$$

(f) Decision: Since $G_H = 12.224$ does not exceed 14.067, the null hypothesis is accepted.

(ii) The results of pairwise comparisons of the distributions of 8 haplotypes:

Chinese/Indians										
	C-T	C-C	G-T	G-C	C+T	C+C	G+T	G+C	Total	$j = 502.078$
Chinese	0	0	11	19	0	31	11	68	140	$k = 482.197$
Indians	0	0	14	16	8	26	10	66	140	$m = 1172.244$
Total	0	0	25	35	8	57	21	134	280	$n = 1383.660$
										$s = 1577.741$
										$G_H = 12.224$
										$df = 7$

Chinese/Malays										
	C-T	C-C	G-T	G-C	C+T	C+C	G+T	G+C	Total	$j = 502.078$
Chinese	0	0	11	19	0	31	11	68	140	$k = 497.168$
Malays	0	0	19	14	3	22	9	73	140	$m = 1188.832$
Total	0	0	30	33	3	53	20	141	280	$n = 1383.660$
										$s = 1577.741$
										$G_H = 8.99$
										$df = 7$

Chinese/Caucasians										
	C-T	C-C	G-T	G-C	C+T	C+C	G+T	G+C	Total	$j = 502.078$
Chinese	0	0	11	19	0	31	11	68	140	$k = 572.452$
Caucasians	0	0	23	8	30	12	13	74	160	$m = 1252.652$
Total	0	0	34	27	30	43	24	142	300	$n = 1503.858$
										$s = 1711.135$
										$G_H = 58.31$
										$df = 7$

Chinese/Japanese										
	C-T	C-C	G-T	G-C	C+T	C+C	G+T	G+C	Total	$j = 502.078$
Chinese	0	0	11	19	0	31	11	68	140	$k = 817.931$
Japanese	0	1	11	26	0	40	7	115	200	$m = 1547.316$

Total	0	1	22	45	0	71	18	183	340	$n = 1751.493$
										$s = 1981.842$
										$G_H = 6.084$
										$df = 7$

Indians/Malays										
	C-T	C-C	G-T	G-C	C+T	C+C	G+T	G+C	Total	$j = 482.197$
Indians	0	0	14	16	8	26	10	66	140	$k = 497.168$
Malays	0	0	9	14	3	22	9	73	140	$m = 1171.451$
Total	0	0	33	30	11	48	19	139	280	$n = 1383.660$
										$s = 1577.741$
										$G_H = 3.99$
										$df = 7$

Indians/Caucasians										
	C-T	C-C	G-T	G-C	C+T	C+C	G+T	G+C	Total	$j = 482.197$
Indians	0	0	14	16	8	26	10	66	140	$k = 572.452$
Caucasians	0	0	23	8	30	12	13	74	160	$m = 1250.280$
Total	0	0	37	24	38	38	23	140	300	$n = 1503.858$
										$s = 1711.135$
										$G_H = 23.292$
										$df = 7$

Indians/Japanese										
	C-T	C-C	G-T	G-C	C+T	C+C	G+T	G+C	Total	$j = 482.197$
Indians	0	0	14	16	8	26	10	66	140	$k = 817.931$
Japanese	0	1	11	26	0	40	7	115	200	$m = 1519.699$
Total	0	1	25	42	8	66	17	181	340	$n = 1751.493$
										$s = 1981.842$
										$G_H = 21.556$
										$df = 7$

Malays/Caucasians										
	C-T	C-C	G-T	G-C	C+T	C+C	G+T	G+C	Total	$j = 497.168$

Malays	0	0	19	14	3	22	9	73	140	$k = 572.452$
Caucasians	0	0	23	8	30	12	13	74	160	$m = 1261.863$
Total	0	0	42	22	33	34	22	147	300	$n = 1503.858$
										$s = 1711.135$
										$G_H = 30.068$
										$df = 7$

Malays/Japanese										
	C-T	C-C	G-T	G-C	C+T	C+C	G+T	G+C	Total	$j = 497.168$
Malays	0	0	19	14	3	22	9	73	140	$k = 817.931$
Japanese	0	1	11	26	0	40	7	115	200	$m = 1537.582$
Total	0	1	30	40	3	62	16	188	340	$n = 1751.493$
										$s = 1981.842$
										$G_H = 15.732$
										$df = 7$

Caucasians/Japanese										
	C-T	C-C	G-T	G-C	C+T	C+C	G+T	G+C	Total	$j = 572.452$
Caucasians	0	0	23	8	30	12	13	74	160	$k = 817.931$
Japanese	0	1	11	26	0	40	7	115	200	$m = 1597.898$
Total	0	1	34	34	30	52	20	189	360	$n = 1871.691$
										$s = 2118.997$
										$G_H = 79.582$
										$df = 7$