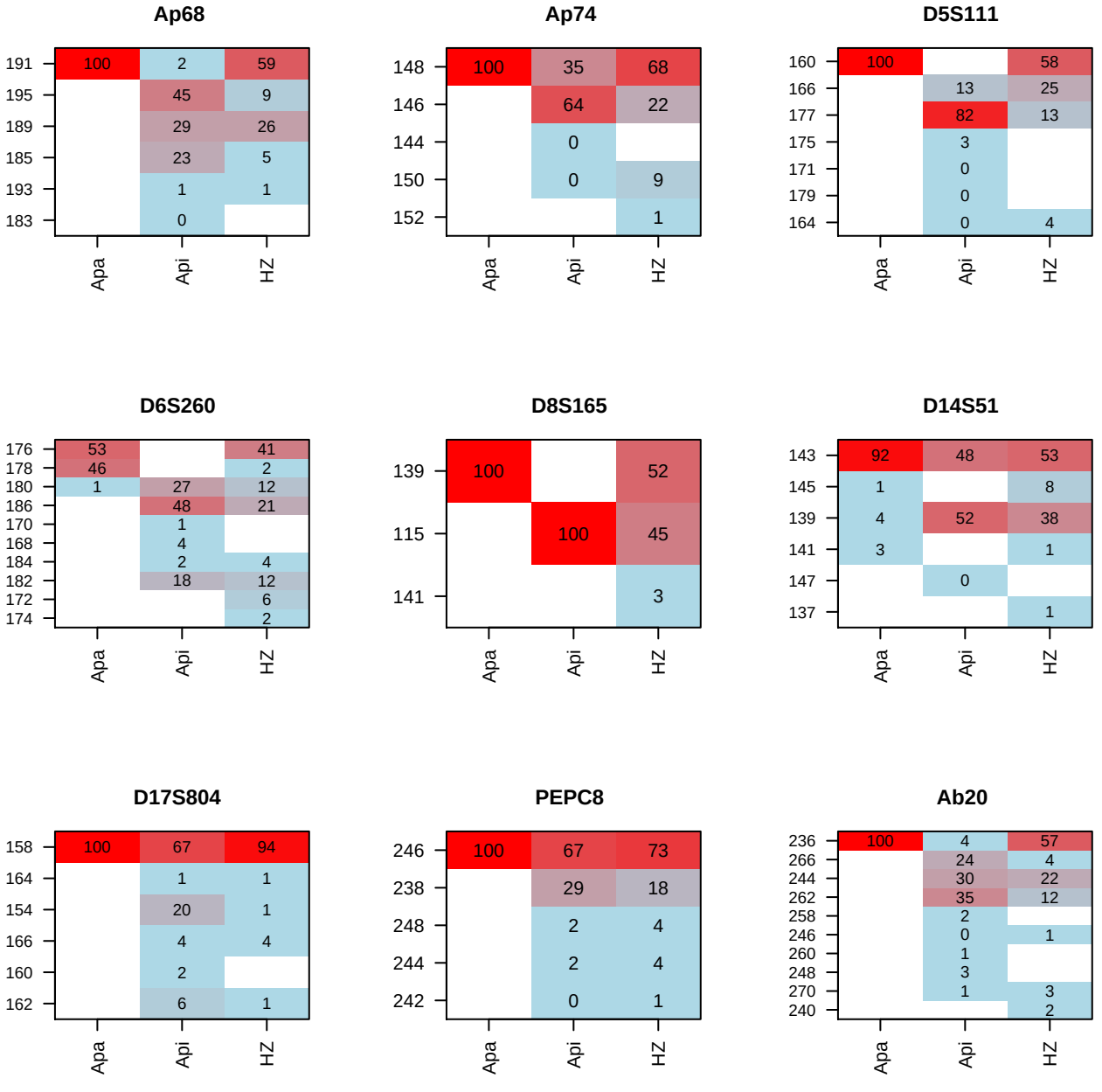
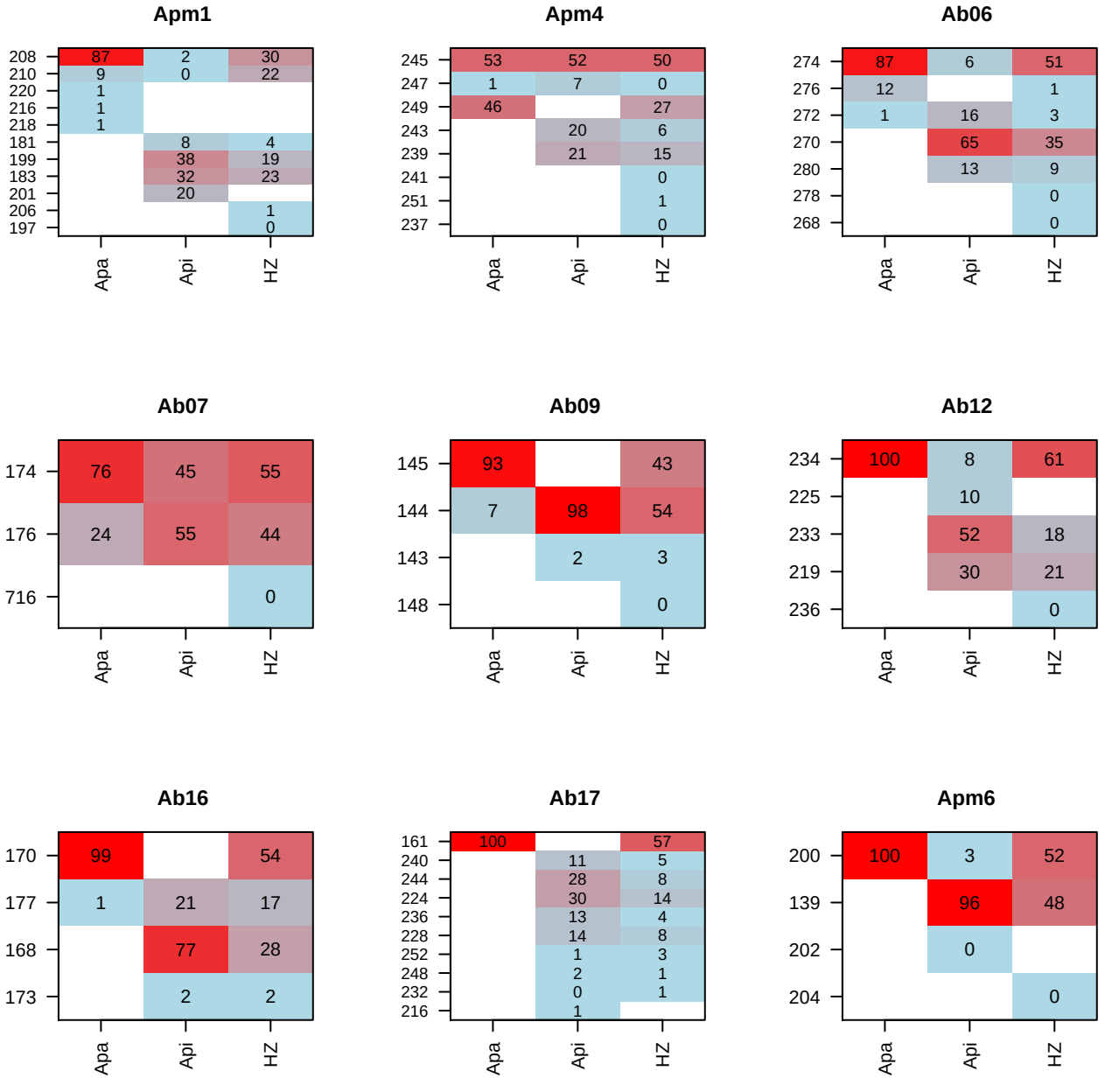
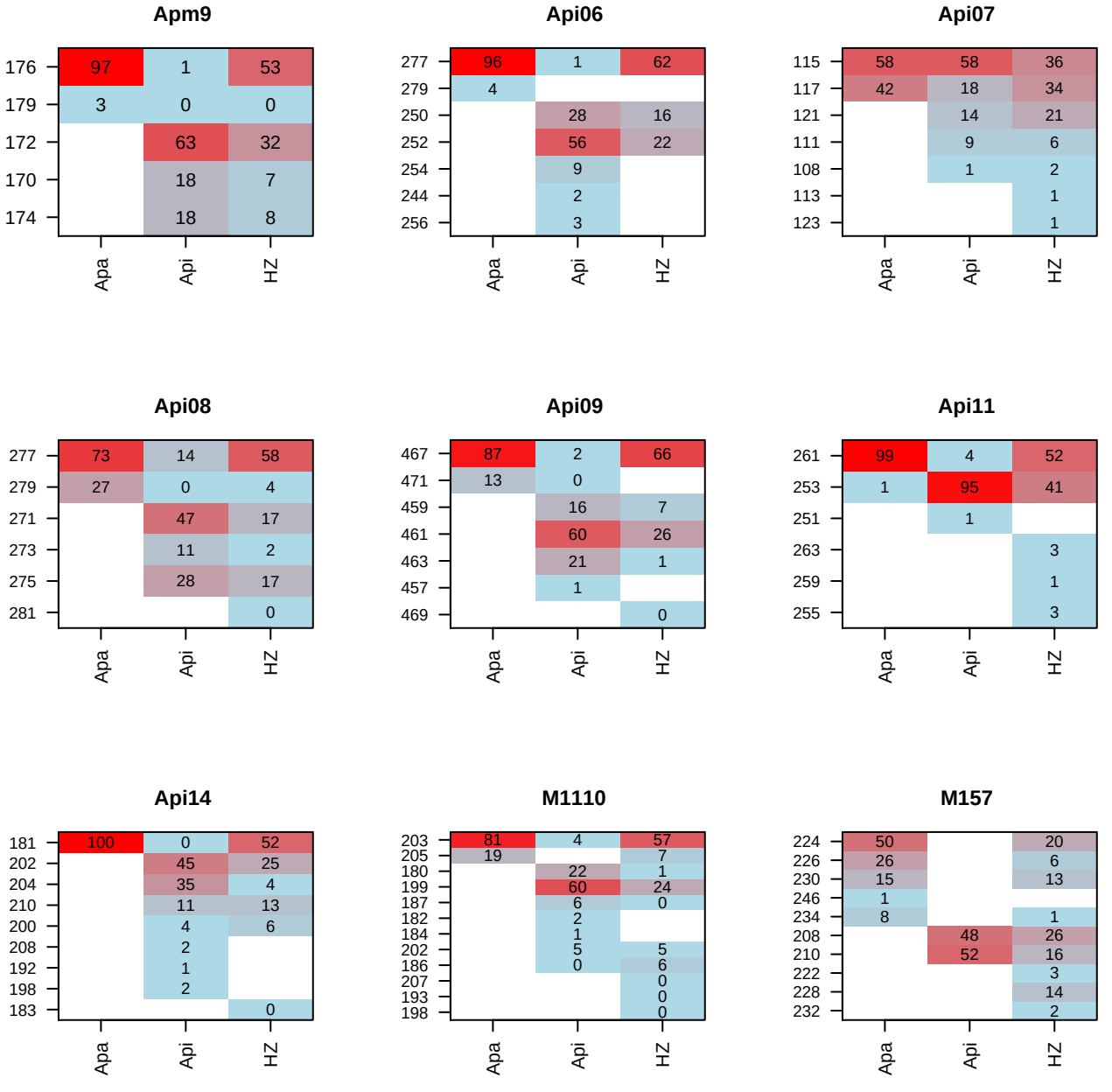
Figure S1


Ap68
191 195 189 185 193 183
100 2 59
45 9
29 26
23 5
1 1
0
Ap74
148 146 144 150 152
100 35 68
64 22
0
0 9
1
D5S111
160 166 177 175 171 179 164
100 58
13 25
82 13
3
0
0
0 4
D6S260
176 178 180 186 170 168 184 182 172 174
53 41
46 2
1 27 12
48 21
1
4
2 4
18 12
6
2
D8S165
139 115 141
100 52
100 45
3
D14S51
143 145 139 141 147 137
92 48 53
1 8
4 52 38
3 1
0
1
D17S804
158 164 154 166 160 162
100 67 94
1 1
20 1
4 4
2
6 1
PEPC8
246 238 248 244 242
100 67 73
29 18
2 4
2 4
0 1
Ab20
236 266 244 262 258 246 260 248 270 240
100 4 57
24 4
30 22
35 12
2
0 1
1
3
1 3
2
Apa Api HZ


Apm1
208 210 220 216 218 181 199 183 201 206 197
87 2 30
9 0 22
1
1
1
8 4
38 19
32 23
20
1 0
Apa Api HZ
Apm4
245 247 249 243 239 241 251 237
53 52 50
1 7 0
46 27
20 6
21 15
0
1
0
Apa Api HZ
Ab06
274 276 272 270 280 278 268
87 6 51
12 1
1 16 3
65 35
13 9
0
0
Apa Api HZ
Ab07
174 176 716
76 45 55
24 55 44
0
Apa Api HZ
Ab09
145 144 143 148
93 43
7 98 54
2 3
0
Apa Api HZ
Ab12
234 225 233 219 236
100 8 61
10
52 18
30 21
0
Apa Api HZ
Ab16
170 177 168 173
99 54
1 21 17
77 28
2 2
Apa Api HZ
Ab17
161 240 244 224 236 228 252 248 232 216
100 57
11 5
28 8
30 14
13 4
14 8
1 3
2 1
0 1
1
Apa Api HZ
Apm6
200 139 202 204
100 3 52
96 48
0
0
Apa Api HZ


Apm9
176
179
172
170
174
97
1
53
3
0
0
63
32
18
7
18
8
Apa
Api
HZ
Api06
277
279
250
252
254
244
256
96
1
62
4
28
16
56
22
9
2
3
Apa
Api
HZ
Api07
115
117
121
111
108
113
123
58
58
36
42
18
34
14
21
9
6
1
2
1
1
Apa
Api
HZ
Api08
277
279
271
273
275
281
73
14
58
27
0
4
47
17
11
2
28
17
0
Apa
Api
HZ
Api09
467
471
459
461
463
457
469
87
2
66
13
0
16
7
60
26
21
1
1
0
Apa
Api
HZ
Api11
261
253
251
263
259
255
99
4
52
1
95
41
1
3
1
3
Apa
Api
HZ
Api14
181
202
204
210
200
208
192
198
183
100
0
52
45
25
35
4
11
13
4
6
2
1
2
0
Apa
Api
HZ
M1110
203
205
180
199
187
182
184
202
186
207
193
198
81
4
57
19
7
22
1
60
24
6
0
2
1
5
0
5
6
0
0
0
Apa
Api
HZ
M157
224
226
230
246
234
208
210
222
228
232
50
20
26
6
15
13
1
8
1
48
26
52
16
3
14
2
Apa
Api
HZ

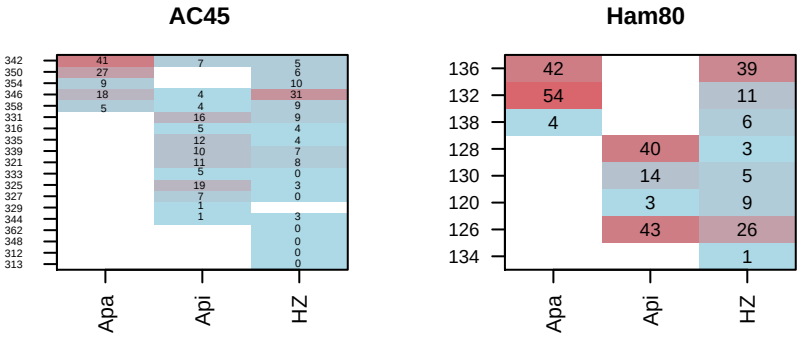
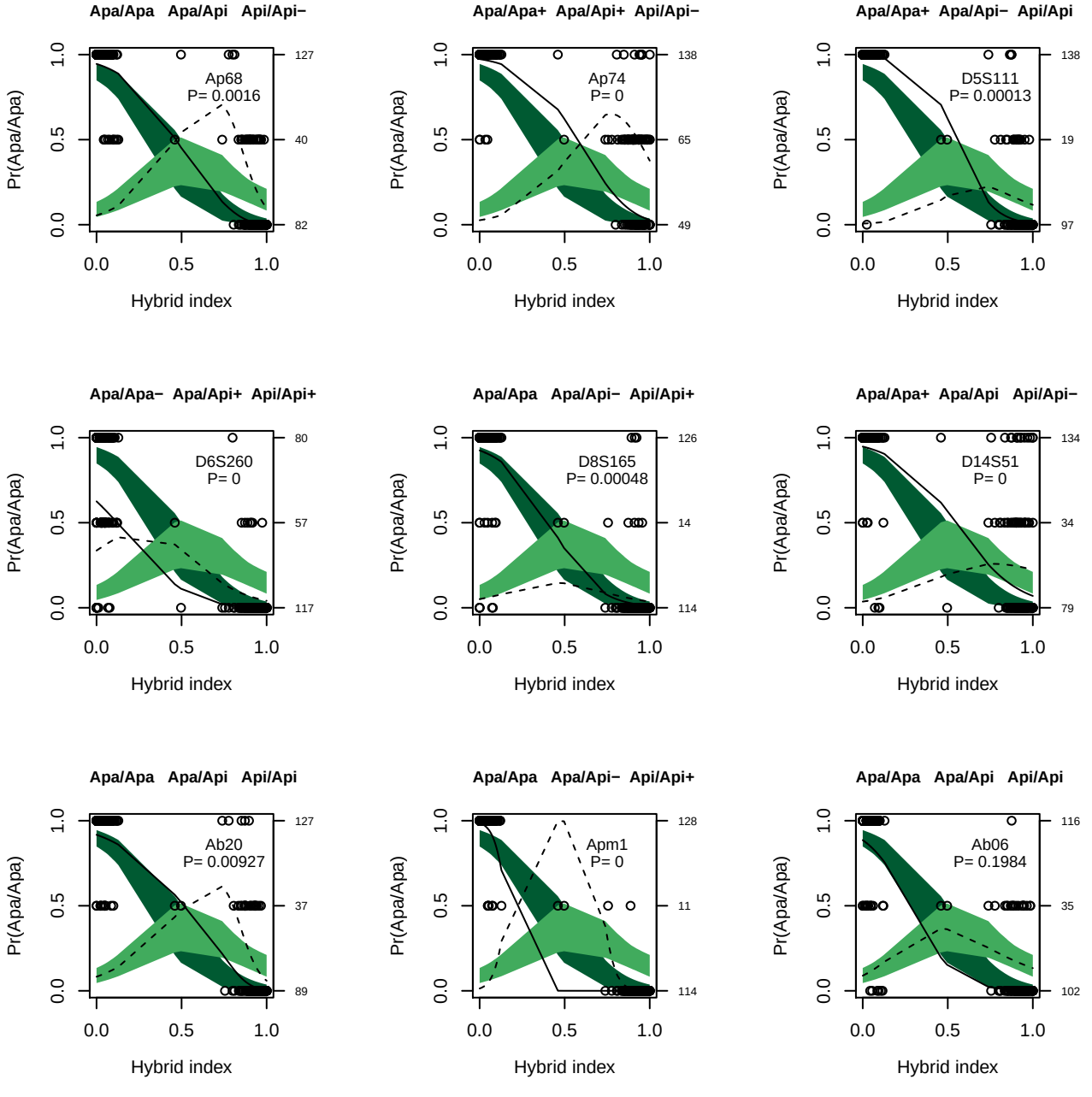
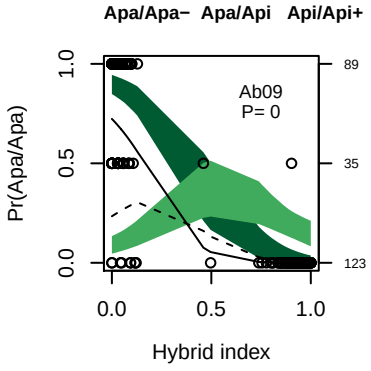
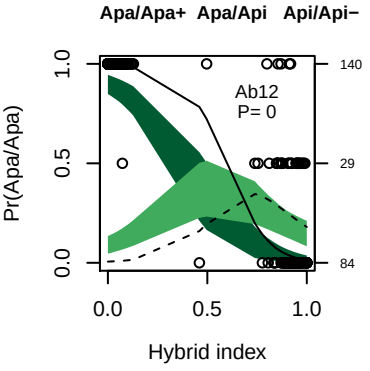


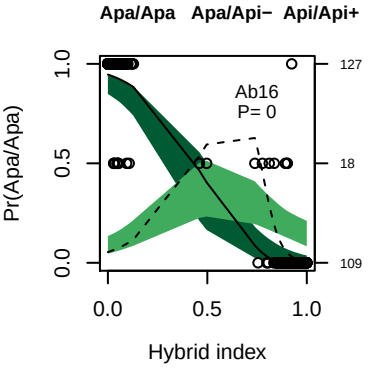
Fig. S1 Per locus heat maps showing the frequencies of alleles (presented as the percentages) by population. For each locus, alleles are denoted by size on the *y*-axis; populations are on the *x*-axis (Apa = *A. palliata* sampled outside the hybrid zone, Api = *A. pigra* sampled outside the hybrid zone, and HZ = individuals sampled in the hybrid zone). In the plot area, warmer colors indicate a higher percentage of individuals with a given genotype. Percentages ≤0.5 were rounded down to 0. We dropped from analyses loci where the most common allele in Apa was also the most common allele in Api. This included D17S804, PEPC8, Apm4, and Api07. We also dropped Ab07 because although the most common allele was different between populations, alternative alleles were present at nearly equal frequency in Api and the locus was not near fixation in Apa.

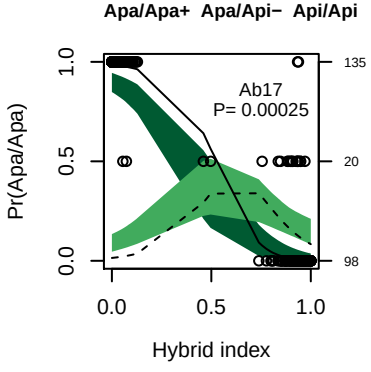
Figure S2A

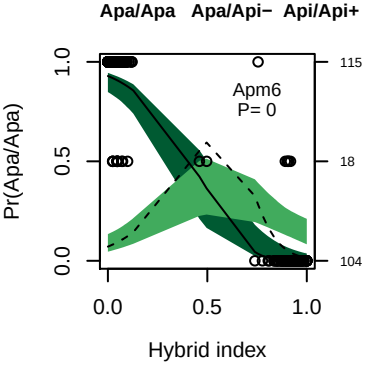

Apa/Apa Apa/Api Api/Api−
Ap68
P= 0.0016
Apa/Apa+ Apa/Api+ Api/Api−
Ap74
P= 0
Apa/Apa+ Apa/Api− Api/Api
D5S111
P= 0.00013
Apa/Apa− Apa/Api+ Api/Api+
D6S260
P= 0
Apa/Apa Apa/Api− Api/Api+
D8S165
P= 0.00048
Apa/Apa+ Apa/Api Api/Api−
D14S51
P= 0
Apa/Apa Apa/Api Api/Api
Ab20
P= 0.00927
Apa/Apa Apa/Api− Api/Api+
Apm1
P= 0
Apa/Apa Apa/Api Api/Api
Ab06
P= 0.1984
Pr(Apa/Apa)
Hybrid index
0.0
0.5
1.0

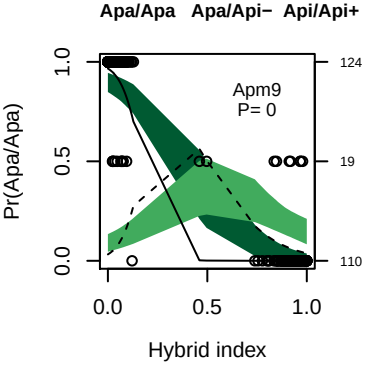

Apa/Apa− Apa/Api Api/Api+
Ab09
P= 0
Pr(Apa/Apa)
Hybrid index
89
35
123

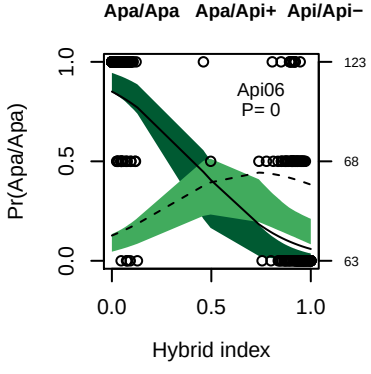

Apa/Apa+ Apa/Api Api/Api−
Ab12
P= 0
Pr(Apa/Apa)
Hybrid index
140
29
84

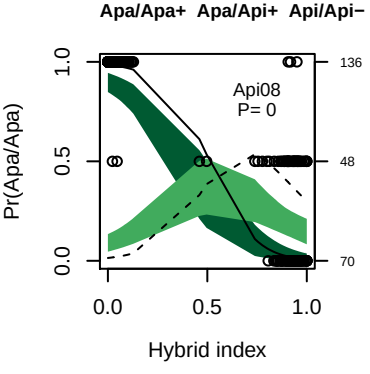

Apa/Apa Apa/Api− Api/Api+
Ab16
P= 0
Pr(Apa/Apa)
Hybrid index
127
18
109

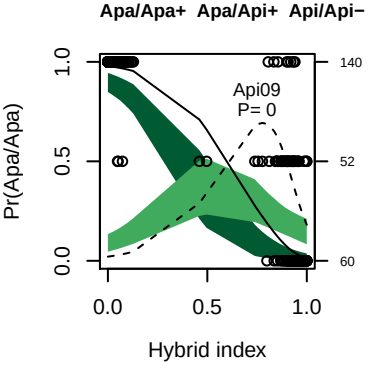

Apa/Apa+ Apa/Api− Api/Api
Ab17
P= 0.00025
Pr(Apa/Apa)
Hybrid index
135
20
98

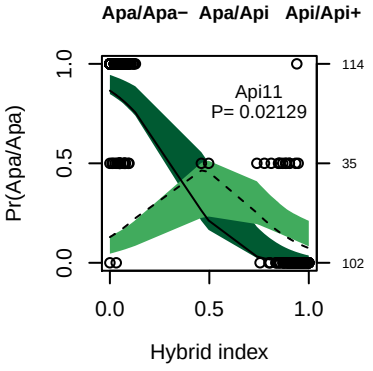

Apa/Apa Apa/Api− Api/Api+
Apm6
P= 0
Pr(Apa/Apa)
Hybrid index
115
18
104

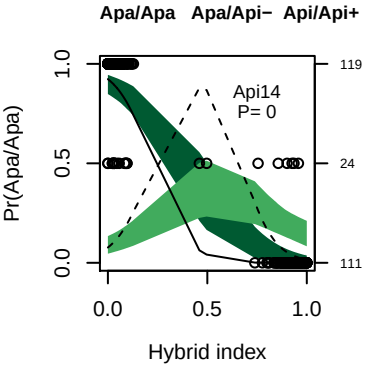

Apa/Apa Apa/Api− Api/Api+
Apm9
P= 0
Pr(Apa/Apa)
Hybrid index
124
19
110

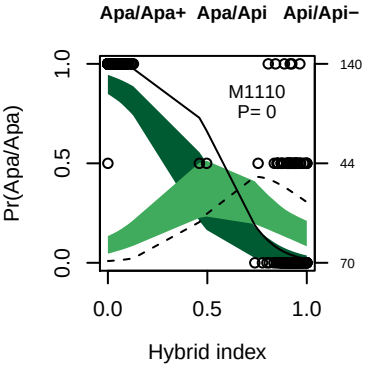

Apa/Apa Apa/Api+ Api/Api−
Api06
P= 0
Pr(Apa/Apa)
Hybrid index
123
68
63

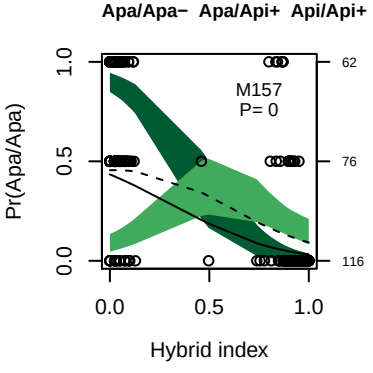

Apa/Apa+ Apa/Api+ Api/Api−
Api08
P= 0
Pr(Apa/Apa)
Hybrid index
136
48
70

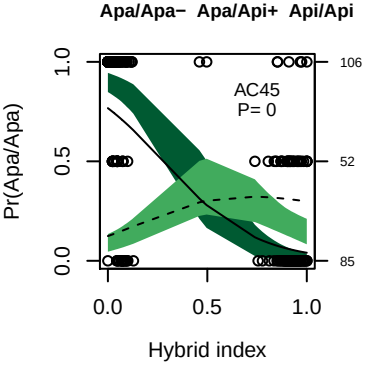

Apa/Apa+ Apa/Api+ Api/Api−
Api09
P= 0
Pr(Apa/Apa)
Hybrid index
140
52
60


Apa/Apa− Apa/Api Api/Api+
Api11
P= 0.02129
Pr(Apa/Apa)
Hybrid index
114
35
102


Apa/Apa Apa/Api− Api/Api+
Api14
P= 0
Pr(Apa/Apa)
Hybrid index
119
24
111


Apa/Apa+ Apa/Api Api/Api−
M1110
P= 0
Pr(Apa/Apa)
Hybrid index
140
44
70


Apa/Apa− Apa/Api+ Api/Api+
M157
P= 0
Pr(Apa/Apa)
Hybrid index
62
76
116


Apa/Apa− Apa/Api+ Api/Api
AC45
P= 0
Pr(Apa/Apa)
Hybrid index
106
52
85

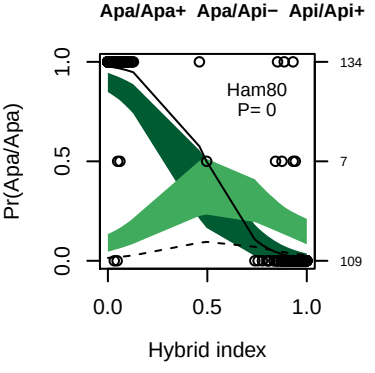
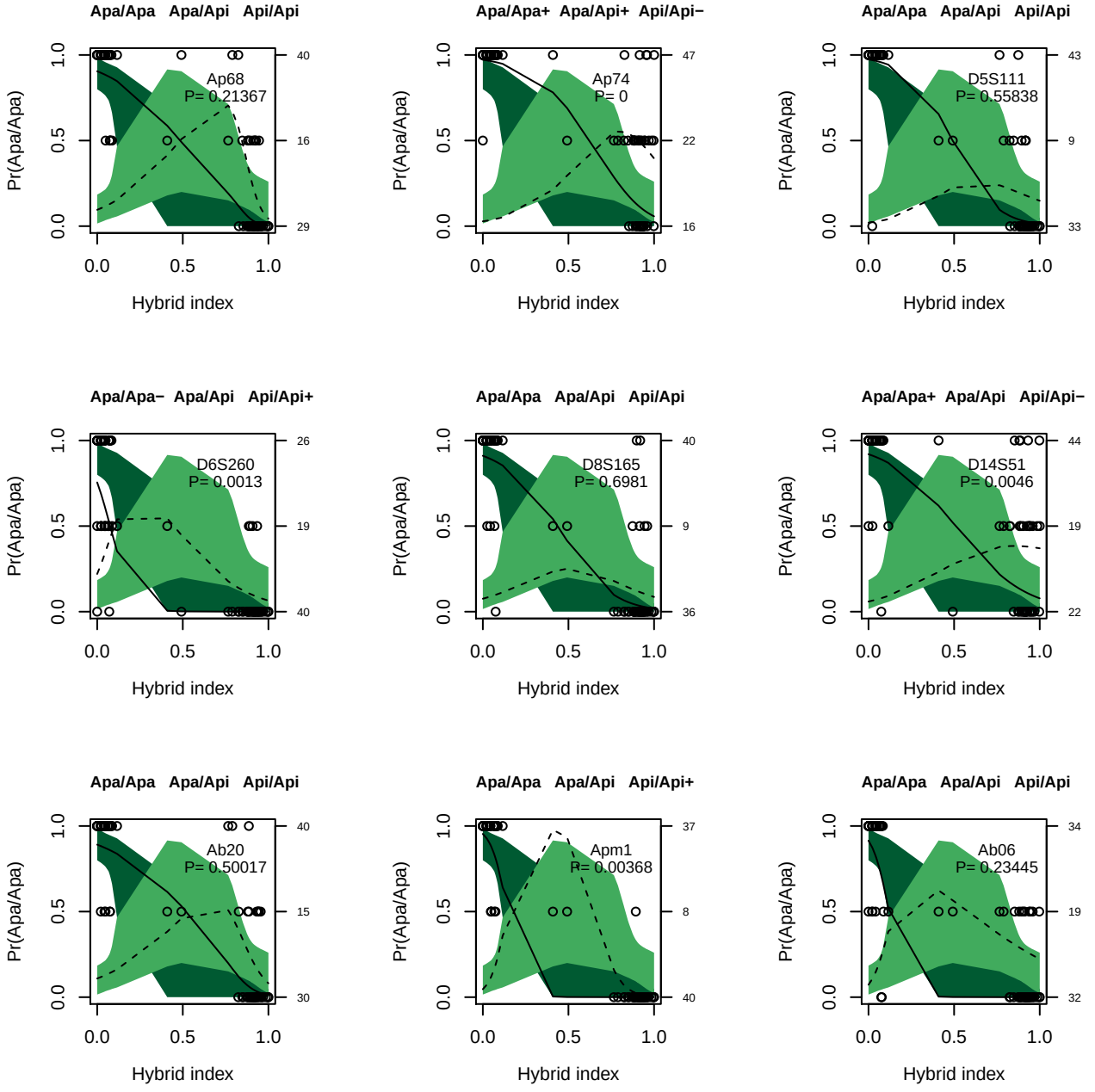
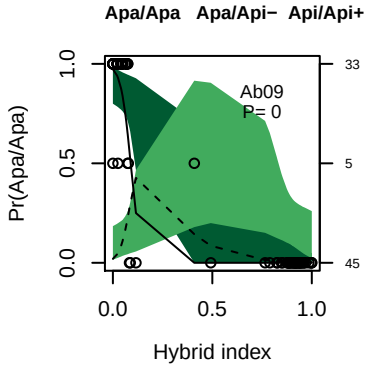
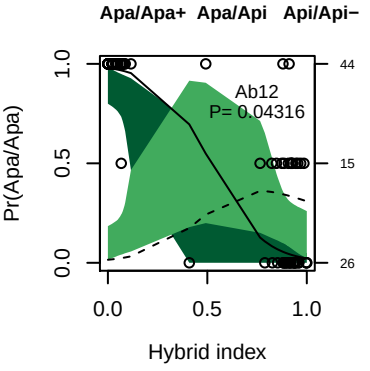
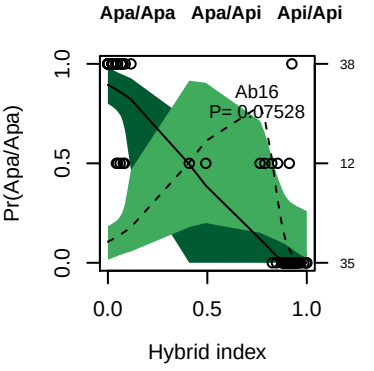

Apa/Apa+ Apa/Api− Api/Api+
Ham80
P= 0
Pr(Apa/Apa)
Hybrid index
134
7
109

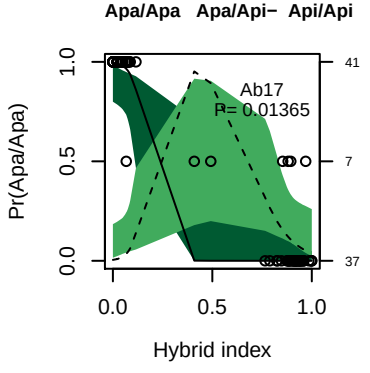
Figure S2B

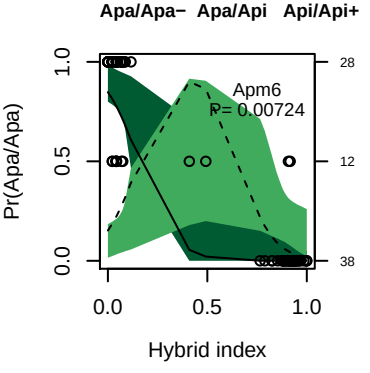

Apa/Apa Apa/Api Api/Api
Ap68
P= 0.21367
Apa/Apa+ Apa/Api+ Api/Api−
Ap74
P= 0
Apa/Apa Apa/Api Api/Api
D5S111
P= 0.55838
Apa/Apa− Apa/Api Api/Api+
D6S260
P= 0.0013
Apa/Apa Apa/Api Api/Api
D8S165
P= 0.6981
Apa/Apa+ Apa/Api Api/Api−
D14S51
P= 0.0046
Apa/Apa Apa/Api Api/Api
Ab20
P= 0.50017
Apa/Apa Apa/Api Api/Api+
Apm1
P= 0.00368
Apa/Apa Apa/Api Api/Api
Ab06
P= 0.23445
Pr(Apa/Apa)
Hybrid index
0.0
0.5
1.0

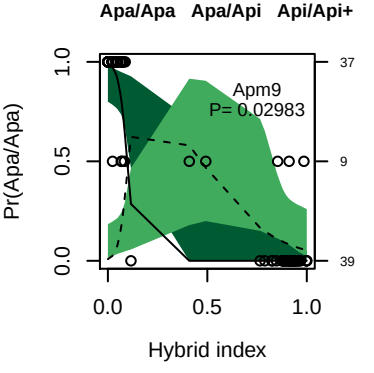

Apa/Apa Apa/Api− Api/Api+
Ab09
P= 0
Pr(Apa/Apa)
Hybrid index

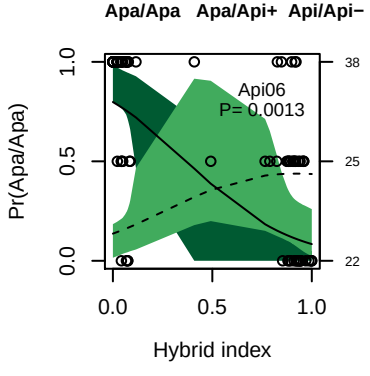

Apa/Apa+ Apa/Api Api/Api−
Ab12
P= 0.04316
Pr(Apa/Apa)
Hybrid index

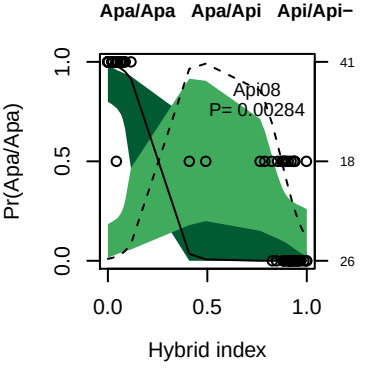

Apa/Apa Apa/Api Api/Api
Ab16
P= 0.07528
Pr(Apa/Apa)
Hybrid index

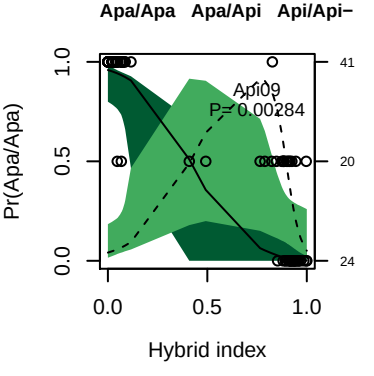

Apa/Apa Apa/Api− Api/Api
Ab17
P= 0.01365
Pr(Apa/Apa)
Hybrid index

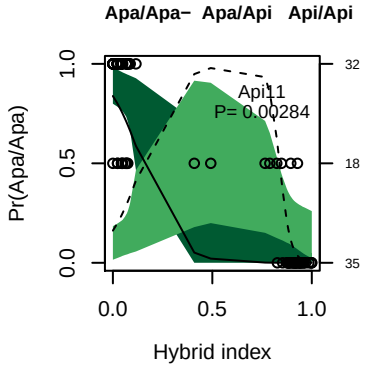

Apa/Apa− Apa/Api Api/Api+
Apm6
P= 0.00724
Pr(Apa/Apa)
Hybrid index

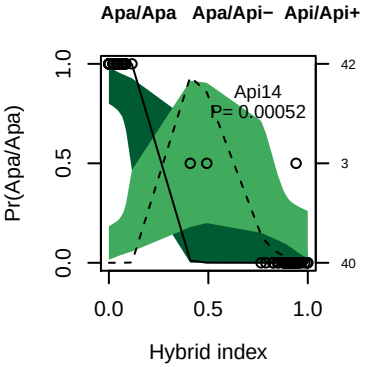

Apa/Apa Apa/Api Api/Api+
Apm9
P= 0.02983
Pr(Apa/Apa)
Hybrid index

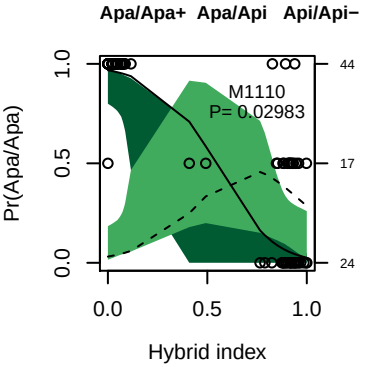

Apa/Apa Apa/Api+ Api/Api−
Api06
P= 0.0013
Pr(Apa/Apa)
Hybrid index

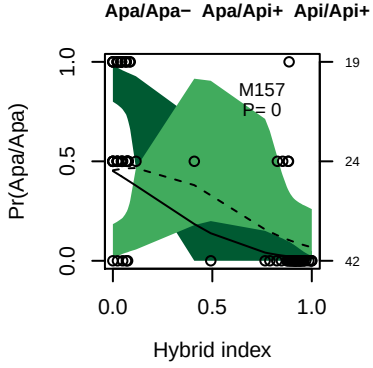

Apa/Apa Apa/Api Api/Api−
Api08
P= 0.00284
Pr(Apa/Apa)
Hybrid index

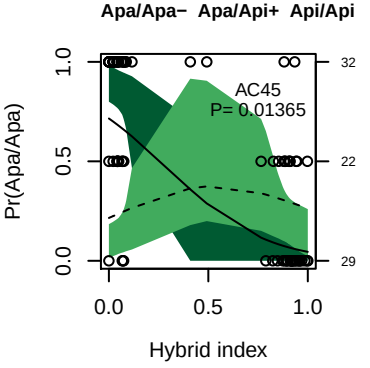

Apa/Apa Apa/Api Api/Api−
Api09
P= 0.00284
Pr(Apa/Apa)
Hybrid index

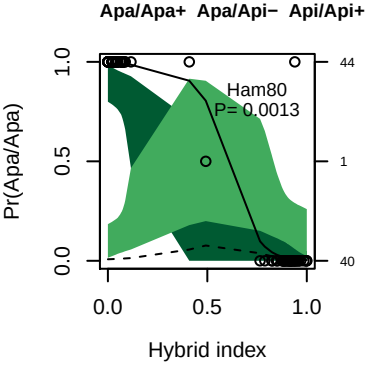


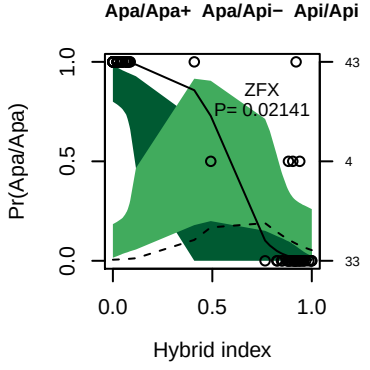












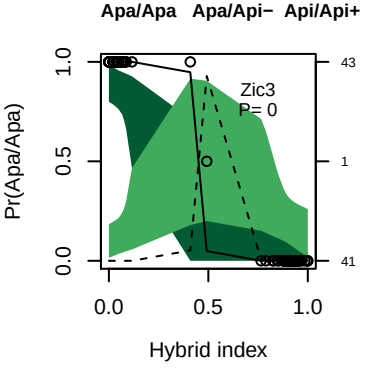


Fig. S2 Individual genomic clines for **(A)** all microsatellite loci based on the full dataset, and **(B)** all microsatellite and X-chromosome loci based on the reduced dataset.

Figure S3

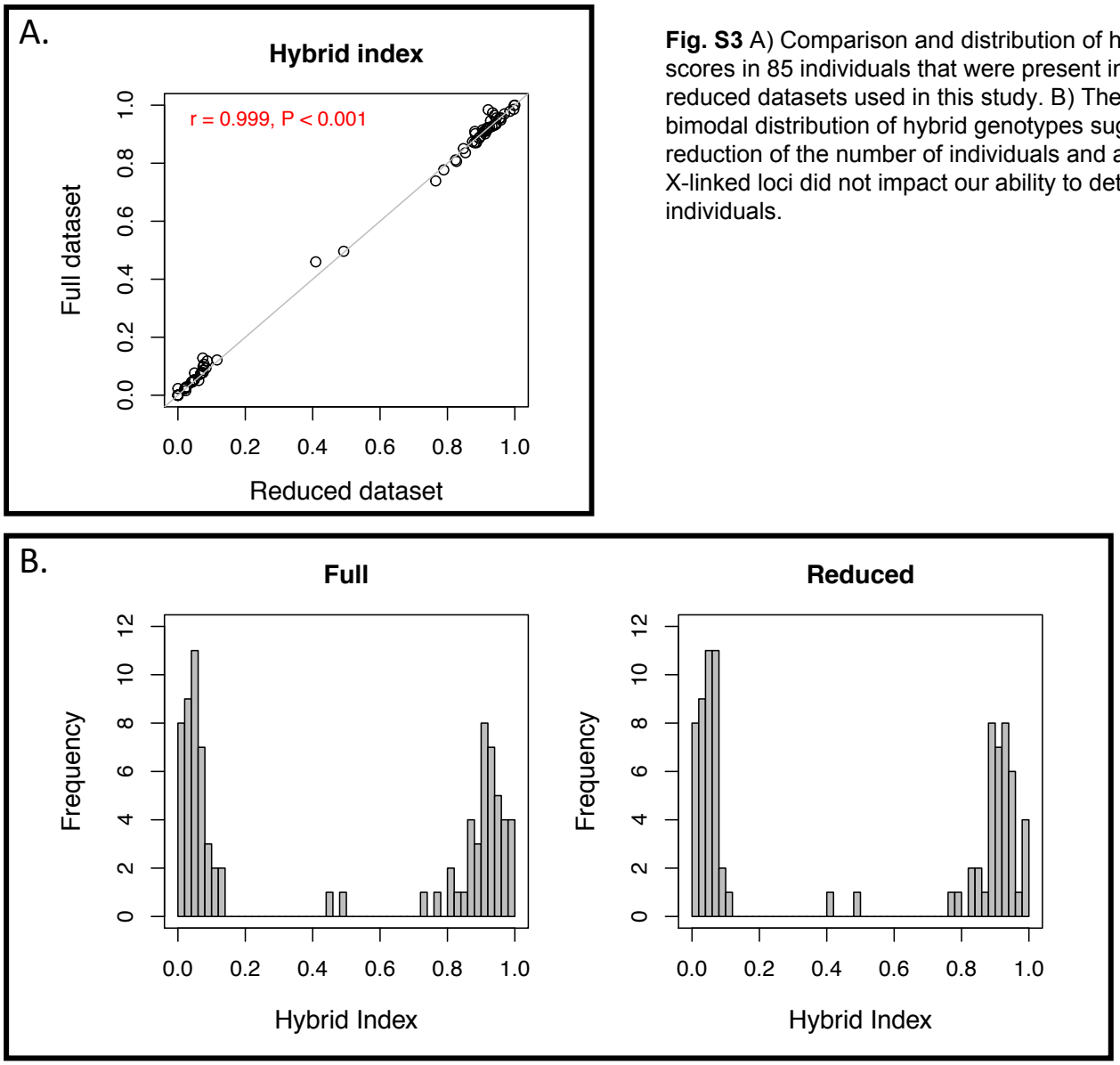


Fig. S3 A) Comparison and distribution of hybrid index (HI) scores in 85 individuals that were present in both full and reduced datasets used in this study. B) The similar bimodal distribution of hybrid genotypes suggests that the reduction of the number of individuals and addition of two X-linked loci did not impact our ability to detect admixed individuals.