

1 **RECRUITMENT OF GROUPE BROODSTOCK ON THE BASIS OF SINGLE**
2 **LOCUS DNA MARKERS**

3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25

Kenneth F. RODRIGUES ^{1*}, Ahmad Z. TANI¹, Syarul N. BAHARUM²

¹*Biotechnology Research Institute, Universiti Malaysia Sabah, Kota Kinabalu, Sabah, Malaysia*

²*Institute of Systems Biology, Universiti Kebangsaan Malaysia, 43600 UKM Bangi, Selangor Malaysia*

*Correspondence: Kenneth Francis Rodrigues, Biotechnology Research Institute, Universiti Malaysia Sabah, 88400, Kota Kinabalu, Sabah, Malaysia. Phone: +6088320000-5599, Fax: +6088320993, e-mail: kennethr@ums.edu.my

26 **Abstract**

27

28 Scientific breeding programs are founded on the screening and recruitment of genetically
29 diverse broodstock, with the ultimate aim of developing heterogeneous breeding populations
30 that host a collection of desirable traits. Single locus DNA markers can be applied to facilitate
31 the process of selection as they are species specific, reliable, reproducible and easy to use.
32 This study set forth to develop a library of single locus DNA markers for two commercially
33 cultured species of groupers, *Epinephelus fuscoguttatus* and *E. corallicola*. DNA was
34 isolated from one representative specimen of each species and utilized to construct shotgun
35 genomic libraries. DNA sequences derived from the library were selected for the
36 development of 42 and 41 single locus DNA markers for *E. fuscoguttatus* and *E. corallicola*
37 respectively. The markers were then tested against randomly selected specimens obtained
38 from the wild. Genotyping results revealed that the species specific primers demonstrated the
39 ability to distinguish between individuals from the same species into distinct operational
40 taxonomic units (OTUs) on the basis of their differential DNA profiles, thus establishing a
41 basis for selection based on genetic heterogeneity. The findings of this study present a strong
42 case for the application of single locus DNA markers as molecular tools for the selection of
43 broodstock on the basis of genotyping.

44

45

46

47

48

49

50 **Keywords:** Grouper, *Epinephelus fuscoguttatus*, *E. corallicola*, Single locus DNA markers.

51 1.0 INTRODUCTION

52 The economic success of the aquaculture industry is founded on the selection and recruitment
53 of high quality broodstock from genetically diverse wild populations. However, the process
54 of selection of wild specimens is confounded by phenotypical similarity and paucity of
55 genetic information. Genomic molecular markers [1] have the potential to revolutionize the
56 aquaculture industry when applied in conjunction with conventional breeding techniques [2].
57 This has formed the basis for approaches that recruit broodstock and seed on the basis of data
58 obtained from Quantitative Trait Loci (QTLs) [3] and Marker Assisted Selection (MAS) [4].
59 These two molecular approaches can have a significant impact on the economics of a fish
60 breeding operation as they offer an avenue for the elimination of genetically inferior
61 germplasm prior to recruitment. Scientists have initiated the process of marker development
62 for finfish by focusing on several commercially exploited species such as *Oreochromis*
63 *niloticus* [5], *Ictalurus punctatus* [6], *Salmo salar* [7] and *Cyprinus carpio* [8]. They have
64 relied on an assortment of molecular markers such as microsatellites [9], Single Nucleotide
65 Polymorphisms (SNPs) [10], Amplified Fragment Length Polymorphisms [11] and Short
66 Sequence Repeats [12] in order to detect genetic polymorphisms that can be exploited by
67 breeders. The practical application of molecular markers to breeding has been discussed in
68 detail [13] and it is interesting to note that highly informative markers such as microsatellites
69 and SNPs require specialized laboratories and analytical techniques, thus putting them
70 beyond the technological reach of commercial breeders. Single locus DNA markers [14] are
71 less informative than microsatellites and SNPs, however they make up for this shortcoming
72 by their simplicity, reproducibility and ability to distinguish individuals within a population.
73 This study set forth to develop single locus DNA markers could be applied for the selection
74 of broodstock purely on the basis of Boolean DNA profiling. The groupers *E. fuscoguttatus*

75 and *E. corallicola* were selected as the target species as they are commercially exploited by
76 the aquaculture industry.

77

78 **2.0 MATERIAL AND METHODS**

79 2.1 Sample collection and DNA isolation

80 The samples for this study were all collected from broodstock being maintained at the Borneo
81 Marine Research Institute, Universiti Malaysia Sabah. DNA was extracted from Fin clips
82 collected from *E. fuscoguttatus* (12) and *E. corallicola* (10) using the DNeasy extraction kit
83 (Qiagen), the concentration of DNA was assessed using a micro-volume UV-Vis
84 Spectrophotometer (GE Healthcare Life Sciences) and the final concentration was adjusted to
85 50 ng/μl using sterile nuclease free water. DNA samples were stored at -80° C.

86

87 2.2 Construction of genomic libraries

88 Partial small insert genomic libraries [15] were constructed using one DNA sample derived
89 from each of the two species of groupers, *E. fuscoguttatus* and *E. corallicola*. Restriction
90 digests were carried out using a combination of six restriction enzymes, *EcoRI/HindIII*,
91 *EcoRI/BamHI*, *BamHI/HindIII*, *KpnI/SalI*, *SacI/KpnI* and *SacI/XbaI*. (New England Biolabs),
92 following which the digested DNA was ligated onto a pUC19 Vector and transformed into
93 chemically competent *Escherichia coli* (TOP10). Recombinant clones from each library were
94 selected randomly from Luria–Bertani plates containing Ampicillin (100 mg/l) and X-Gal (50
95 mg/l). Plasmid DNA were extracted and purified using GeneJET plasmid purification kit
96 (Fermentas) and sequenced using BigDye Terminator 2.0 Cycle Sequencing Ready Reaction
97 Kit (Life Technologies, USA) on an ABI Prism 3770 automated DNA sequencer (Applied
98 Biosystems). Sequences were deposited at the NCBI GenBank and assigned accession
99 numbers (Tables 1.0 and 3.0).

100

101 2.3 Primer design

102 One pair of primers was designed per individual DNA sequence using the online Primer3
103 software [16]. The annealing temperature was set (T_a) at 60 °C and regions with potential
104 secondary structures, high G: C ratio and runs of a single nucleotide, were excluded. PCR
105 grade primers were synthesized (IDT Technologies, Singapore).

106

107 2.4 Genotyping

108 PCR amplification was performed in final volume of 20 μ l containing 1.2 μ l $MgCl_2$
109 (1.5mM), 0.4 μ l dNTPs (0.2mM each), 4 μ l 1x *GoTaq* buffer (Promega), 1 U *Taq* DNA
110 polymerase (Promega), 1 μ l of each primer (5 μ M), 2 μ l template DNA and nuclease free
111 water. Amplification was performed using a thermal cycler (MJ research, PTC-200) under
112 the following conditions: pre-denaturation at 95°C for 3 min, followed by 30 cycles of
113 denaturation (30 sec at 95°C), annealing (40 sec at 58°C), extension (2 min at 72°C) and final
114 extension (10 min at 72°C). PCR products were resolved by electrophoresis on a 1.5% Tris-
115 Boric Acid EDTA agarose gel, stained with Ethidium bromide and the gel was analyzed
116 using a gel documentation system (Alpha Innotech, San Leandro, CA).

117

118 2.5 Scoring of PCR amplicons and data analysis

119 PCR amplicons were resolved on a 1.5% Tris – Boric Acid – EDTA (TBE) agarose gel,
120 stained in a solution of Ethidium Bromide (50 μ g/ml) for 10 min following which the gels
121 were viewed using a UV transilluminator (Alpha Innotech, USA). Bands were scored as “1”
122 for present and “0” for absent resulting in a binary score matrix. To test the reproducibility of
123 the amplification pattern the PCR was repeated at least twice. Only unambiguous and clear
124 amplicons were scored and chosen for Jaccard's similarity coefficient analysis. The UPGMA

125 phenogram was constructed using the online software DendroUPGMA
126 (<http://genomes.urv.cat/UPGMA/>) [17]. Distance and Similarity matrices were computed
127 based on the Dice Coefficient with 100 replicates. Operational Taxonomic Units (OTUs)
128 were determined on the basis of the Cophenetic Correlation Coefficient (CPCC) [18] and
129 phenograms were rendered graphically using the online software PhyloWidget
130 (<http://www.phylowidget.org/>) [19].

131

132 **3.0 RESULTS**

133 3.1 Single Locus DNA Markers for *E. fuscoguttatus*

134 Six genomic libraries yielded 341 clones of which 68 were randomly selected for sequencing.
135 Primers were designed to amplify 42 loci (Table 1.0). 37 primers yielded single amplicons
136 whereas the remaining 5 primers (EFJ006, EFJ018, EFP010, EFJAAC2 and EFP003)
137 amplified more than one locus. The total number of polymorphic loci was 21 (Table 2.0). The
138 phenogram of *E. fuscoguttatus* graphically depicts the OTUs (Figure 1.0). The individuals
139 clustered into three major clades. Clade 1 consisted of OTUs EF001, EF006, EF008, EF005,
140 EF004 and EF010. Clade 2 consisted of OTUs EF002, EF009, EF03X, EF02X and EF003
141 and Clade 3 contained one OTU EF007. Within clade 1, OTUs EF001 and EF006 were
142 grouped together with a similarity of 96%. Both of these OTUs were connected to 4 nodes
143 containing 4 different OTUs namely; EF008, EF005, EF004 and EF010. OTU EF006
144 indicating highly a higher degree of similarity to two inter-joining nodes containing OTUs
145 EF008 and EF005 with a similarity of 96% and 95% respectively. OTU EF005 was highly
146 similar to OTU EF004 with 93% similarity. Within clade 2, OTUs EF009 and EF03X
147 clustered with a similarity of 97%. Both OTUs were connected with three other nodes. OTU
148 EF009 was 95% similar to OTUs EF02X, EF002 and EF003. Clade 3 was represented by
149 only one individual OTU EGF007.

150

151 3.2 Single Locus DNA Markers for *E. corallicola*

152 Six genomic libraries yielded 220 clones of which 52 were randomly selected for sequencing.

153 Primers were designed to amplify 41 loci (Table 3.0) which yielded single amplicons (Table

154 4.0). The phenogram of *E. corallicola* graphically depicts the OTUs (Figure 2.0). The

155 phenogram depicts three major clades. Clade 1 was composed of OTUs CC001, CC009,

156 CC006 and CC008. Clade 2 comprised OTUs CC003, CC004, CC002, CC010, CC007 and

157 CC005. In clade 1, OTUs CC001 and CC009 exhibited 81% similarity. Both OTUs were

158 linked to another set of 2 nodes containing 2 different OTUs namely; CC006 and CC008.

159

160 **4.0 DISCUSSION**

161 4.1 Single Locus DNA Markers for *E. fuscoguttatus*

162 The tiger grouper, *E. fuscoguttatus* is highly sought after by fish breeders as it adapts well to

163 commercial aquaculture and mariculture systems. The genetic profile indicated a high degree

164 of similarity with 31 primers amplifying consistently across the 12 samples and 15 primers

165 exhibiting differential profiles. This implies that the breeding population is not as genetically

166 diverse as compared to *E. corallicola* and may require the acquisition and screening of

167 additional recruits from the wild. Earlier reports [20] based on genotyping using

168 microsatellites have arrived at similar conclusions regarding the abundance and diversity of

169 wild populations of *E. fuscoguttatus*. Single locus DNA markers can be tested for Mendelian

170 inheritance and applied for marker assisted selection of intraspecific grouper hybrids.

171

172 4.2 Single Locus DNA Markers for *E. corallicola*

173 These are the first reported genomic molecular markers for *E. corallicola*. The amplification

174 profiles revealed a high level of intraspecific genetic diversity as the ten individuals tested

175 exhibited unique genetic fingerprints implying that the wild population is genetically diverse.
176 A similar study conducted using microsatellites in a closely related species *Plectropomus*
177 *maculatus* led to the discovery of highly polymorphic loci which have potential applications
178 in broodstock management [21]. Single locus DNA markers can be applied to develop
179 linkage maps as in the case of *E. aeneus* where 222 microsatellite loci were utilized to
180 construct a linkage map representing 24 chromosomes [22]. Advances in next generation
181 DNA sequencing technologies have led to the development of novel markers such as SNPs as
182 reported in *E. coioides* [23] and microsatellites with intra specific applications [24]. The
183 development of a database of markers is essential for the development of management
184 strategies, however markers which require extensive technical expertise and complex analysis
185 will not be relevant to aquaculture as there is no cost benefit advantage. Under these
186 circumstances single locus markers offer an economical alternative to SNPs.

187

188

189 4.3 Implications for broodstock management

190 Grouper breeders rely on wild germplasm in order to develop inbred lines. The selection of
191 seed is done on a random basis and not on the basis of genetic diversity. There are two
192 primary reasons for this, the first is the lack of suitable species specific markers for genetic
193 profiling and the second is the lack of technical expertise to interpret the data derived from
194 highly informative microsatellite DNA loci and SNPs. The objective of this study was to
195 develop molecular markers which could be applied for diagnostic testing in a simple
196 laboratory setup comprising a thermal cycler, gel electrophoresis system and imaging systems
197 which are can be accessed by fish breeders. The markers which have been developed can be
198 scored directly purely on the basis of amplification or non-amplification. Previous studies
199 [25] that have attempted to develop molecular markers for groupers have utilized Random

200 Amplified Polymorphic DNA (RAPD) which are difficult to reproduce due to the low degree
201 of species specificity and high number of PCR artefacts. Furthermore, the ability of the
202 markers to resolve intraspecific genetic polymorphism makes them ideal for population
203 diversity studies and the construction of linkage maps for mapping quantitative traits.

204

205

206

207

208 **5.0 Conclusion**

209 This study demonstrated that species specific single locus DNA markers can be applied for
210 the genotyping of groupers recruited from the wild for the purpose of breeding. We
211 developed 42 and 41 novel species specific DNA markers for *E. fuscoguttatus* and *E.*
212 *corallicola* respectively and applied them to resolve intraspecific diversity. These markers
213 will be of assistance to fish breeders during the process of broodstock selection and will
214 facilitate the process of developing genetically diverse breeding populations.

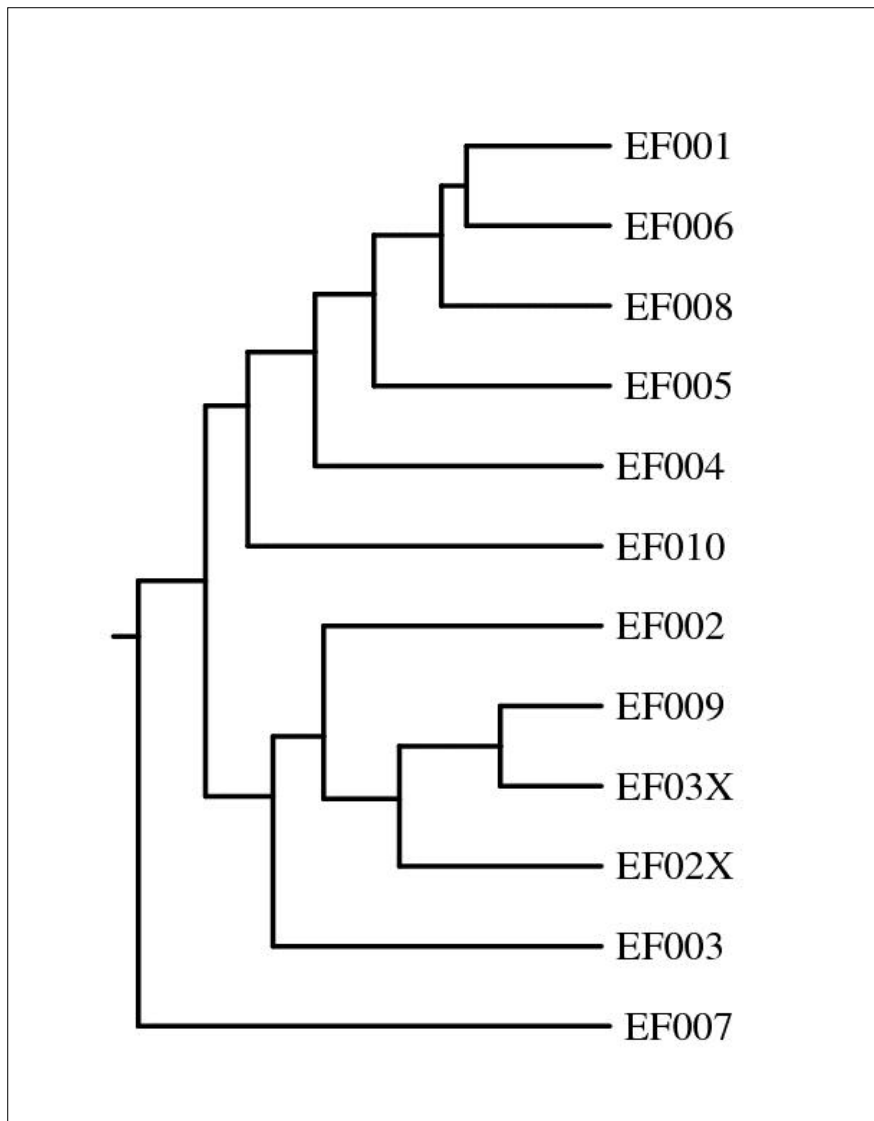
215

216

217 **Acknowledgements**

218 This study was funded by the Ministry of Agriculture, Government of Malaysia, Grant
219 Number SCF-2010-SF1010

220



221

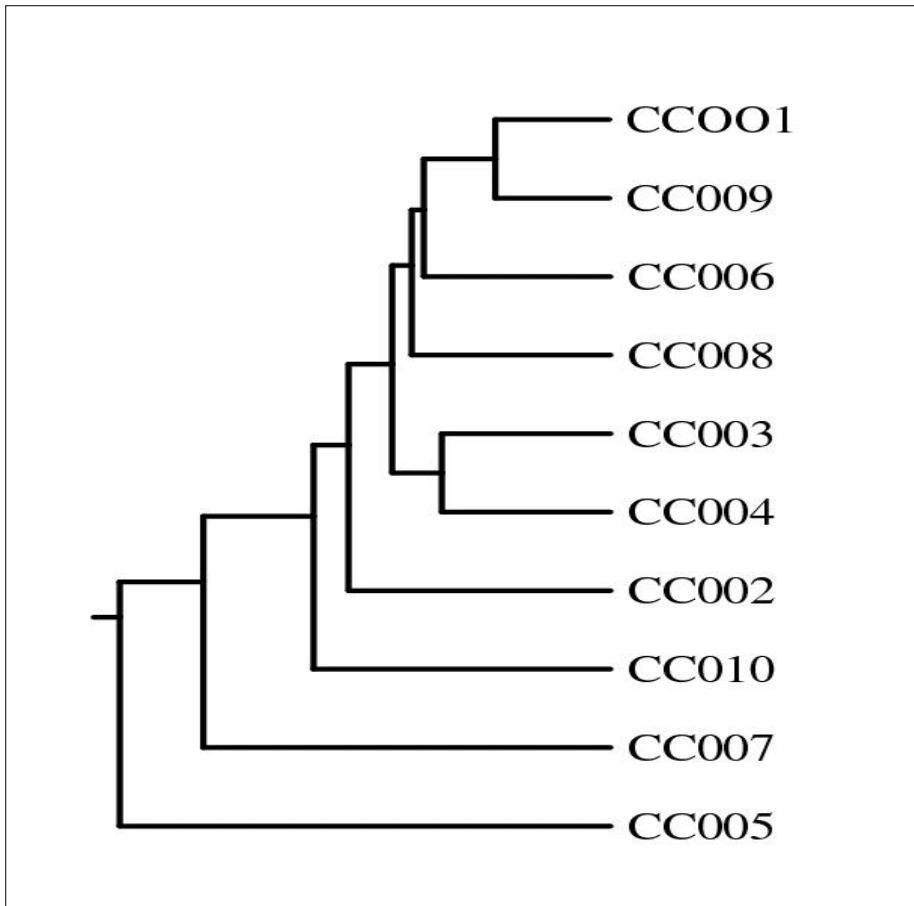
222

223 Fig. 1.0: Phenogram of 12 *E. fuscoguttatus* OTU's resulting from the UPGMA cluster

224 analysis of the OTU x OTU correlation matrix. Cluster 1 comprises EF001, EF006, EF008,

225 EF005, EF004 and EF010. Cluster 2 consists of EF002, EF009, EF003X, EF002X and

226 EF003. Cluster 3 is composed on only one individual EF007.



227

228 Figure 2.0: Phenogram of 10 *E. corallicola* OTU's resulting from the UPGMA cluster
229 analysis of the OTU x OTU correlation matrix. The high degree of intraspecific genetic
230 diversity is evident from the distribution of the nodes.

231

232

233

234

235

236

237

238

239

240 **REFERENCES**

- 241 [1] **Liu, Z. J. and Cordes, J. F.** 2004 DNA marker technologies and their application in
242 aquaculture genetics. *Aquaculture* 238: 1 – 37.
- 243 [2] **Davis, G.P. and Hetzel, D.J.** 2000. Integrating molecular genetic technology with
244 traditional approaches for genetic improvement in aquaculture species. *Aquaculture*
245 *Research*, 31: 3 – 10. (DOI: 10.1046/j.1365-2109.2000.00438.x)
- 246 [3] **Sakamoto, T., Danzmann, R.G., Okamoto, N., Ferguson, M.M. and Ihssen, P.E.**
247 1999. Linkage analysis of quantitative trait loci associated with spawning time in rainbow
248 trout (*Oncorhynchus mykiss*). *Aquaculture*, 173: 33 – 43.
- 249 [4] **Fuji, K., Hasegawa, O., Honda, K., Kumasaka, K., Sakamoto, T. and Okamoto, N.**
250 **2007.** Marker-assisted breeding of a lymphocystis disease-resistant Japanese flounder
251 (*Paralichthys olivaceus*). *Aquaculture*, 272: 291 – 295.
- 252 [5] **Kocher, T.D., Lee, W.J., Sobolewska, H., Penman, D. and McAndrew, B.** 1998. A
253 genetic linkage map of a cichlid fish, the tilapia (*Oreochromis niloticus*). *Genetics*, 148: 1225
254 – 1232.
- 255 [6] **Waldbieser, G.C., Bosworth, B.G., Nonneman, D.J. and Wolters, W.R.** 2001. A
256 microsatellite-based genetic linkage map for channel catfish, *Ictalurus punctatus*. *Genetics*,
257 158: 727 – 734.
- 258 [7] **Gilbey, J., Verspoor, E., McLay, A. and Houlihan, D.** 2004. A microsatellite linkage
259 map for Atlantic salmon (*Salmo salar*). *Animal genetics*, 35: 98 – 105.
- 260 [8] **Sun, X. and Liang, L.** 2004. A genetic linkage map of common carp (*Cyprinus carpio*
261 L.) and mapping of a locus associated with cold tolerance. *Aquaculture*, 238: 165 – 172.
- 262 [9] **Magoulas, A., Bartley, D. and Basurco, B.** 1998. Application of molecular markers to
263 aquaculture and broodstock management with special emphasis on microsatellite DNA.
264 *Cahiers Options Mediterranes*, 34: 153 – 168.

- 265 [10] **Hayes, B., Laerdahl, J.K., Lien, S., Moen, T., Berg, P., Hindar, K., Davidson, W.S.,**
266 **Koop, B.F., Adzhubei, A. and Høyheim, B.** 2007. An extensive resource of single
267 nucleotide polymorphism markers associated with Atlantic salmon (*Salmo salar*) expressed
268 sequences. *Aquaculture*, 265: 82 – 90.
- 269 [11] **Liu, Y.G., Chen, S.L., Li, B.F., Wang, Z.J. and Liu, Z.** 2005. Analysis of genetic
270 variation in selected stocks of hatchery flounder, *Paralichthys olivaceus*, using AFLP
271 markers. *Biochemical systematics and ecology*, 33: 993 – 1005.
- 272 [12] **Maltagliati, F., Lai, T., Casu, M., Valdesalici, S. and Castelli, A.** 2006. Identification
273 of endangered Mediterranean cyprinodontiform fish by means of DNA inter-simple sequence
274 repeats (ISSRs). *Biochemical systematics and ecology*, 34: 626 – 634.
- 275 [13] **Ferguson, M.M. and Danzmann, R.G.** 1998. Role of genetic markers in fisheries and
276 aquaculture: useful tools or stamp collecting? *Canadian Journal of Fisheries and Aquatic*
277 *Sciences*, 55: 1553 – 1563.
- 278 [14] **Karl, S.A. and Avise, J.C.** 1993. PCR-based assays of mendelian polymorphisms from
279 anonymous single-copy nuclear DNA: techniques and applications for population genetics.
280 *Molecular Biology and Evolution*, 10: 342 – 361.
- 281 [15] **Sambrook, J., Fritsch, E.F. and Maniatis, T.** 1989. *Molecular cloning* (Vol. 2, pp. 14-
282 9). New York: Cold spring harbor laboratory press.
- 283 [16] **Rozen, S. and Skaletsky, H.** 1999. Primer3 on the WWW for general users and for
284 biologist programmers. In *Bioinformatics methods and protocols* (pp. 365-386). Humana
285 Press.
- 286 [17] **Garcia-Vallve, S. and Puigbo, P.** 2009. DendroUPGMA: A dendrogram construction
287 utility. *Universitat Rovira i Virgili*.
- 288 [18] **Rohlf, F.J. and Sokal, R.R.** 1962. The description of taxonomic relationships by factor
289 analysis. *Systematic Zoology*, 11: 1 – 16.

- 290 [19] **Jordan, G.E. and Piel, W.H.** 2008. PhyloWidget: web-based visualizations for the tree
291 of life. *Bioinformatics*, 24: 1641 – 1642.
- 292 [20] **Gao, C., Wang, L., Fan, B., Yang, S., Meng, Z. and Lin, H.** 2012. Isolation and
293 Characterization of Microsatellite Markers from the Brown-marbled Grouper, *Epinephelus*
294 *fuscoguttatus*. *Journal of the World Aquaculture Society*, 43: 442 – 446.
- 295 [21] **Zhu, Z.Y., Lo, L.C., Lin, G., Xu, Y.X. and Yue, G.H.** 2005. Isolation and
296 characterization of polymorphic microsatellites from red coral grouper (*Plectropomus*
297 *maculatus*). *Molecular Ecology Notes*, 5: 579 – 581.
- 298 [22] **Dor, L., Shirak, A., Gorshkov, S., Band, M.R., Korol, A., Ronin, Y., Curzon, A.,**
299 **Hulata, G., Seroussi, E. and Ron, M.** 2014. Construction of a microsatellites-based linkage
300 map for the white grouper (*Epinephelus aeneus*). *G3: Genes| Genomes| Genetics*, 4: 1455 –
301 1464.
- 302 [23] **You, X., Shu, L., Li, S., Chen, J., Luo, J., Lu, J., Mu, Q., Bai, J., Xia, Q., Chen, Q. and**
303 **Cai, Y.** 2013. Construction of high-density genetic linkage maps for orange-spotted grouper
304 *Epinephelus coioides* using multiplexed shotgun genotyping. *BMC genetics*, 14: 113.
- 305 [24] **Ramirez, M.A., Patricia-Acevedo, J., Planas, S., Carlin, J.L., Funk, S.M. and**
306 **McMillan, W.** 2006. New microsatellite resources for groupers (Serranidae). *Molecular*
307 *Ecology Notes*, 6: 813 – 817.
- 308 [25] **Govindaraju, G.S. and Jayasankar, P.** 2004. Taxonomic relationship among seven
309 species of groupers (genus *Epinephelus*; family Serranidae) as revealed by RAPD
310 fingerprinting. *Marine Biotechnology*, 6: 229 – 237. (DOI: 10.1007/s10126-003-0021-9)
- 311
- 312
- 313
- 314

315 **Table 1.0:** Molecular markers developed for genotyping of *E. fuscoguttatus* indicating the genomic locus, GenBank accession number, primer
 316 designation, sequences of forward and reverse primers, expected product size and annealing temperatures.

No.	Genomic Locus	GenBank Accession No.	Primer designation	Primer Sequences 5' – 3'	Expected Product Size (bp)	Annealing Temperature Ta (°C)
1	EFJ002A	JN048832	EFJ002F	TTG GGA TGG GGT CTA AGA GA	294	58
			EFJ002R	ACC CCA GGT TTC TTT TCA GC		
2	EFJ005	JN048835	EFJ005F	TTT CGT TGT AGC GCT TGA TG	345	58
			EFJ005R	TGC ACA CTC TTG GCA TTC TC		
3	EFJ006	JN048836	EFJ006F	CGT CTC TCC ACG GGA TAT TT	253	55
			EFJ006R	CCG TGA CAA CTT TGA CCA TC		
4	EFJ016	JN048846	EFJ016F	GGG CAG CAT TAT GTC TCC AT	185	58
			EFJ016R	TGT CTG TCC CTC CCT ACA CC		
5	EFJ018A	JN048848	EFJ018F	CCT GTC TCT GGA AGC CTC AC	157	58
			EFJ018R	CCT GCA ACG TAG TGT GGG TA		
6	EFJ022	JN048852	EFJ022F	ATG TGC CAT GCA ATC TGT GT	332	58
			EFJ022R	ACT GCT GTC CAT CCA TCT CC		
7	EFP007	JN048861	EFP007F	GAA GTA TGG GGG CAA TGA TG	624	58
			EFP007R	TTT TTG TGG GGC TTT GCT AC		
8	EFP009	JN048863	EFP009F	GCT GAG TGA TCT GGC ATC AA	178	58
			EFP009R	ATG CTC CAG AAG ACG AGG AA		
9	EFP010	JN048864	EFP010F	CAT GGC AGC AGA ATA AAC CA	192	58
			EFP010R	CAG GAA GAG GGG AAG AAG TG		

10	EFP013	JN048867	EFP013F	ACG GAC CTC TGG GAG AAA CT	379	59
			EFP013R	GAT GTC CCA GAA AGG CAA AA		
11	EFPHI003	JN159896	EFPHI003F	ACA AGG CCA AAG CAA AGA GA	550	58
			EFPHI003R	GGG TGG AGG AAG AAC ACA AA		
12	EFPHI004	JN159897	EFPHI004F	TTT GTC TCC CTC CCT CAA TG	265	58
			EFPHI004R	GCT AGC ATG ATC CCG ATG TT		
13	EFPHI006	JN159899	EFPHI006F	CTA GCT GTG GCA GAC AGA CG	214	58
			EFPHI006R	AGG GAC ACT GGT TGT GGA AC		
14	EFJAAC2	JN048828	EFJAAC2F	TGT GAA AAT GGG TGA AGT CG	161	58
			EFJAAC2R	GTA TGG CCC TGC AAA GGT AA		
15	EFJCTT1	JN048829	EFJCTT1F	TCC TGC ACA ACT CCA CAG AG	288	58
			EFJCTT1R	CAA GCA TGT CTG CCT TTT GA		
16	EFJ003	JN048833	EFJ003F	TTT GCA GTG TAG GCC AGA TG	340	55
			EFJ003R	GTA AGC AGG GCA AGG AAA AC		
17	EFJ007	JN048837	EFJ007F	AAG ATC GCT GGA GAC CAG AA	288	55
			EFJ007R	AAT CGT CAG TCG CTT CAC CT		
18	EFJ008	JN048838	EFJ008F	GGG GAA GCT CTG TCT GAA AA	173	55
			EFJ008R	TTC ATT CTG TCC CCA GAA CC		
19	EFJ009	JN048839	EFJ009F	GCA AAC TCT GCA CTC ACC AG	203	55
			EFJ009R	TCT GGG ATG CCT ACG TGA AT		
20	EFJ013	JN048843	EFJ013F	GCA CCT TGA GGG AGC TAG TG	244	55
			EFJ013R	GTC AGC AGA AGC CAC TTT CC		
21	EFJ020	JN048850	EFJ020F	TCA GTG ACC CCT GTG TGT GT	372	55
			EFJ020R	GTG CTT GTT TTT GCC ACT GA		

22	EFJ021	JN048851	EFJ021F	GTC ACA ACA CTG GGA ACG TG	476	55
			EFJ021R	GGC AGC CAT GGT TTA TGT CT		
23	EFP003	JN048857	EFP003F	TCA TCT AAT GTG CGC TGC TC	185	55
			EFP003R	TGC TGT TAA TGC GTG AGG AC		
24	EFP005	JN048859	EFP005F	AGA GCG GAG CTT GTT CTC AC	358	55
			EFP005R	GAG TGT GCC TGC ATG AGT GT		
25	EFP006	JN048860	EFP006F	AGC ACG TTT GAG CAG GAG AT	466	55
			EFP006R	CAG GGA GGG TCA AGA TTT CA		
26	EFPHI002	JN159895	EFPHI002F	AGA GGC TGG CTG TGT CAA CT	217	55
			EFPHI002R	AAA CAT CCC ATC AGG CTG TT		
27	EFJAAC1	JN048827	EFJAAC1F	CAT CGT GGT ATG CAC CTC TG	285	55
			EFJAAC1R	TCA AAC AGG TCG TCC ACA AA		
28	EFPHI001	JN159894	EFPHI001BF	GTT CAG ACG TGC TCA GCG TA	189	58
			EFPHI001BR	TTA GTA AAC GCA CGC TGG TG		
29	EFJ014	JN048844	EFJ014AF	ACT GCG ACA TCG TAT CGT GA	119	60
			EFJ014AR	GGC CTT TAC AGC ACT GAG ATG		
30	EFP012	JN048866	EFP012AF	AAT GGC CAG ACT GGT TCA AG	112	62
			EFP012AR	CAA GGT TGG ACG TGT TGT TG		
31	EFEH001	JN944339	EFEH001B1F	AAA GAG CCC GTT CTG TCT CA	111	58
			EFEH001B1R	GGG GGT GTT GAT GCT GTA AA		
32	EFEX002	JN944340	EFEX002YBF	TTG AGT GTG CTT GCT GAT CC	147	62
			EFEX002YBR	ATG CGA GCT CCA GGT AGA AA		
33	EFEX003	JN944342	EFEX003YBF	CCC AAA GTG CTG TTG CAG TA	142	58
			EFEX003YBR	TTC GCC AAG ATC TGG TA GC		

34	EFHX003	JN944347	EFHX003YBF	GGG TTC GCT TGT CAC ACT TT	243	58
			EFHX003YBR	GTG ACC TTT CCT CCA CCA GA		
35	EFXB003	JN944350	EFXB003YBF	GCC TAA TAG CAT GCC AGG TG	244	58
			EFXB003YBR	GCC CAA CAC AGG TCA GAA GT		
36	EFXP001	JN944352	EFXP001YBF	CAA TGG ACT CAG GAC CTG CT	114	60
			EFXP001YBR	ACG GTG GAT AAA CCA AGA CG		
37	EFBP001	JN944336	EFBP001AF	GAC CAA CAC CAA TCC AGT CC	126	55
			EFBP001AR	GAG ACG AGA ACC AGG ACA GC		
38	EFEX001	JN944340	EFEX001AF	CAG CCG ACC AAC ACT CAC TA	344	55
			EFEX001AR	CCT AGT GAC GCG AGG CTA TC		
39	EFEX004	JN944343	EFEX004AF	GGC CCG TGT CTC ACT ATG TT	149	55
			EFEX004AR	TGG GGG AAG ACA ACA CTT TC		
40	EFEX005	JN944344	EFEX005AF	CTT AGG CAG ACG GTG TGT GA	288	55
			EFEX005AR	CTG GGG GAG GTT TTA CGT TT		
41	EFXB001	JN944348	EFXB001AF	CTG CAT GCA CCT GAC AGA CT	182	55
			EFXB001AR	CAG GCA TTT GAT CTG GTC CT		
42	EFXB003	JN944350	EFXB003AF	CCA GAT GGC CTC AAA TCC TA	400	55
			EFXB003AR	TGT GAC TCT GCA GGA ACA GG		

317

318

319

320

321

322

323 Table 2.0: Intra-specific genetic profiling of *E. fuscoguttatus* broodstock collected from the wild. '1' indicates the presence of a PCR amplicon of
 324 the expected product size, '0' indicate the absence of a PCR amplicon. Primers EFJ006, EFJ018, EFP010, EFJAAC2 and EFP003 yielded more
 325 than one PCR amplicon and these were scored separately.

326

No.	Genomic Locus	Observed Product Sizes (bp)	EF02X Control DNA	EF 001	EF 002	EF 003	EF 004	EF 005	EF 006	EF 007	EF 008	EF 009	EF 0010	EF 03X
1	EFJ002	294	1	1	0	0	1	1	1	1	1	1	1	1
2	EFJ005	345	1	1	1	1	1	1	1	1	1	1	1	1
3	EFJ006A	253	1	1	1	0	1	1	1	1	1	1	1	1
3a	EFJ006B	~200	0	1	1	1	1	1	1	1	1	1	1	0
4	EFJ016	185	1	1	1	1	1	1	1	1	1	1	1	1
5	EFJ018A	157	1	1	1	1	0	0	1	1	0	1	1	1
5b	EFJ018B	~180	0	1	0	0	1	1	1	0	1	0	0	0
6	EFJ022	332	1	1	1	1	1	1	1	1	1	1	1	1
7	EFP007	624	1	1	1	0	1	1	1	0	1	1	1	1
8	EFP009	178	1	1	1	1	1	1	1	1	1	1	1	0
9	EFP010A	192	1	1	1	1	1	1	1	1	1	1	1	1
9a	EFP010B	~210	0	1	1	1	1	1	1	1	1	1	1	1
9b	EFP010C	~270	0	1	0	0	0	0	0	0	1	0	1	0
10	EFP013	379	1	1	1	1	1	1	1	1	1	1	1	1
11	EFPHI003	550	1	1	1	1	1	1	1	1	1	1	1	1
12	EFPHI004	265	1	1	1	1	1	1	1	1	1	1	1	1
13	EFPHI006	214	1	1	1	1	1	1	1	1	1	1	1	1
14	EFJAAC2A	161	1	1	1	1	1	0	0	0	0	1	0	1
14a	EFJAAC2B	~180	0	1	0	0	0	1	1	1	1	0	0	0

15	EFJCTT1	288	1	1	1	1	1	1	1	0	1	1	0	1
16	EFJ003	340	1	1	1	1	1	1	1	1	1	1	1	1
17	EFJ007	288	1	0	1	0	0	0	1	1	1	1	0	1
18	EFJ008	173	1	1	1	1	1	1	1	1	1	1	1	1
19	EFJ009	203	1	1	1	1	0	1	1	1	1	1	1	1
20	EFJ013	244	1	1	1	1	1	1	1	1	1	1	1	1
21	EFJ020	372	1	1	1	1	1	1	1	0	1	1	1	1
22	EFJ021	476	1	1	1	1	1	1	1	0	1	1	1	1
23	EFP003A	185	1	1	0	1	0	1	1	1	0	1	0	1
23a	EFP003B	~210	0	1	1	0	0	0	1	0	1	0	1	0
24	EFP005	358	1	0	0	0	0	0	0	0	0	0	0	0
25	EFP006	466	1	0	1	0	0	1	0	0	0	0	0	0
26	EFPHI002	217	1	1	1	1	1	1	1	1	1	1	1	1
27	EFJAAC1	285	1	1	1	1	1	1	1	1	1	1	1	1
28	EFPHI001	189	1	1	1	1	1	1	1	1	1	1	1	1
29	EFJ014	119	1	1	1	1	1	1	1	1	1	1	1	1
30	EFP012	112	1	1	1	1	1	1	1	1	1	1	1	1
31	EFEH001	111	1	1	1	1	1	1	1	1	1	1	1	1
32	EFEX002	147	1	1	1	1	1	1	1	1	1	1	1	1
33	EFEX003	142	1	1	1	1	1	1	1	1	1	1	1	1
34	EFHX003	243	1	1	1	1	1	1	1	1	1	1	1	1
35	EFXB003	244	1	1	1	1	1	1	1	1	1	1	1	1
36	EFXP001	114	1	1	1	1	1	1	1	1	1	1	1	1
37	EFBP001	126	1	1	1	1	1	1	1	1	1	1	1	1
38	EFEX001	344	1	1	1	1	1	1	1	1	1	1	1	1
39	EFEX004	149	1	1	1	1	1	1	1	1	1	1	1	1
40	EFEX005	288	1	1	1	1	1	1	1	1	1	1	1	1
41	EFXB001	182	1	1	1	1	1	1	1	1	1	1	1	1
42	EFXB003	400	1	1	1	1	1	1	1	1	1	1	1	1
		TOTAL	15/21	18/21	15/21	11/21	12/21	15/21	17/21	11/21	16/21	15/21	13/21	13/21

	Similarity	%	71	86	71	52	57	71	81	52	76	71	62	62

327 Table 3.0: Molecular markers developed for genotyping of *E. corallicola* indicating the genomic locus, GenBank accession number, primer
328 designation, sequences of forward and reverse primers, expected product size and annealing temperatures.

NO	Genomic Locus	GenBank Accession No.	Primer designation	Primer Sequences 5' – 3'	Expected Product Size (bp)	Annealing Temperature Ta (°C)
1	CCBP001	JX684019	CCBP001AF	GGT GTG AGA TGG GCT ACC AG	144	58
			CCBP001AR	TTG CCT CAC AGA GTT TGC AC		
2	CCBP002	JX684020	CCBP002AF	TCA TTC TTC CCT GGA AGA GG	178	58
			CCBP002AR	CTG TTG AGC GTG TGT GTG TG		
3	CCBP003	JX684021	CCBP003AF	TAG GCG TTC CCT GTG ATT GT	159	58
			CCBP003AR	GCC CAA TAG CCA CAT GAA CT		
4	CCBP004	JX684022	CCBP004AF	AAG ACG TGA TCC CTG TGG AC	155	58
			CCBP004AR	TGG AGG CTG TTG AAA GAG GT		
5	CCBP005	JX684023	CCBP005AF	TAA AGC CAC GTG AGT GTT CG	252	58
			CCBP005AR	AGC GCC TAG CTC TAT GGT CA		
6	CCBP006	JX684024	CCBP006AF	TAG CAA GGC AAG GCC TCT AA	264	58
			CCBP006AR	CGG TCA AAC ACA CAC AGG AC		
7	CCBP007	JX684025	CCBP007AF	GTG GTC TCG TGG GTG TTG TT	202	58
			CCBP007AR	AGC CAG TCT CAG CAG AGG AA		
8	CCBP008	JX684026	CCBP008AF	GGT TGC CAA AGA AAC TGC TC	213	58
			CCBP008AR	TCC TCC AGG TCT TGC TCT GT		

9	CCBP009	JX684027	CCBP009AF	GAG AAG GGT TCA TTG GTG GA	242	58
			CCBP009AR	ACG GCC AGT TTA ATG TCA GC		
10	CCBH001	JX684028	CCBH001AF	GGA CAC AGC CAG GTT TCA GT	225	58
			CCBH001AR	CCC CCG ACC ACC TAA ATT AT		
11	CCBH002	JX684029	CCBH002AF	TCC CTG CCT CTC TGT TCA CT	272	58
			CCBH002AR	CAT TTC CCC CTC CTT CTC TC		
12	CCBH003	JX684030	CCBH003AF	GGG ACA GGT GAG GCT AAC AT	234	58
		31323334	CCBH003AR	CAG GGT CAG TTC ACC GTT TT		
13	CCBH008	JX684035	CCBH008AF	CCA CAA AGA AAA GCC TGG AC	288	58
			CCBH008AR	GTA ACA CTC GCC ACA CAT CG		
14	CCBH009	JX684036	CCBH009AF	ACC GTG TCC ATC CCT TTA TG	249	58
			CCBH009AR	GCT TCA CAA TGA GCC ACA GA		
15	CCBH010	JX684037	CCBH010AF	CCC TAT TGG CCT CAC TTT CA	291	58
			CCBH010AR	ACT TCC GTT GTC CCA CTG TC		
16	CCBH011	JX684038	CCBH011AF	CCA GTG CCC AAA CCT AGA AG	228	58
			CCBH011AR	TGG TCT CCA GAG CTG AGG TT		
17	CCBH012	JX684039	CCBH012AF	GAC ATG GTC ACA CCA ACA GC	210	58
			CCBH012AR	GGC GAA CTT ATT GGA CCG TA		
18	CCBH013	JX684040	CCBH013AF	CTG GCT CCC TGT AAA ATC CA	276	58
			CCBH013AR	GGA GAG CCC TGA TAG CTG AA		
19	CCBH014	JX684041	CCBH014AF	CTT TCC TTA CAG GCC CAT CA	114	58
			CCBH014AR	GTG CCC CAC CAT CAA ATA TC		
20	CCBH015	JX684042	CCBH015AF	CAA AAA CCG CTA GAG GTC CA	245	58
			CCBH015AR	AAC CAG GAT CTC GAT TGC AG		

21	CCBS001	JX684044	CCBS001AF	GAC GTC AGC ACT CGG AAG TT	204	58
			CCBS001AR	CGA GAG TCC CAT TCC GAC TA		
22	CCBS002	JX684044	CCBS002AF	GAC GGA GCA GTG AGT GAC AA	344	58
			CCBS002AR	GCG TGT TTC CAT CCA CTA CA		
23	CCBS004	JX684046	CCBS004AF	TGG TTC TTC CCA TAG GCA AC	312	58
			CCBS004AR	CGG GAC CAG ATT TTA CGA GA		
24	CCBS005	JX684047	CCBS005AF	GGC TCA AGC GTC AGA TCT TC	209	58
			CCBS005AR	ACT TTC TGT GCA GCA TGT CG		
25	CCEB001	JX684048	CCEB001AF	GTG TGA ACA TGC CCT GAT TG	305	58
			CCEB001AR	CCG ATG TGC TGG AGT ACA GA		
26	CCEB002	JX684049	CCEB002AF	GAA ACA CGA GCA GAG CTG AA	319	58
			CCEB002AR	CGG GTC TCA TCC AAG AGA AA		
27	CCEB003	JX684050	CCEB003AF	TAA GCG AGG GGC ATC TAT TG	214	58
			CCEB003AR	CTG TTT GAT GGG ACA CAT GC		
28	CCEB004	JX684051	CCEB004AF	GCC GAG AGT AAC ACG GAA AA	309	58
			CCEB004AR	GCT AAC ATG GGT GGG ACA TT		
29	CCEB005	JX684052	CCEB005AF	CTC CCT GGC TAG CAC GTT TA	216	58
			CCEB005AR	TTG CTG AGT GGC GTG TAA TC		
30	CCEB006	JX684053	CCEB006AF	AAA GGC TAT GCG AGA CTG GA	225	58
			CCEB006AR	CGC AAG GGT AAA CAG GTG AT		
31	CCEB008	JX684055	CCEB008AF	CAT GCT CCT GAT GTG CCT TA	380	58
			CCEB008AR	TAT GTC AGC CAT GTC CGT GT		
32	CCEH002	JX684057	CCEH002AF	GAG GCG GTT TTG ACT GTG AT	222	58
			CCEH002AR	AAT CGA CCG TCC ACT TTG TC		

33	CCEH003	JX684058	CCEH003AF	GTG GTG TGT GAG GTG ATC CT	338	58
			CCEH003AR	TGA CCG CAC AAA CTA AGC TG		
34	CCEH004	JX684059	CCEH004AF	TGA GTG CTT GGA CTT TGT GC	389	58
			CCEH004AR	GGG CTC TCA ACC TGA ATC AA		
35	CCSP001	JX684060	CCSP001AF	TTT GCT GCC ACA CTT GAG AC	255	58
			CCSP001AR	CCC CAT CAG GCA ATG TTT AG		
36	CCSP004	JX684063	CCSP004AF	ATT TCC AGA CTG GGT GTT GC	284	58
			CCSP004AR	TGG AGC ATA GCT GTC ACC AG		
37	CCSP005	JX684064	CCSP005AF	TAG TTG TTG ACG GGC CTC TT	249	58
			CCSP005AR	CCT GGC CAT TCT TAT CGA TG		
38	CCSP006	JX684065	CCSP006AF	TTC AGC CCG TCT CAG ACT TT	298	58
			CCSP006AR	TCT CCC CTC AGC TTA CAT GG		
39	CCSP007	JX684066	CCSP007AF	ACC AGG AAG CCC AGA AAA T	286	58
			CCSP007AR	GGG AGT GCT TAG CAG AAT CG		
40	CCHX002	JX684067	CCHX002AF	GCT ATG AAC GCA GGT CAA CA	230	58
			CCHX002AR	CCT GCT GTA CGT GTC ATG CT		
41	CCXP001	JX684068	CCXP001AF	ACT GGT GTT CAT CCG TAG CC	252	58
			CCXP001AR	AAG GGG CCA ATT TAG TAC CC		

329

330

331

332

333

334 **Table 4.0:** Intra-specific genetic profiling of *E. corallicola* broodstock collected from the wild. '1' indicates the presence of a PCR amplicon of
 335 the expected product size, '0' indicate the absence of a PCR amplicon.

336

NO	Genomic Locus	Observed Product Size (bp)	CC001 Control	CC 002	CC 003	CC 004	CC 005	CC 006	CC 007	CC 008	CC 009	CC 010
1	CCBP001	144	1	0	1	1	0	1	0	1	0	0
2	CCBP002	178	1	0	1	0	0	1	0	0	0	0
3	CCBP003	159	1	1	1	1	0	1	0	0	1	0
4	CCBP004	155	1	0	1	1	0	1	0	0	1	0
5	CCBP005	252	1	0	0	0	1	0	0	0	0	0
6	CCBP006	264	1	1	0	0	0	1	0	0	1	0
7	CCBP007	202	1	0	0	0	0	1	0	0	1	0
8	CCBP008	213	1	0	1	0	0	0	0	0	1	0
9	CCBP009	242	1	0	1	0	0	0	0	1	1	0
10	CCBH001	225	1	1	1	1	0	0	0	0	0	0
11	CCBH002	272	1	1	0	0	0	1	0	1	1	1
12	CCBH003	234	1	0	1	0	0	0	0	1	1	0
13	CCBH008	288	1	0	0	0	0	0	0	1	0	0
14	CCBH009	249	1	0	0	0	0	1	0	1	1	0
15	CCBH010	291	1	0	0	0	0	0	1	0	0	0

16	CCBH011	228	1	0	1	0	0	1	1	1	1	1
17	CCBH012	210	1	0	1	0	0	0	0	0	1	0
18	CCBH013	276	1	0	1	1	0	0	0	0	1	1
19	CCBH014	114	1	0	1	1	0	1	1	0	1	0
20	CCBH015	245	1	0	0	0	0	0	0	0	1	0
21	CCBS001	204	1	0	0	0	0	1	0	0	1	0
22	CCBS002	344	1	0	0	0	0	1	0	1	0	0
23	CCBS004	312	1	0	0	0	0	0	0	1	0	0
24	CCBS005	209	1	0	0	0	0	0	0	1	1	0
25	CCEB001	305	1	0	0	0	0	0	0	1	1	1
26	CCEB002	319	1	0	0	0	0	0	0	1	0	0
27	CCEB003	214	1	0	0	0	0	1	1	1	1	1
28	CCEB004	309	1	0	1	0	0	1	1	1	1	0
29	CCEB005	216	1	1	1	1	1	1	1	0	1	0
30	CCEB006	225	1	0	0	0	0	0	0	1	1	0
31	CCEB008	380	1	1	1	1	0	1	0	1	1	0
32	CCEH002	222	1	1	1	1	1	1	0	1	1	0
33	CCEH003	338	1	1	1	0	0	0	0	1	1	1
34	CCEH004	389	1	1	1	0	0	0	0	0	0	1
35	CCSP001	255	1	1	1	1	1	1	1	0	1	1
36	CCSP004	284	1	1	1	1	0	1	0	0	1	1
37	CCSP005	249	1	1	1	1	0	1	1	0	1	1
38	CCSP006	298	1	1	1	1	0	1	0	0	0	1
39	CCSP007	286	1	0	0	0	0	0	0	0	1	0

40	CCHX002	230	1	0	0	0	0	1	0	0	0	0
41	CCHXP001	252	1	0	1	0	0	1	0	0	0	0
		TOTAL	41/41	13/41	23/41	13/41	3/41	23/41	8/41	18/41	28/41	11/41
	Similarity	%	100	32	56	32	7	56	20	44	68	27

337

338