

1 **QTL and genetic analysis controlling fiber quality traits using**
2 **paternal backcross population in Upland Cotton**

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4 **Lingling Ma¹, Ying Su¹, Yumei Wang², Hushai Nie¹, Yupeng Cui¹, Cheng**
5 **Cheng¹, Meiyang Wang¹, Jinping Hua^{1,*}**

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7 ¹ Laboratory of Cotton Genetics, Genomics and Breeding /Beijing Key Laboratory of Crop
8 Genetic Improvement /Key Laboratory of Crop Heterosis and Utilization of Ministry of Education,
9 College of Agronomy and Biotechnology, China Agricultural University, Beijing 100193, China

10 ² Institute of Cash Crops, Hubei Academy of Agricultural Sciences, Wuhan 430064, Hubei, China

11

12 * Corresponding author: College of Agronomy and Biotechnology, China Agricultural University,
13 Beijing 100193, China. E-mail: jinping_hua@cau.edu.cn

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15 **ABSTRACT**

16

17 In present study, F₁₄ recombinant inbred line (RIL) population was backcrossed to
18 paternal parent for a paternal backcross (BC/P) population, deriving from one Upland
19 cotton hybrid. Three repetitive BC/P field trials and one BC/M field trial were
20 performed including both two BC populations and the original RIL population. Totally,
21 for fiber quality traits, 24 novel QTLs were detected and 13 QTLs validated previous
22 results. And 19 quantitative trait loci (QTL) in BC/P populations explained 5.01% -
23 22.09% of phenotype variation (PV). Among the 19 QTLs, three QTLs were detected
24 simultaneously in BC/M population. The present study provided novel alleles of male

25 parent for fiber quality traits with positive genetic effects. Particularly, *qFS-Chr3-1*
26 controlling fiber strength explained 22.09% of PV in BC/P population, which
27 increased 0.48 cN/tex for fiber strength. A total of seven, two, eight, two and six
28 QTLs explained over 10.00% of PV for fiber length, fiber uniformity, fiber strength,
29 fiber elongation and fiber micronaire, respectively. In the RIL population, six
30 common QTLs detected in more than one environment such as *qFL-Chr1-2*,
31 *qFS-Chr5-1*, *qFS-Chr9-1*, *qFS-Chr21-1*, *qFM-Chr9-1* and *qFM-Chr9-2*. Two
32 common QTLs of *qFE-Chr2-2* (TMB2386-SWU12343) and *qFM-Chr9-1*
33 (NAU2873-CGR6771) explained 22.42% and 21.91% of PV. In addition, a total of
34 142 and 46 epistatic QTLs and QTL \times environments (E-QTLs and QQEs) were
35 identified in RIL-P and BC/P populations, respectively.

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38 **Keywords: fiber quality traits, common QTL, paternal backcross population,**

39 **Upland cotton**

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42 **INTRODUCTION**

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44 Upland cotton (*Gossypium hirsutum* L.) is one of the most important sources of
45 natural textile fiber. Among four cultivated species, Upland cotton shows higher yield
46 potential and stronger adaptation to diverse environments than Sea island cotton (*G.*
47 *barbadense*), *G. arboreum* and *G. herbaceum*, and accounts for more than 92% of
48 cultivated cotton worldwide (Zhang *et al.* 2015a). But fiber quality of Upland cotton
49 is not as good as that of Sea Island cotton. To meet the diverse demands of textile

50 industry, it is a key target to improve fiber quality in breeding project of Upland
51 cotton.

52 Generally, fiber quality traits consisted of fiber length (FL), fiber uniformity
53 (FU), fiber strength (FS), fiber elongation (FE), and fiber micronaire (FM). Different
54 traits have different genetic mechanisms. Among 4892 QTLs in Cotton QTLdb
55 database (Yu *et al.* 2014), 494, 289, 470, 287 and 395 were detected for FL, FU, FS,
56 FE and FM, respectively (<http://www2.cottonqtl.org:8081/>, CottonQTLdb, newly
57 released V2.3 on January 24, 2018).

58 A total of 151, 132, 91, 118 and 234 QTLs were meta-analyzed for QTL-rich
59 regions for FL, FU, FS, FE and FM, respectively (Said *et al.* 2013). A number of
60 QTLs were located on Chr 5, Chr 19 and Chr 21 (Said *et al.* 2013, 2015). For fiber
61 quality, the most QTLs were detected based on mapping in recombinant inbred lines
62 (RIL) populations of Upland cotton (Wu *et al.* 2009; Sun *et al.* 2012; Ning *et al.* 2014;
63 Tan *et al.* 2014; Shang *et al.* 2015; Tang *et al.* 2015; Zhang *et al.* 2015b; Jamshed *et*
64 *al.* 2016; Li *et al.* 2016). However, RIL population can be only used to dissect
65 additive and additive \times additive effects and not to dissect dominance and
66 dominance-related genetic effects because lacking of heterozygous genotypes.
67 Recently, RIL populations as permanent mapping populations, were used to develop
68 backcross populations in rice (Mei *et al.* 2005) and cotton (Shang *et al.* 2016d), which
69 allows performing repetitive trials as doing in 'immortalized' F₂ population (Hua *et al.*
70 2002, 2003). Seven QTLs controlled fiber length and fiber strength by using
71 backcross population deriving from Guazuncho 2 \times VH8-4602 (Lacape *et al.* 2005).
72 And 44 QTLs for fiber quality traits were detected on Chr 1, Chr 9 and Chr 21 using
73 (CCRI 8 \times Pima 90-53) \times CCRI 8 BC₁F₁ interspecific population (Yang *et al.* 2015).
74 Shang *et al.* (2016d) detected 17, 6, 15, 11 and 21 QTLs for FL, FU, FS, FE and FM,

75 respectively, in F₉ RIL and F₉BC₁ progenies of a hybrid ‘Xinza 1’, While Wang *et al.*
76 (2016) detected 22, 14, 17, 3 and 20 QTLs for the five traits in another two parental
77 F₈BC₁ populations. In Wang’s work (2016), two markers of NAU5530 and CIR099
78 flanking *qFL-c19-2*, *qFU-LG3-1* and *qFS-LG3* were same in Shang’s work (2016d).
79 Using a map of single nucleotide polymorphism (SNP) markers, one fiber length
80 hotspot on Chr 5 carrying three QTLs was observed (Li *et al.* 2016). Additionally,
81 four potential candidate genes for fiber length on Chr Dt7 were found using
82 genotyping by sequencing by genome-wide association studies (GWAS) (Su *et al.*
83 2016). Previous studies indicated that the RIL population and its two BCF₁
84 populations which derived from the same parents increased the power of QTL
85 detection in cotton (Shang *et al.* 2016d; Wang *et al.* 2016). Therefore, it is also
86 available to dissect QTLs for fiber quality using multiple populations at the same time
87 on Upland cotton. Cotton genomes for diploid species (Paterson *et al.* 2012; Wang *et al.*
88 *et al.* 2012; Li *et al.* 2014; Du *et al.* 2018) and tetraploid genomes (Zhang *et al.* 2015; Li
89 *et al.* 2015c; Yuan *et al.* 2015; Liu *et al.* 2015) had been released recently, so as recent
90 genomics researches in cotton (Fang *et al.* 2017a; Wang *et al.* 2018). These genomics
91 analysis in cotton facilitate applications of SNP markers (Ali *et al.* 2018) and GWAS
92 for fiber quality (Fang *et al.* 2017b; Ma *et al.* 2018b). It is very important to detect
93 novel QTLs and to validate the reported QTLs using diverse populations. In our
94 previous study, serial genetic analyses were performed in multiple segregating
95 populations including F₂, F_{2:3}, RIL and BC/M population derived from the hybrid
96 ‘Xinza 1’ across multiple years and various locations (Liang *et al.* 2013; Liang *et al.*
97 2015; Shang *et al.* 2015, 2016a,b,c,d; Ma *et al.* 2017, 2018a, 2019). In previous study,
98 111 quantitative trait loci (QTLs) were detected for fiber quality using four
99 populations derived from RIL (XZ) and backcross (XZV) hybrids (Shang *et al.*

100 2016d). Recently, a total of 55 QTLs were detected which distributed in 21
101 chromosomes using BC/M population in three locations (Ma *et al.* 2017). In addition,
102 32 QTLs at five stages and 24 conditional QTLs at four intervals were detected for
103 plant height in different years or populations or stages (Ma *et al.* 2018a). And 26 and
104 27 QTLs including heterotic loci were identified in TC/P and TC/M populations,
105 respectively (Ma *et al.* 2019). In addition, 10 and 16 clusters improved more than one
106 trait for fiber quality and yield and yield-components, respectively (Ma *et al.* 2017;
107 Ma *et al.* 2019). In order to identify and validate genetic components related fiber
108 quality traits, we further developed BCF₁ progenies population based on RIL
109 population by backcrossing with the paternal parent of ‘Xinza 1’. Here we termed as
110 paternal backcross population (BC/P population for short). We generated additional
111 177 BCF₁ crosses for BC/P populations by backcrossing the 177 RI lines as current
112 female parents to GX100-2 (the original male parent), respectively. Detection of new
113 and novel QTLs and comparison analysis were performed for fiber quality traits using
114 BC/P, BC/M and RIL populations together.

115

116 **MATERIALS AND METHODS**

117

118 **Plant materials and populations development**

119 The intraspecific F₁₄ recombinant inbred lines (RIL) were inbred for 177 individuals,
120 which were derived from an Upland cotton hybrid “Xinza 1” (GX 1135 × GX 100-2)
121 by single seed descent method (Shang *et al.* 2016a). The parental backcross (BC/P)
122 population was obtained by backcrossing the original male parent (GX100-2) to 177
123 RI lines, respectively. The maternal backcross (BC/M) population referred to the
124 previous study (Ma *et al.* 2017; Ma *et al.* 2019). The control set was performed in

125 each experimental trial, including GX100-2, “Xinza 1”, GX1135 and a competition
126 hybrid “Ruiza 816” in Yellow River Region.

127 In present study, we named the maternal and paternal backcross populations as BC/M
128 and BC/P populations for short, respectively, and similarly referred RIL-M population
129 and RIL-P population as RIL population used in BC/M field trials and in BC/P field
130 trials, respectively.

131

132 **Field arrangement, sampling and trait evaluation**

133 Three BC/P field trials and one maternal BC trial were conducted in 2015 and 2016 in
134 two locations in China, E1: Quzhou Experimental Station in Handan City, and E2:
135 Guoxin Seed Company Ltd in Cangzhou City (Ma *et al.* 2017, 2018a, 2019). The field
136 trials were designed and planted same to the previous study for BC field trials (Shang
137 *et al.* 2016a; Ma *et al.* 2017, 2018a, 2019). Field management followed the local
138 conventional standard field practice.

139 Twenty-five naturally opening bolls in the middle of plants were hand-harvested
140 for each plot at mature stage in three environments, respectively. Fiber samples were
141 ginned and sampled for measurements of fiber quality traits with HVI 900 instrument
142 (USTER_ HVISPECTRUM, SPINLAB, USA) at Cotton Fiber Quality Inspection and
143 Test Center of Ministry of Agriculture (Anyang, China) (Shang *et al.* 2016d). The
144 fiber quality traits included 2.5% fiber span length (FL, mm), fiber uniformity
145 (FU, %), fiber strength (FS, cN/tex), fiber elongation (FE), and fiber micronaire (FM)
146 as usual.

147

148 **Genetic Map and Data Analysis**

149 The genetic map based on RIL population published before (Shang *et al.* 2016c), in
150 which a total of 653 loci based on SSR markers distributed on 31 linkage groups and
151 anchored on 26 chromosomes, covering 3889.9 cM (88.20%) of cotton genome with
152 average interval of 6.2 cM (Ma *et al.* 2017, 2018a, 2019). The genotype for each
153 maternal F₁₄BC₁ was deduced on the basis of the RIL genotype used as the parent for
154 backcross (Shang *et al.* 2016a, b, c).

155 Basic statistical analysis was implemented by the software SPSS (Version 19.0,
156 SPSS, Chicago). Using the variance analysis, heritability was calculated in the
157 equation as $h^2 = \delta^2_G / [\delta^2_G + (\delta^2_{G \times E}) / env]$, where δ^2_G and $\delta^2_{G \times E}$ refers to the genotypic
158 variance and genotype-by-environment interaction variance, respectively, and *env* to
159 the number of the environments.

160 Composite interval mapping (CIM) method was used for QTL mapping in the
161 confidence interval of 95%. The software QTL Cartographer (Version 2.5) (Zeng *et al.*
162 1994; Wang *et al.* 2007) was used to map single-locus QTL and to estimate the
163 genetic effect. The threshold of LOD was estimated to declare a suggestive QTL after
164 1000 permutation times, whereas QTL in another environment or population with
165 LOD of at least 2.0 was considered as common QTL (Liang *et al.* 2013; Shang *et al.*
166 2015, 2016d). According to the position linked and shared common markers, QTLs
167 detected in different populations were regarded as common QTL (Shao *et al.* 2014;
168 Shang *et al.* 2016d; Ma *et al.* 2017).

169 The QTL IciMapping 4.1 (www.isbreeding.net) was conducted by the two-locus
170 analysis using inclusive composite interval mapping (ICIM) method (Shang *et al.*
171 2016d; Ma *et al.* 2017).. The main-effect QTL (M-QTL) and its environmental
172 interaction (QTL \times environment, QE), epistatic QTLs (E-QTLs) and its
173 environmental interactions (QTLs \times environment, QQE) were conducted using RIL-P

174 and BC/P datasets under multiple environments in three parental TC trials. A
175 threshold LOD 2.5 and 5 scores were used to declare significant M-QTL and E-QTLs,
176 respectively.

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178

179 **Data availability**

180 All of our raw data are available as Supporting Information Table S6 for
181 phenotype values of fiber quality traits of BC/M population in three field trials in this
182 study, Table S7 for phenotype values of fiber quality traits in field trial of BC/P
183 population in this study, and Supporting Information Table S8A for genotypes of RIL
184 population (Shang *et al.* 2016a), Table S8B for genotypes of BC/M population (Ma *et*
185 *al.* 2017), and Table S8C for genotypes of BC/P population.

186

187

188 **RESULTS**

189

190 **Trait Performance in Two Populations**

191 The ‘original’ maternal parent 'GX1135' of Xinza 1 performed differently with the
192 ‘original’ male parent 'GX100-2' for five fiber quality traits (**Table 1**). The hybrid
193 ‘Xinza 1’ showed no significant hybrid vigor of F_1 for fiber quality traits ranging
194 from -3.17% to 1.53% of mid-parent heterosis (MPH). Among different traits, larger
195 phenotypic variation was observed for fiber length (FL), fiber strength (FS) and fiber
196 micronaire (FM), ranging from 2.63% to 8.53% in both BC and RIL populations; And
197 lighter phenotypic variation presented with 0.87% - 1.23% for fiber uniformity (FU)
198 and fiber elongation (FE) in BC and RIL populations.

199 Genotype variance and environment variance for five traits showed significant
200 variation at level of 0.05 in RIL and BC populations (**Table 2**). Fiber length (FL) and
201 fiber uniformity (FU) increased in BC/P population in comparison with that in BC/M
202 population, whereas fiber micronaire (FM) reduced. Fiber length (FL) and fiber
203 strength (FS) showed larger heritability of 91.82% and 91.10% in RIL-P population,
204 respectively. The heritability decreased to 86.63% and 81.93% for FL and FS in BC/P
205 population, respectively (**Table 2**). The result indicated that wider range of
206 phenotypic variation and bigger heritability in RIL-P population were showed in BC/P
207 population for five fiber quality traits.

208

209 **Correlation Analysis among Fiber Quality Traits in Multiple Populations**

210 The significant correlation coefficients were calculated among five fiber quality traits
211 in BC/P, BC/M, RIL-P and RIL-M populations in 2015E2, 2016E1 and 2016E2
212 (Table 3). Fiber length (FL) correlated significantly and positively with fiber
213 uniformity (FU), fiber strength (FS) and fiber elongation (FE) in these populations
214 except FU in 2016E1. However, fiber micronaire (FM) showed significant negative
215 correlation with FL and FS in the populations. This result was similar to the previous
216 research (Liang et al, 2013; Shang et al, 2016d; Ma et al, 2019).

217 The correlations were similar tendency among BC/P and BC/M populations. In
218 both BC/P and BC/M populations, no significant correlation was showed between FU
219 and FS. However, the majority of correlation values decreased in both BC/P and
220 BC/M populations in comparison with correlation values in RIL population after
221 backcrossing to either of parents.

222

223 **Single Locus QTL Analysis**

224 In four field trials, a total of 37 QTLs controlling fiber quality were detected in three
225 corresponding populations of BC/P, RIL-P, BC/M and RIL-M, explaining 5.01% -
226 22.42% of PV (phenotypic variance) (**Table 4, Figure 1**). These QTLs anchored on
227 17 chromosomes, respectively.

228 For fiber length, six, one and five QTLs were identified in BC/P, BC/M and RIL
229 populations, respectively. The *qFL-Chr5-2* was simultaneously identified in 2015E2
230 and 2016E1, explaining 7.46% and 7.82% of PV, respectively. The *qFL-Chr1-2* was
231 simultaneously detected in 2016E1 and 2016E2, explaining 7.01% and 6.91% of PV,
232 respectively. The *qFL-Chr19-1* explaining 17.98% of PV in BC/P population was
233 verified in RIL population with 11.05% of PV. Among five QTLs detected in RIL
234 population, three QTLs showed additive effects originated from GX1135 alleles
235 whereas three QTLs showed additive effects offered by GX100-2 alleles. Three QTLs
236 *qFL-Chr5-1*, *qFL-Chr5-2* and *qFL-Chr5-3* were distributed on chromosome 5 (Chr 5),
237 and three QTLs *qFL-Chr1-1*, *qFL-Chr1-2* and *qFL-Chr1-3* were distributed on Chr 1.

238 A total of five QTLs were detected for fiber uniformity (FU) explaining 8.76% -
239 11.86% of PV, which distributed on four chromosomes. Four QTLs and one were
240 identified in BC/P and RIL populations, respectively. No common QTL was identified
241 in multiple populations or multiple environments. The *qFU-Chr6-1* increased FU
242 providing alleles by GX1135 in RIL population.

243 For fiber strength (FS), a total of six QTLs were detected on four chromosomes,
244 explaining 6.27% - 22.09% of PV. Two common QTLs were identified. The
245 *qFS-Chr3-1* was detected in BC/P population alone explaining high to 22.09% of PV
246 in 2016E2. The *qFS-Chr3-1* increased 0.48 cN/tex fiber strength in 2016E2. The
247 *qFS-Chr9-1* was simultaneously detected in RIL population in 2016E1 and 2016E2,
248 providing alleles by female parent GX100-2 in both environments. The QTL

249 explained 9.23% of PV in 2016E2 and 11.01% of PV in 2016E1. All of four QTLs
250 provided increasing effect alleles donated by female parent GX100-2 in both
251 environments in RIL population. However, *qFS-Chr9-1* increased 0.46 cN/tex and
252 0.47 cN/tex fiber strength in 2016E1 and 2016E2. The *qFS-Chr21-2* was detected in
253 BC/P, BC/M and RIL populations at the same time across 2016E1 and 2016E2,
254 explaining 6.27% - 13.37% of PV. Four QTLs distributed on A-subgenome of Chr 2,
255 Chr 3, Chr 9 whereas the two remaining QTLs distributed on D-subgenome of Chr 21.

256 Six, two and six QTLs for fiber elongation (FE) were identified in the BC/P,
257 BC/M and RIL populations, respectively. Four common QTLs were detected in at
258 least two populations, including *qFE-chr2-2*, *qFE-chr2-3*, *qFE-chr3-1*, and
259 *qFE-chr21-2*. The *qFE-chr2-3* detected in BC/P population was verified in BC/M and
260 RIL populations, which explained 7.02% of PV on average. The *qFE-chr3-1*
261 explaining 12.17% of PV in BC/P population were also detected in BC/M population
262 in the same environment of 2016E2. The *qFE-Chr2-2* explained 22.42% of PV in RIL
263 population in 2016E1 and was observed in BC/M population in 2016E2. The
264 *qFE-Chr21-2* detected in BC/P population was also identified in RIL population.

265 A total of 5 QTLs underlying fiber micronaire were located on 5 chromosomes.
266 The *qFM-Chr9-2* was identified in BC/M and RIL populations in 2016E2 explaining
267 14.53% and 21.91% of PV, respectively. At the same time, the QTL were detected in
268 three environments of 2015E2, 2016E1 and 2016E2. Another common QTL
269 *qFM-Chr15-1* was simultaneously detected in RIL population in 2016E1 and in BC/M
270 population in 2016E2, explaining 12.36% and 5.46% of PV, respectively. All of six
271 QTLs detected in RIL population increased over 0.10 fiber micronaire value, which
272 donating increasing additive effect alleles by GX1135, containing *qFM-Chr9-1*,
273 *qFM-Chr9-2*, *qFM-Chr12-1*, *qFM-Chr14-1*, *qFM-Chr14-2*, and *qFM-chr15-1*. On

274 summary, 19 QTL explained 10.14-22.09% of PV on average in BC/P population in
275 2015E2, 2016E1 and 2016E2. Among them, a total of eight QTLs explained larger
276 than 10% of PV. Then, we identified 8 QTLs in BC/M population, explained 9.03% of
277 PV on average. At last, 20 QTLs existed in RIL-P and RIL-M populations explaining
278 on average 10.39% of PV in four environments above. Totally, 12 common QTLs
279 were detected in multiple environments or in multiple populations of BC/P, BC/M,
280 RIL-P and RIL-M populations (Table 4, S5).

281

282 **Pleiotropic Effects**

283 We also observed 5 pleiotropic regions controlling at least two fiber quality traits
284 on 2 chromosomes of Chr 9, Chr18 and Chr 21 (Figure 1). Of these, a pleiotropic
285 region flanking with SWU15511- SWU15413 on Chr 9 increased the values for FL
286 and FS, showing increasing additive effects originated from alleles of GX100-2. The
287 NAU2873-CGR6771 on Chr 9 contributed alleles to FS but also increased the FM.
288 The region of SWU0830-HAU2004-CGR5602 contained *qFU-Chr21-1* in BC/P
289 population and *qFE-Chr21-1* in RIL-P population. And SWU0189-CGR5808 on Chr
290 21 flanked along *qFS-Chr21-1*, *qFS-Chr21-2* and *qFE-Chr21-2*, all of which showing
291 increasing additive effects originated from alleles of GX100-2. The region of
292 SWU15511- SWU15413 on Chr 18 controlled fiber length and fiber elongation at the
293 same time.

294

295 **Digenic and Environmental Interactions in Three BC/P Trials**

296 In the three repetitive BC/P trials, a total of 38 and 56 M-QTLs and environmental
297 interactions (QTL \times environment, QE) were identified in BC/P and RIL-P populations,
298 respectively (Table 5, Table S1, S2). Of these, they explained 2.53% - 3.13% and

299 2.63% - 3.41% of PV on average in the populations, respectively. Environmental
300 effect prevailed in both BC/P and RIL-P populations. However, environment and
301 M-QTL interacted with 1.24% of PV in the BC/P population while with 0.90% of PV
302 in RIL-P population.

303 Then, 46 and 142 E-QTLs and their environmental interactions (digenic
304 interactions \times environment, QQE) were respectively identified in BC/P and RIL-P
305 populations, respectively (**Table S3, S4**). Eighteen pairs of E-QTL and QQE
306 explained 4.17% of PV on average in RIL-P population, while nine pairs of E-QTL
307 and QQE explained 2.58% of PV on average in BC/P populations (**Table 5**). On
308 average, the number of both types of M-QTL and E-QTL was larger in RIL
309 populations than that in BC populations. To our surprise, epistatic interactions
310 contributed more to fiber quality than M-QTLs did in RIL-P population.

311 Totally, 20 (42.5%) and 101 (71.13%) pairs of E-QTLs and QQE contained
312 M-QTLs and QEs in BC/P and RIL-P populations, respectively (**Table 6**). We
313 detected about 3-fold epistatic QTLs in RIL populations than QTLs in BC/P
314 population, and 19.01% M-QTLs participated epistasis between M-QTL and M-QTL.
315 Three types of epistasis were checked: I) both loci were M-QTLs; II) either locus
316 between two loci was M-QTL; III) both loci were no M-QTLs (Shang *et al.* 2016d;
317 Ma *et al.* 2019). Apparently, 27 (57.45%) epistatic QTLs of type III was the most
318 popular type in epistatic styles in BC/P population whereas it was 31 (52.11%)
319 epistatic QTLs of type II in RIL-P population (Table 6). The results indicated that
320 epistasis played more vital role in improving fiber quality both in RIL populations of
321 Upland cotton. The result was consistent to the previous result that epistatic QTLs
322 with significant additive \times additive effects were identified for fiber quality traits
323 (Wang *et al.* 2017; Ma *et al.*, 2019).

324

325

326 **DISCUSSION**

327 In present study, the paternal BC (BC/P) population was constructed to explore the
328 genetic mechanism for fiber quality, following the maternal BC (BC/M) population
329 (Shang *et al.* 2016d; Ma *et al.* 2017, 2019). The backcross design has the obvious
330 advantages: (I) dissecting the genetic components between paternal and maternal
331 backcross populations; (II) identifying more new and novel QTLs for important traits
332 using multiple corresponding populations (BC/P, BC/M and RIL) originated from the
333 same hybrid; and (III) allowing to generate enough hybrid seeds when needed, similar
334 to IF₂ population.

335 Here, we detected 19 and 8 QTLs alone in BC/P and BC/M populations,
336 respectively. Three QTLs for fiber strength and fiber elongation shared in both BC
337 populations, including *qFS-Chr21-2*, *qFE-Chr2-3* and *qFE-Chr3-1*. The result
338 indicated that remaining elite alleles (84.21%) showed increasing additive effects
339 originated from male parent for fiber quality in BC/P population. Therefore, the
340 present study was significant for separating the novel elite alleles of male parent for
341 fiber quality.

342 The identification of stable QTLs (including common QTLs) across multiple
343 environments and multiple populations plays an essential role in marker-assisted
344 selection (MAS) (Jamshed *et al.* 2016). In present study, a total of 12 common QTLs
345 were simultaneously identified in more than one environment(s) or population(s)
346 (**Table 4**). They distributed on Chr 1, Chr 2, Chr 3, Chr 5, Chr 9, Chr 15, Chr 19 and
347 Chr 21. In present study, a total of 13 single locus QTLs (35.14%) for fiber quality
348 were common in comparison with the previous studies in multiple years and multiple

349 locations see Table S5 (Shang *et al.* 2016d; Ma *et al.* 2017). The QTLs verified each
350 other in the RIL population and its BC progenies, suggesting that it is reasonable and
351 effective to map QTLs using different populations across multiple environments and
352 multiple years. The experiment design and the continuous study in our lab contributed
353 to these results in the present study. Among these 13 QTLs, 10 QTLs explained larger
354 than 10% of PV. Five QTLs were identified in Shang *et al.*' results (2016d) and Ma *et*
355 *al.*' results (2017), including *qFL-Chr5-1*, *qFL-Chr5-2*, *qFL-Chr5-3*, *qFS-Chr21-1*
356 *and qFE-Chr2-1* (Table S5). For example, region of NAU4034- SWU17713 flanking
357 with *qFL-chr5-1* explained 12.31% of PV on average across 2012 and 2015 in
358 multiple locations. The QTL increased 0.31 mm fiber length (FL) on average,
359 suggesting the major roles and important regions for FL. These verified QTLs were
360 valuable for follow-up breeding program, so as to facilitate fine mapping and
361 favorable gene pyramiding project (Shao *et al.* 2014).

362 The epistatic effects and environmental interactions existed commonly for fiber
363 quality traits as well as other traits. At two-locus level, we detected a number of
364 interactions under environments for fiber quality traits in both populations (**Table 5**).
365 Three types of epistasis combinations were observed (**Table 6**). However, epistasis
366 QTLs influenced fiber quality by Type III (57.45%) in BC/P population. Differently,
367 epistasis influenced fiber quality by Type I and Type II (71.13%) in RIL population.
368 In addition, 3-fold epistasis QTLs was detected in RIL-P population than that in BC/P
369 population. The results indicating that epistasis played roles in different genetic mode
370 to control fiber quality. Especially, no E-QTL was identified for fiber uniformity (FU).
371 Another interesting result detected that epistasis is another vital genetic effect
372 affecting fiber quality traits (Shang *et al.* 2016d). Similarly to the previous study,

373 Wang *et al.* (2006) indicated that both epistasis effect and single-locus effect of QTLs
374 played important genetic roles in cotton fiber quality.

375 In the present study, the five QTLs increased fiber micronaire (FM) values from
376 0.06-0.18 (**Table 4**). The mean values ranged from 4.71-5.18 on average in the RIL-P
377 and BC/P populations of Xinza 1. In fact, fiber quality ranks from B grade (3.5-3.6,
378 4.3-4.9) to C grade (<3.4, >5.0) for fiber micronaire, in which the fiber change larger
379 thickness to be worse. At the same time, FM displayed negative correlation with FL,
380 FU, FS and FE. Therefore, we should avoid exploiting these QTL regions for FM
381 when breeding in cotton. Therefore, we will not focus on the region of
382 NAU2873-CGR6771 on Chr 9, contributing alleles to FS and increased the FM values.
383 At the same time, larger lint yield and well fiber quality are the key aims in cotton
384 breeding program. However, negative correlation between yield and fiber quality
385 hinders the cotton breeding (Yang *et al.* 2015). Many important heterotic loci were
386 detected to increase yield or yield-components in previous studies in our lab (Shang *et*
387 *al.* 2016a; Ma *et al.* 2019). Some heterotic loci were also identified for improving
388 fiber quality in present and previous studies (Shang *et al.* 2016d; Ma *et al.* 2017). The
389 important pleiotropic regions should be paying more attention in further research so as
390 to improve fiber quality and to increase yield in breeding program.

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394 **AUTHOR CONTRIBUTIONS**

395 LM performed the experiments, analyzed the data and prepared the manuscript. YW maintained
396 the experimental platform and attended bench work. YS, HN, YC, CC and MW attended field
397 experiments and data collection. JH conceived the experiments, provided experimental platform
398 and revised the manuscript.

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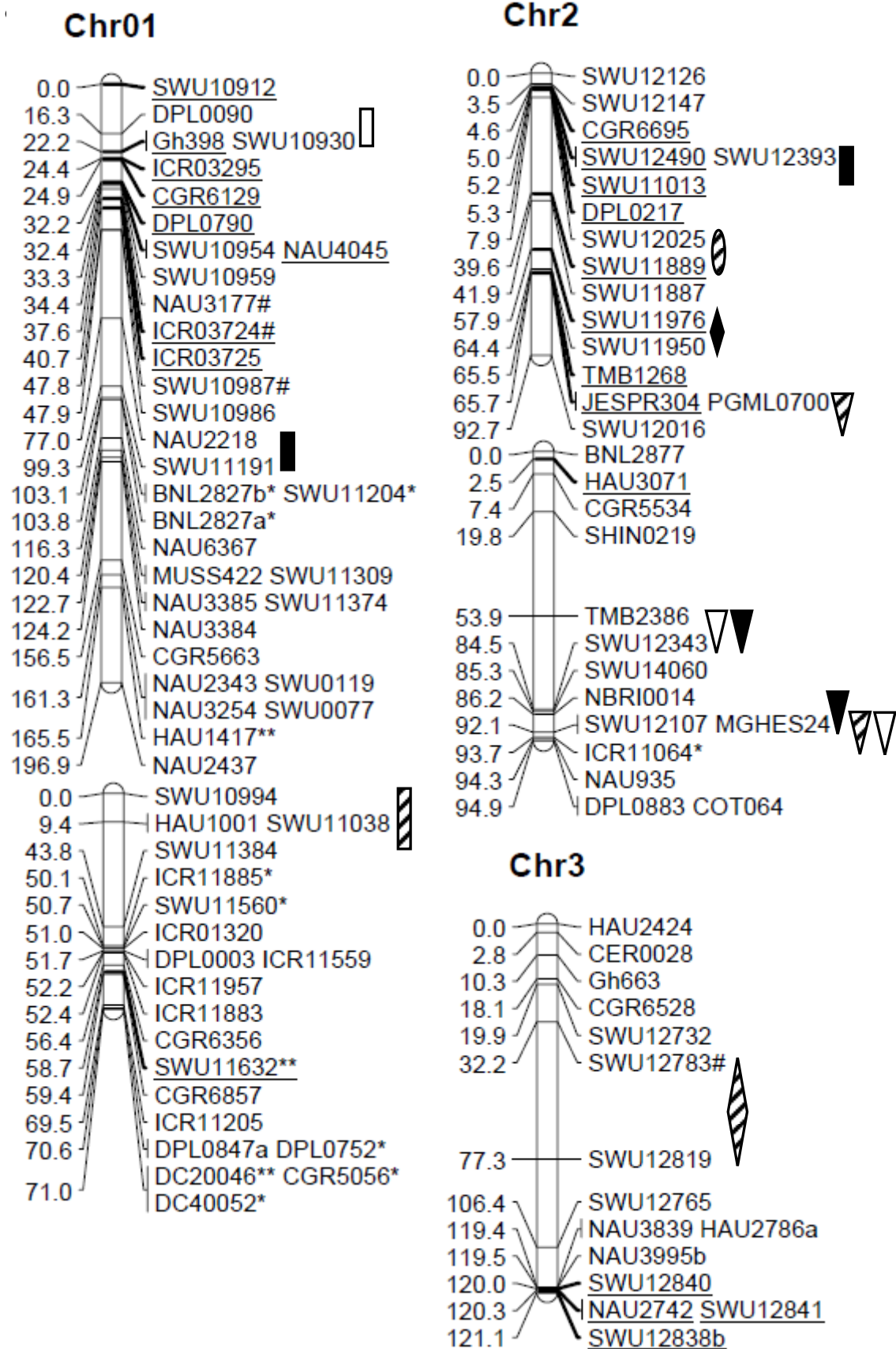
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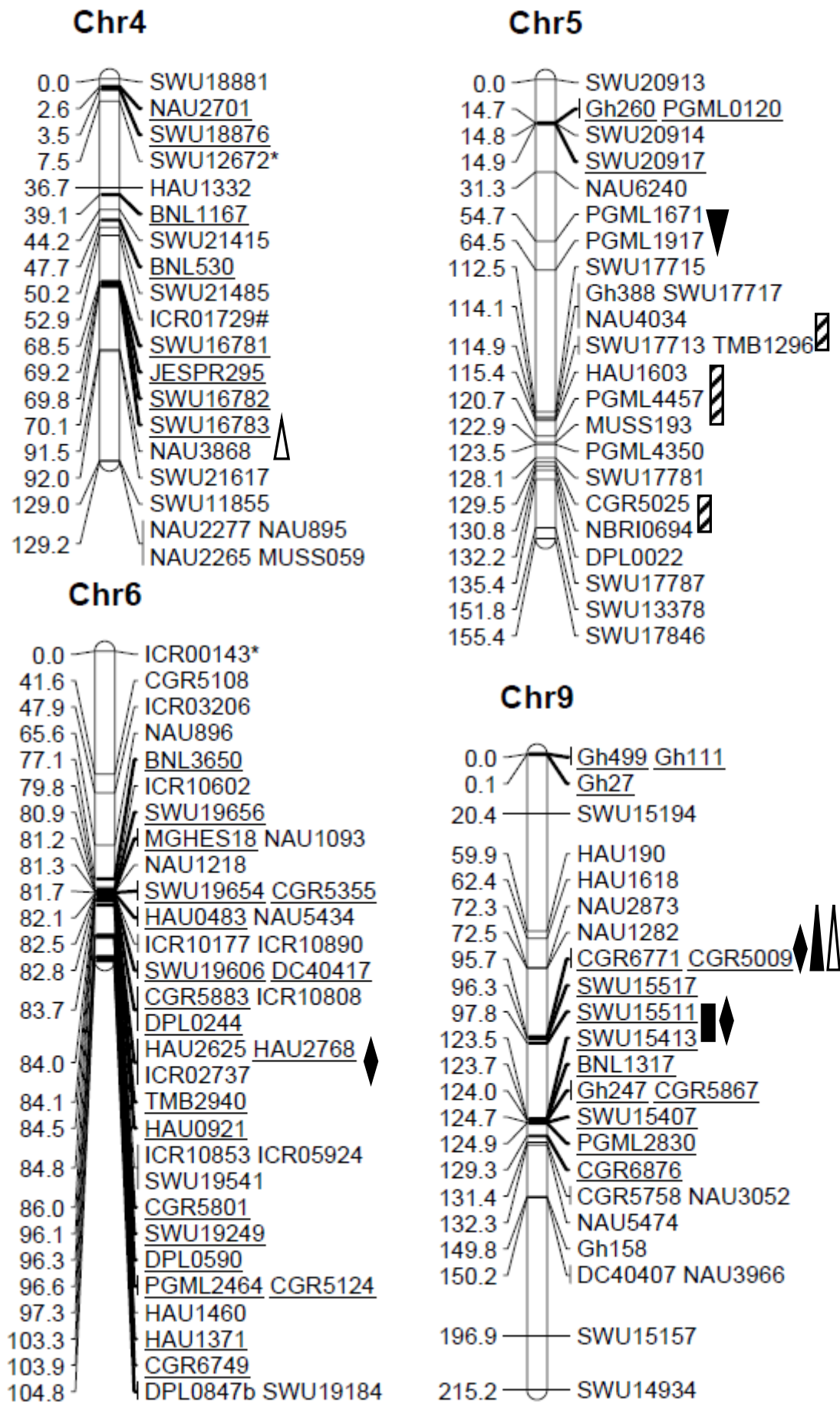
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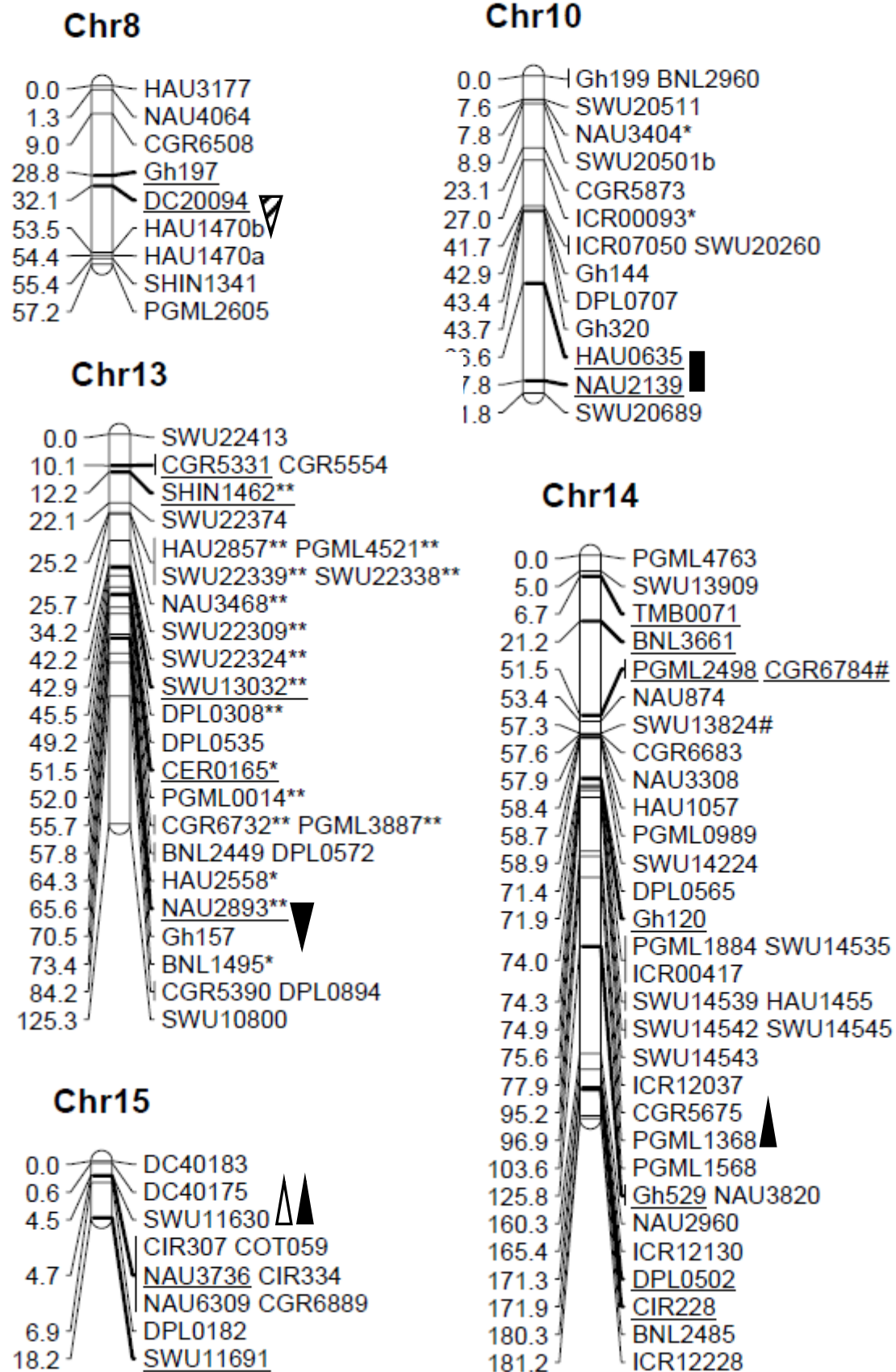
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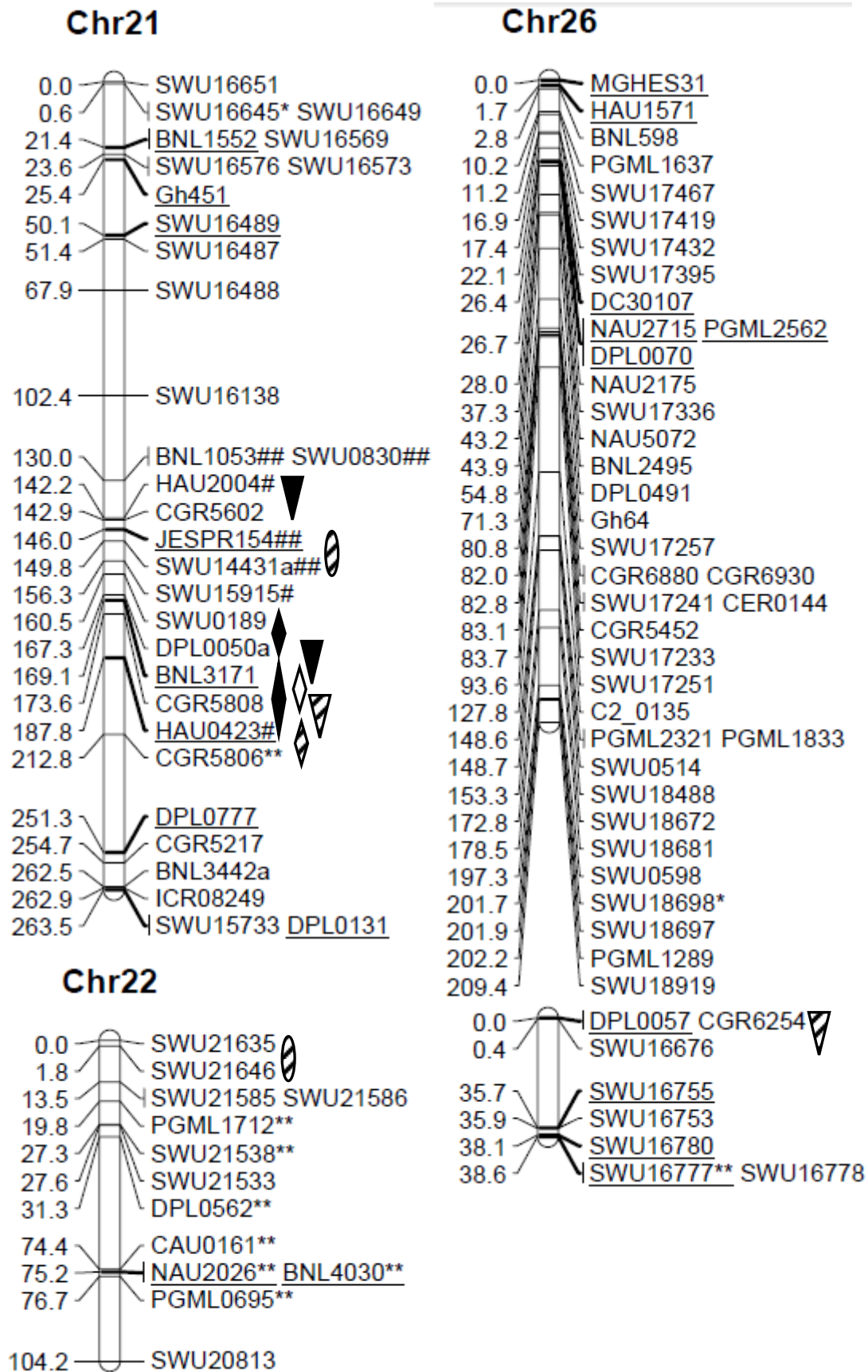
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570 **Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any
571 commercial or financial relationships that could be construed as a potential conflict of interest.









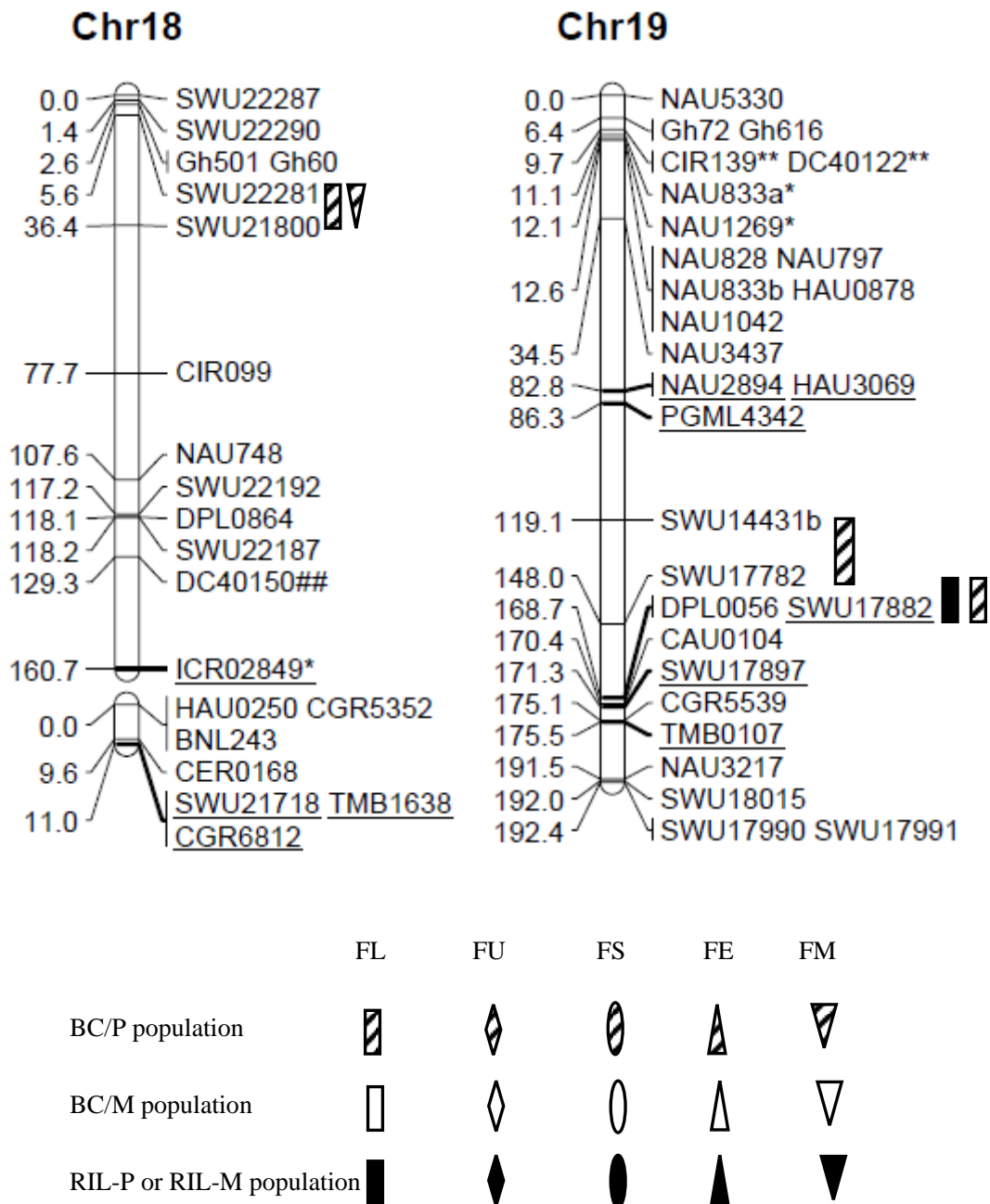


Figure 1 Locations of QTLs controlling fiber quality traits in BC/P and BC/M trials

* and ** (# and ##), marker showed respectively segregation distortion significant at P = 0.05 and 0.01 levels; markers with * and ** skewed toward the GX1135 alleles, and markers with # and ## skewed toward the GX100-2 alleles.

Table 1 Descriptive statistical analysis of fiber quality traits in multiple populations and the control set

Trait	Env.	BC/P			RIL-P			GX1135	GX100-2	Xinza 1	Ruiza 816
		Mean	Range	CV%	Mean	Range	CV%				
FL/mm	2016E1	30.38±0.80	27.70-32.95	2.63	30.36±1.07	26.35-33.75	3.54	31.15	30.40	30.73	31.15
	2015E2	31.08±0.69	29.20-33.00	2.21	30.95±0.95	28.60-33.20	3.07	30.44	30.10	31.05	31.15
	2016E2	29.42±0.78	26.65-31.45	2.64	29.15±1.08	26.00-31.60	3.70	28.92	28.80	30.35	30.35
	<u>2016E2</u>	<u>29.26±0.95</u>	<u>26.50-31.70</u>	<u>3.25</u>	<u>29.14±1.2</u>	<u>26.05-32.75</u>	<u>4.12</u>	29.28	29.38	28.90	29.80
FU	2016E1	86.28±0.76	83.75-88.30	0.88	85.99±0.85	82.85-88.05	0.98	86.43	85.43	85.78	86.43
	2015E2	86.06±0.70	83.70-87.90	0.81	85.79±0.82	82.70-88.35	0.96	85.28	86.50	86.13	86.08
	2016E2	85.29±1.02	81.75-87.40	1.20	84.95±1.05	80.85-87.05	1.23	84.60	85.35	85.45	86.00
	<u>2016E2</u>	<u>85.14±0.98</u>	<u>82.25-87.40</u>	<u>1.15</u>	<u>84.90±1.21</u>	<u>80.2-87.45</u>	<u>1.42</u>	85.43	86.05	85.05	86.20
FS/(cN/tex)	2016E1	28.81±0.94	26.05-30.85	3.25	28.99±1.25	24.65-32.30	4.32	31.85	30.13	30.23	31.85
	2015E2	30.63±0.99	28.15-33.60	3.22	30.80±1.42	27.50-34.30	4.62	29.20	28.57	28.15	30.85
	2016E2	29.11±1.02	26.45-32.45	3.50	29.03±1.38	25.6-33.90	4.75	28.50	28.70	30.18	31.08
	<u>2016E2</u>	<u>29.39±1.08</u>	<u>26.75-31.85</u>	<u>3.68</u>	<u>29.12±1.41</u>	<u>25.5-32.75</u>	<u>4.83</u>	29.20	28.35	29.28	31.10
FE	2016E1	6.81±0.06	6.55-7.00	0.87	6.80±0.07	6.55-6.95	1.09	6.98	6.90	6.90	6.98
	2015E2	6.99±0.06	6.85-7.20	0.84	6.99±0.08	6.80-7.25	1.16	6.78	6.77	6.83	6.78
	2016E2	6.74±0.06	6.55-6.90	0.88	6.72±0.07	6.50-7.00	1.08	6.67	6.70	6.75	6.80
	<u>2016E2</u>	<u>6.72±0.07</u>	<u>6.55-6.90</u>	<u>0.99</u>	<u>6.71±0.08</u>	<u>6.55-6.90</u>	<u>1.17</u>	6.73	6.70	6.70	6.75
FM	2016E1	4.81±0.34	3.95-5.70	7.12	4.86±0.41	3.80-5.75	8.53	5.33	5.10	4.50	5.33
	2015E2	4.76±0.27	4.15-5.40	5.59	4.71±0.36	3.65-5.65	7.65	5.06	5.10	5.35	5.18
	2016E2	4.93±0.24	4.30-5.70	4.92	4.97±0.37	4.10-5.90	7.45	5.33	4.55	4.98	5.55
	<u>2016E2</u>	<u>5.18±0.25</u>	<u>4.60-5.80</u>	<u>4.80</u>	<u>5.02±0.36</u>	<u>3.90-5.90</u>	<u>7.04</u>	5.40	5.13	5.00	5.38

Env., two testing locations (E1, Handan, E2, Cangzhou) in 2015 and 2016.

Mean referred to the mean value ± standard deviation. CV%, coefficient of variation.

Data without underline was from the recombinant inbred line (RIL-P) and backcross (BC/P) populations in paternal BC trials; Data with underlines was from the RIL-M and BC/M populations in maternal BC trials.

Table 2 Results of ANOVA and heritability for yield and its components in different populations from two backcross trials

Trait	Source of variation	MS				MS				
		RIL-P	H^2 [§]	BC/P	H^2	RIL-M	H^2	BC/M	H^2	
FL	G	4.753**	91.82%	2.072**	86.63%	2.072**	5.213**	91.78%	2.021**	79.62%
	E	291.886**		240.054**		240.054**	269.064**		297.752**	
	G×E	0.864		0.652		0.652	0.955		1.053	
	Error	0.814		0.615		0.615	0.888		0.998	
FU	G	1.880*	71.06%	1.490*	69.35%	1.490*	2.828**	78.69%	1.785*	72.00%
	E	110.536**		95.792**		95.792**	259.923**		272.103**	
	G×E	1.55		1.368		1.368	1.524		1.364	
	Error	1.494		1.214		1.214	1.548		1.437	
FS	G	7.906**	91.10%	3.044**	81.93%	3.044**	8.901**	89.71%	4.039**	81.95%
	E	369.073**		333.408**		333.408**	159.82**		85.482**	
	G×E	1.625*		1.365		1.365	2.07		1.71	
	Error	1.381		1.298		1.298	1.989		1.919	
FE	G	0.022**	86.83%	0.010**	79.87%	0.010**	0.032**	88.26%	0.014**	78.81%
	E	6.779**		6.063**		6.063**	6.453**		6.614**	
	G×E	0.007		0.005		0.005	0.009**		0.008	
	Error	0.006		0.005		0.005	0.007		0.007	
FM	G	0.576**	89.00%	0.261**	81.25%	0.261**	0.439**	85.33%	0.202**	76.37%
	E	6.24**		2.636**		2.636**	11.665**		13.089**	
	G×E	0.154**		0.117		0.117	0.158		0.131	
	Error	0.119		0.128		0.128	0.137		0.112	

G, genotype, E, environment, G×E, genotype×environment. †Mean square. §Heritability.

‘*’ and ‘**’ indicate that the correlation is significant at 0.05 and 0.01 probability levels, respectively.

Table 3 Correlation analyses between five fiber quality traits in RIL population and its TC progenies

Trait	Env.	FL		FU		FS		FE	
		RIL	BC	RIL	BC	RIL	BC	RIL	BC
FU	2016E1	0.013	-0.096						
	2015E2	0.226**	0.222**						
	2016E2	0.497**	0.381**						
	<u>2016E2</u>	<u>0.438**</u>	<u>0.178*</u>						
FS	2016E1	0.656**	0.616**	-0.030	-0.083				
	2015E2	0.718**	0.699**	0.217**	0.075				
	2016E2	0.754**	0.581**	0.403**	0.060				
	<u>2016E2</u>	<u>0.784**</u>	<u>0.525**</u>	<u>0.305**</u>	<u>0.043</u>				
FE	2016E1	0.659**	0.617**	0.128	0.105	0.530**	0.511**		
	2015E2	0.627**	0.476**	0.369**	0.163*	0.507**	0.533**		
	2016E2	0.754**	0.737**	0.454**	0.252**	0.710**	0.696**		
	<u>2016E2</u>	<u>0.813**</u>	<u>0.535**</u>	<u>0.414**</u>	<u>0.249**</u>	<u>0.751**</u>	<u>0.486**</u>		
FM	2016E1	-0.237**	-0.202**	0.295**	0.314**	-0.320**	-0.404**	-0.015	0.016
	2015E2	-0.439**	-0.334**	0.088	0.049	-0.428**	-0.390**	-0.102	0.047
	2016E2	-0.443**	-0.124	-0.053	0.093	-0.497**	-0.261**	-0.206**	0.004
	<u>2016E2</u>	<u>-0.426**</u>	<u>-0.277**</u>	<u>0.063</u>	<u>0.142</u>	<u>-0.434**</u>	<u>-0.482**</u>	<u>-0.219**</u>	<u>-0.020</u>

‘*’, ‘**’ indicate that the correlation is significant at 0.05 and 0.01 probability levels, respectively.

RIL, recombinant inbred line population in maternal and paternal testcross trials, respectively; BC, backcross populations including maternal and paternal BC (BC/M and BC/P) populations.

Figures underlined referred to QTLs identified in one BC/M trial, the remaining QTLs identified in three BC/P trials.

Table 4 Single-locus QTLs in paternal and maternal backcross experiments by composite interval

QTL	Env.	Flanking markers		mapping method					
				BC			RIL		
				LOD	Effect value	Var%	LOD	Effect value	Var%
<u><i>qFL-Chr1-1</i></u>	<u>2016E2</u>	<u>DPL0090</u>	<u>Gh398</u>	<u>4.57</u>	<u>0.32</u>	<u>10.66</u>			
<i>qFL-Chr1-2</i>	2016E1	NAU2218	SWU11191				3.70	0.29	7.10
	2016E2	NAU2218	SWU11191				3.30	0.29	6.91
<i>qFL-Chr1-3</i>	2015E2	SWU10994	HAU1001	3.24	-0.19	7.76			
	2015E2	SWU11038	SWU11384	3.33	-0.26	14.77			
<i>qFL-Chr2-1</i>	2016E1	SWU12393	SWU11013				4.24	0.31	8.25
<i>qFL-Chr2-2</i>	2016E1	SWU11950	TMB1268	3.05	0.19	5.70			
<i>qFL-Chr5-1</i>	2015E2	NAU4034	SWU17713	3.80	0.19	7.70			
<i>qFL-Chr5-2</i>	2016E1	HAU1603	PGML4457	3.55	0.22	7.46			
	2015E2	PGML4457	MUSS193	3.44	0.19	7.82			
<i>qFL-Chr5-3</i>	2016E1	CGR5025	NBRI0694	5.57	0.26	10.49			
<i>qFL-Chr9-1</i>	2016E1	SWU15511	SWU15413				3.53	-0.28	6.78
<i>qFL-Chr10-1</i>	2016E1	SWU20260	Gh144				2.88	-0.25	5.19
<i>qFL-Chr10-2</i>	2016E2	HAU0635	NAU2139				4.76	-0.52	17.90
<i>qFL-Chr18-1</i>	2016E1	SWU22290	Gh501				3.10	-0.26	5.91
<i>qFL-Chr18-2</i>	2016E1	SWU22281	SWU21800	4.15	-0.23	7.83			
<i>qFL-Chr19-1</i>	2015E2	SWU14431b	SWU17782	3.88	0.30	17.98			
	2015E2	SWU17782	DPL0056	3.16	0.24	11.35			
	2016E2	SWU17782	DPL0056				5.28	0.41	11.05
<i>qFL-Chr21-1</i>	2016E2	SWU0189	DPL0050a				3.22	-0.30	7.20
<i>qFL-Chr24-1</i>	2016E1	SWU13267	BNL1521	2.81	-0.21	6.66			
<i>qFL-Chr25-1</i>	2016E2	BNL3594	DPL0282	2.71	-0.18	5.52			
<i>qFU-Chr2-1</i>	2016E1	SWU12025	SWU11889	3.91	-0.28	11.30			
<i>qFU-Chr2-2</i>	2016E2	MGHES24	ICR11064	2.64	0.26	6.02			
<i>qFU-Chr4-1</i>	2016E1	SWU16783	NAU3868				2.86	0.24	7.76
<u><i>qFU-Chr5-1</i></u>	<u>2016E2</u>	<u>TMB1296</u>	<u>HAU1603</u>	<u>3.05</u>	<u>0.26</u>	<u>6.77</u>			
<i>qFU-Chr6-1</i>	2016E1	DPL0244	HAU2625				5.77	0.30	11.86

QTL	Env.	Flanking markers		BC			RIL		
				LOD	Effect value	Var%	LOD	Effect value	Var%
<i>qFU-Chr7-1</i>	2016E2	NAU3181	SHIN0376				2.60	0.27	6.51
<i>qFU-Chr9-1</i>	2016E1	NAU1282	CGR6771				2.77	0.20	5.40
<i>qFU-Chr11-1</i>	2016E2	TMB0628	HAU0639				2.57	0.24	5.23
<i>qFU-Chr13-1</i>	<u>2016E2</u>	<u>SWU22309</u>	<u>SWU22324</u>	<u>2.52</u>	<u>-0.24</u>	<u>5.72</u>			
<i>qFU-Chr14-1</i>	2016E2	CIR228	BNL2485	2.67	0.25	5.53			
<i>qFU-Chr21-1</i>	2015E2	SWU0830	HAU2004	3.51	0.22	9.05			
<i>qFU-Chr21-2</i>	2015E2	JESPR154	SWU14431a	3.99	0.22	8.76			
<i>qFU-Chr22-1</i>	2015E2	SWU21635	SWU21646	4.24	0.22	8.86			
<i>qFU-Chr22-2</i>	2015E2	SWU21533	DPL0562	2.77	-0.18	5.69			
<i>qFS-Chr1-1</i>	2016E2	NAU3384	CGR5663				2.94	0.52	13.70
<i>qFS-Chr2-1</i>	2016E2	SWU11976	SWU11950				3.96	0.45	9.66
<i>qFS-Chr3-1</i>	2016E2	SWU12783	SWU12819	3.84	0.48	22.09			
<i>qFS-Chr5-1</i>	2016E1	NAU6240	PGML1671				2.73	0.38	9.23
	2016E2	NAU6240	PGML1671				3.23	0.46	11.01
<i>qFS-Chr9-1</i>	2016E1	NAU1282	CGR6771				4.75	-0.46	13.20
	2016E2	NAU1282	CGR6771				2.97	-0.47	11.30
<i>qFS-Chr9-2</i>	2016E1	SWU15511	SWU15413				5.08	-0.41	10.04
<i>qFS-Chr20-1</i>	2016E1	CGR5548	SWU20675				2.89	-0.31	5.90
<i>qFS-Chr21-1</i>	2016E2	SWU0189	DPL0050a				3.40	-0.41	8.42
<i>qFS-Chr21-2</i>	<u>2016E2</u>	<u>BNL3171</u>	<u>CGR5808</u>	<u>2.97</u>	<u>-0.29</u>	<u>6.90</u>	2.89	-0.35	6.27
	2016E1	CGR5808	HAU0423				5.31	-0.46	13.37
	2016E2	CGR5808	HAU0423				4.24	-0.44	9.62
	2016E2	HAU0423	CGR5806	5.18	-0.34	10.14			
<i>qFS-Chr21-2</i>	2016E2	CGR5217	BNL3442a	2.87	-0.25	5.62			
<i>qFE-Chr1-1</i>	2016E1	NAU2218	SWU11191				2.61	0.02	5.13
<i>qFE-Chr2-1</i>	2016E1	PGML0700	SWU12016	3.62	0.02	6.90			
<i>qFE-Chr2-2</i>	2016E1	TMB2386	SWU12343				5.46	0.04	22.42
	<u>2016E2</u>	<u>TMB2386</u>	<u>SWU12343</u>	<u>2.53</u>	<u>0.02</u>	<u>5.71</u>			
<i>qFE-Chr2-3</i>	2016E1	NBRI0014	SWU12107				3.99	0.02	8.03
	2016E2	MGHES24	ICR11064	2.70	0.01	5.66			

QTL	Env.	Flanking markers		BC			RIL		
				LOD	Effect value	Var%	LOD	Effect value	Var%
	<u>2016E2</u>	<u>MGHES24</u>	<u>ICR11064</u>	<u>3.47</u>	<u>0.02</u>	<u>7.37</u>			
<i>qFE-Chr3-1</i>	2016E2	SWU12783	SWU12819	4.79	0.02	12.17			
	2016E2	SWU12819	SWU12765	<u>2.72</u>	<u>-0.02</u>	<u>8.84</u>			
<i>qFE-Chr5-1</i>	2016E2	PGML1671	PGML1917				3.72	0.02	7.75
<i>qFE-Chr13-1</i>	2016E1	NAU2893	Gh157				3.48	0.02	7.02
<i>qFE-Chr13-2</i>	2016E1	BNL1495	CGR5390				2.96	0.02	7.77
<i>qFE-Chr15-1</i>	2016E2	DPL0182	SWU11691	2.63	0.02	6.60			
<i>qFE-Chr18-1</i>	2016E1	SWU22281	SWU21800	2.59	-0.01	5.01			
<i>qFE-Chr21-1</i>	2016E2	HAU2004	CGR5602				4.41	0.03	9.19
<i>qFE-Chr21-2</i>	2016E1	CGR5808	HAU0423	3.02	-0.01	5.77			
	2016E2	DPL0050a	BNL3171				4.54	-0.03	9.48
<i>qFE-Chr24-1</i>	2016E1	SWU13267	BNL1521	3.24	-0.02	6.20			
<i>qFE-Chr26-1</i>	2015E2	CGR6254	SWU16676	3.90	0.02	8.49			
<i>qFM-Chr1-2</i>	2016E2	CGR5663	NAU2343	2.79	0.06	5.80			
<i>qFM-Chr2-1</i>	2015E2	SWU12025	SWU11889	3.25	-0.09	12.38			
<u><i>qFM-Chr4-1</i></u>	<u>2016E2</u>	<u>JESPR295</u>	<u>SWU16782</u>	<u>2.50</u>	<u>0.08</u>	<u>5.31</u>			
<u><i>qFM-Chr4-2</i></u>	<u>2016E2</u>	<u>SWU16783</u>	<u>NAU3868</u>	<u>3.98</u>	<u>0.13</u>	<u>13.96</u>			
<i>qFM-Chr5-1</i>	2016E2	PGML1671	PGML1917	3.25	-0.07	8.30			
<i>qFM-Chr8-1</i>	2016E1	DC20094	HAU1470b	3.49	-0.09	7.00			
<i>qFM-Chr9-1</i>	2016E1	HAU190	HAU1618				2.59	0.10	5.30
<i>qFM-Chr9-2</i>	2015E2	NAU1282	CGR6771				2.83	0.12	5.96
	2016E1	NAU2873	NAU1282				4.16	0.12	7.70
	<u>2016E2</u>	<u>NAU2873</u>	<u>NAU1282</u>	<u>3.65</u>	<u>0.10</u>	<u>7.81</u>	4.98	0.12	10.34
	<u>2016E2</u>	<u>NAU1282</u>	<u>CGR6771</u>	<u>3.85</u>	<u>0.14</u>	<u>14.53</u>	5.94	0.18	21.91
<i>qFM-Chr10-1</i>	2016E1	SWU20501b	CGR5873	3.33	0.11	9.21			
<i>qFM-Chr10-2</i>	2016E1	ICR00093	ICR07050	2.77	0.08	5.56			
<i>qFM-Chr12-1</i>	2016E1	Gh631	HAU1321				3.16	0.13	9.45
<i>qFM-Chr14-1</i>	2016E1	CGR5675	PGML1368				4.04	0.12	8.04
<i>qFM-Chr14-2</i>	2016E1	PGML1568	Gh529				3.06	0.13	9.23
<i>qFM-Chr15-1</i>	2016E1	DC40175	SWU11630				6.04	0.15	12.36

QTL	Env.	Flanking markers		BC			RIL		
				LOD	Effect value	Var%	LOD	Effect value	Var%
	<u>2016E2</u>	<u>DC40175</u>	<u>SWU11630</u>	<u>2.57</u>	<u>0.06</u>	<u>5.46</u>			
<i>qFM-Chr21-1</i>	2015E2	SWU0189	DPL0050a	3.34	0.07	6.94			
<i>qFM-Chr26-1</i>	2016E1	Gh64	SWU17257	3.09	-0.09	7.61			

These single locus QTLs were detected by the software QTL Cartographer (version 2.5). Env.: Environment in 2015 and 2016; E1: Handan; E2: Cangzhou. RIL, recombinant inbred line population in maternal and paternal backcross trials, respectively; BC, backcross populations including maternal and paternal BC (BC/M and BC/P) populations. Bold figures indicated the stable QTL detected in more than two environments or populations simultaneously. Figures underlined referred to QTLs identified in BC/M population in 2016E2, the remaining QTLs identified in BC/P population. Effect value: the genetic expectation of one QTL effect when estimated from the mean values of populations, additive effect in RIL population and the additive and dominance effects in BC populations. Var (%), phenotypic variation explained by a single QTL.

Table 5 Summary on M-QTL and E-QTLs controlling fiber quality traits in BC/P and RIL-P datasets in BC/P trials

Trait	BC/P			RIL-P		
	n	V(A)%	V(AE)%	n ^b	V(A)% ^c	V(AE)%
M-QTL ^a						
FL	11	3.13	0.70	13	2.63	0.27
FU	3	3.02	3.00	7	3.15	2.40
FS	11	2.53	0.67	14	2.92	0.25
FE	0	-	-	12	2.77	0.59
FM	13	2.61	0.99	10	3.41	1.01
Mean	-	2.82	1.34	-	2.98	0.90
E-QTL ^a	n	V(AA)%	V(AAE)%	n	V(AA)% ^c	V(AAE)%
FL	16	3.44	0.30	52	4.33	0.22
FU	11	1.93	2.12	0	-	-
FS	5	3.32	0.52	44	4.15	0.24
FE	1	0.76	0.01	18	4.42	0.24
FM	13	3.44	0.73	28	3.77	0.23
Mean	-	2.58	0.74	-	4.17	0.23

^a M-QTLs and E-QTLs refer to the main effect QTL and epistasis QTLs by environments.

^b The number of QTLs.

^c V(A)%, V(AAE)%, V(AA)% and V(AAE)%, the total proportion of phenotypic variation on average explained by single QTL, epistatic QTLs (AA) and them by environments (AE or AAE) at the current scanning position, respectively.

Table 6 Types of epistasis detected for fiber quality traits in the RIL-P and BC/P populations

Trait	Type of epistasis ^a							
	RIL-P				BC/P			
	I	II	III	Total	I	II	III	Total
Fiber length	8	29	15	52	2	5	9	16
Fiber uniformity	0	0	0	0	2	5	4	11
Fiber strength	10	22	12	44	0	1	5	6
Fiber elongation	4	6	8	18	0	0	1	1
Micronaire	5	17	6	28	1	4	8	13
Total	27	74	31	142	5	15	27	47

^a type I, both loci were M-QTLs, type II, either locus among two loci was M-QTL, and type III, both loci were no

M-QTLs.

Table S2 Epitasis effects and environmental interactions detected for yield and its components in RIL-P population

Trait	Chri	Left Marker	Right Marker	Chrij	Left Marker	Right Marker	LOD	V(AA)
FL	1	CGR6129	DPL0790	3	SWU12840	NAU2742	5.81	4.27
	1	SWU10912	DPL0090	4	BNL1167	SWU21415	5.27	3.53
	3	SWU12840	NAU2742	6	SWU19541	CGR5801	5.26	4.00
	5	PGML1671	PGML1917	9	NAU1282	CGR6771	6.99	5.35
	9	CGR6876	CGR5758	9	SWU15157	SWU14934	5.40	3.61
	3	SWU12783	SWU12819	11	CGR5421	ICR08245	5.26	4.02
	5	CGR5025	NBRI0694	11	NAU3695	DPL0050b	5.08	3.88
	1	CGR5663	NAU2343	11	NAU1014	ICR10344	5.25	4.02
	11	PGML2202	CGR6580	12	NAU943	DPL0303	5.33	3.97
	6	CGR5801	SWU19249	12	DPL0303	COT107	5.24	3.85
	5	SWU20917	NAU6240	14	SWU14224	DPL0565	6.29	4.56
	13	BNL1495	CGR5390	14	SWU14224	DPL0565	5.95	4.52
	1	HAU1417	NAU2437	14	NAU3820	NAU2960	5.80	4.14
	11	SWU15972	TMB0628	15	DPL0182	SWU11691	7.81	5.88
	7	CER0036	PGML1916	16	HAU1129	NAU2984	5.68	3.83
	14	SWU14545	SWU14543	16	ICR00010	SWU10038	5.56	3.95
	4	SWU18881	NAU2701	17	ICR03391	SWU12838a	6.95	5.01
	12	HAU1316	NAU3519	17	ICR03391	SWU12838a	5.83	3.98
	1	NAU6367	MUSS422	17	NAU3765	SWU14627	5.80	3.80
	1	NAU3177	ICR03724	18	SWU21800	CIR099	5.09	4.03
	11	SWU15972	TMB0628	19	NAU3437	NAU2894	5.78	4.48
	3	SWU12840	NAU2742	21	SWU16487	SWU16488	7.12	5.14
	12	DPL0732	Gh631	21	SWU0189	DPL0050a	9.78	6.47
	11	NAU1014	ICR10344	21	CGR5217	BNL3442a	5.46	4.00
	11	SWU15972	TMB0628	22	DPL0562	CAU0161	5.16	3.77
	17	SWU12818	CGR5576	24	CGR5202	Gh298	5.40	3.32
	10	HAU0635	NAU2139	24	PGML4657	Gh454	5.24	4.00
	1	HAU1417	NAU2437	24	SWU13267	BNL1521	6.26	4.89
	19	NAU3437	NAU2894	24	HAU2504	SWU13736	5.54	4.24
	5	SWU20913	Gh260	25	SWU19848	CGR6864	5.90	3.88
	22	PGML0695	SWU20813	25	DPL0282	SWU19763	7.18	5.38
	21	CGR5808	HAU0423	25	Gh220	SWU19434	5.98	3.80
	18	CIR099	NAU748	26	BNL598	PGML1637	6.33	4.77
	21	SWU0830	HAU2004	26	DPL0491	Gh64	7.30	4.86
	22	DPL0562	CAU0161	26	Gh64	SWU17257	6.70	4.96
	12	DPL0732	Gh631	26	SWU17233	SWU17251	5.05	3.75
	14	NAU874	SWU13824	26	C2_0135	PGML2321	5.38	3.71
	13	SWU22413	CGR5331	26	SWU18488	SWU18672	8.22	6.19
	19	SWU17882	CAU0104	26	SWU18672	SWU18681	5.74	4.37
	23	SWU14807	PGML4185	26	SWU18681	SWU0598	5.68	4.40
5	PGML1917	SWU17715	27	ICR11883	CGR6356	5.88	4.52	
22	SWU21635	SWU21646	28	BNL2877	HAU3071	7.19	5.24	
16	SWU10056	SWU10037	28	HAU3071	CGR5534	5.06	3.71	
4	SWU18876	SWU12672	28	CGR5534	SHIN0219	6.58	4.77	
24	SWU13745	Gh273	28	CGR5534	SHIN0219	5.66	3.77	
2	PGML0700	SWU12016	28	CGR5534	SHIN0219	5.69	4.21	
3	SWU12819	SWU12765	28	SHIN0219	TMB2386	5.66	4.20	
9	NAU1282	CGR6771	29	DC20127	DPL0252	6.06	4.45	
20	SWU20246	SWU20501a	29	BNL3261	CGR5111	5.39	3.85	

	3	CER0028	Gh663	15	CGR6889	<u>DPL0182</u>	7.02	5.47
	13	DPL0894	SWU10800	16	SWU10627	PGML1309	5.20	4.09
	11	<u>NAU2152</u>	<u>NAU5428</u>	19	SWU17882	CAU0104	6.21	4.92
	6	ICR00143	CGR5108	21	SWU0830	HAU2004	5.74	4.67
	1	DPL0090	Gh398	21	SWU0830	HAU2004	5.37	4.13
	19	SWU17882	CAU0104	21	CGR5217	BNL3442a	6.71	5.36
	9	NAU5474	Gh158	22	PGML1712	SWU21538	5.41	4.01
	19	NAU3437	NAU2894	24	BNL1521	HAU2504	5.17	4.10
	24	SWU13150	<u>PGML4657</u>	24	SWU13745	Gh273	5.06	4.13
	11	CER0098	CGR5421	26	SWU18488	SWU18672	5.34	3.73
	19	SWU17882	CAU0104	26	SWU18681	SWU0598	6.36	4.52
	3	HAU2424	CER0028	26	SWU18681	SWU0598	5.43	4.14
	7	NAU1357	SWU10067	27	ICR11205	DPL0847a	5.09	4.19
	12	NAU943	DPL0303	28	NBRI0014	SWU12107	6.39	4.76
FM	2	SWU11889	SWU11887	11	NAU2152	NAU5428	5.22	3.25
	10	HAU0635	NAU2139	11	NAU2152	NAU5428	6.08	3.86
	6	CGR5801	SWU19249	11	CER0098	CGR5421	5.07	3.31
	9	HAU190	<u>HAU1618</u>	11	NAU3695	DPL0050b	5.81	3.63
	7	NAU1357	SWU10067	11	CGR6580	SWU15972	5.79	3.78
	5	CGR5025	NBRI0694	13	DPL0535	CER0165	7.51	4.44
	3	SWU12732	SWU12783	14	SWU13909	TMB0071	5.62	3.49
	5	SWU20913	Gh260	14	TMB0071	BNL3661	5.69	3.19
	14	SWU13909	TMB0071	16	ICR00010	SWU10038	5.91	3.70
	1	NAU3384	CGR5663	17	NAU3765	SWU14627	5.74	3.52
	1	CGR5663	NAU2343	18	SWU22287	SWU22290	7.40	4.67
	5	CGR5025	NBRI0694	18	DC40150	ICR02849	7.72	4.83
	3	SWU12819	SWU12765	19	HAU3069	PGML4342	5.75	3.17
	9	Gh27	SWU15194	20	SWU1259	SWU20033	5.23	3.46
	13	SWU22309	SWU22324	20	SWU20035	DPL0319	6.07	2.96
	7	NAU1357	SWU10067	21	Gh451	SWU16489	5.98	3.38
	9	NAU3966	SWU15157	21	SWU16488	SWU16138	5.46	2.74
	8	CGR6508	Gh197	21	SWU16138	BNL1053	6.88	4.36
	12	NAU943	DPL0303	21	SWU16138	BNL1053	6.66	4.31
	19	NAU3437	NAU2894	21	CGR5602	JESPR154	5.90	3.52
	23	SWU14807	PGML4185	25	HAU1382	SWU19848	5.37	3.53
	21	SWU15915	SWU0189	26	SWU17336	NAU5072	7.67	3.95
	11	SWU15972	TMB0628	28	HAU3071	CGR5534	5.12	3.08
	3	SWU12732	SWU12783	28	CGR5534	SHIN0219	5.93	3.81
	20	SWU20035	DPL0319	28	CGR5534	SHIN0219	5.45	3.05
	24	SWU13745	Gh273	28	CGR5534	SHIN0219	6.39	3.93
	4	SWU18876	SWU12672	28	SHIN0219	TMB2386	10.11	6.68
	25	HAU1382	SWU19848	28	TMB2386	SWU12343	6.33	4.00

The result detected by software ICIMapping 4.1. E01 and E03, Cangzhou in 2015 and 2016; E02, Handan in 2016. Chi and C analysis. AA is the epistatic effect between loci i and j. AAE is the effect of the environmental interaction of epistasis. AA environment interactions in E1, E2, E3 and E4, respectively. V(AA)% and V(AAE)%, percentage of the total variation explained between E-QTLs and QEs with the M-QTLs and QEs in RIL populations. Markers in bold a

V(AAE)	AA	AAE01	AAE02	AAE03
0.20	-0.21	0.05	-0.06	0.01
0.28	0.20	-0.07	0.06	0.01
0.09	-0.21	0.02	0.02	-0.04
0.10	-0.24	0.00	0.03	-0.03
0.36	-0.20	-0.02	-0.07	0.09
0.19	0.21	-0.05	0.05	0.00
0.06	-0.20	0.03	-0.01	-0.02
0.00	-0.21	0.01	0.00	-0.01
0.00	0.21	-0.02	0.01	0.01
0.19	0.20	-0.03	0.06	-0.02
0.22	-0.22	0.06	-0.01	-0.05
0.07	-0.22	-0.01	-0.03	0.04
0.28	-0.21	0.04	0.04	-0.07
0.10	-0.25	0.04	0.00	-0.05
0.29	-0.21	0.07	-0.07	0.00
0.19	-0.21	0.06	-0.02	-0.04
0.30	-0.24	0.06	0.01	-0.07
0.38	-0.21	0.08	0.02	-0.09
0.64	-0.21	0.12	-0.08	-0.05
0.10	0.21	-0.02	0.04	-0.02
0.03	-0.22	0.03	-0.02	0.00
0.36	0.24	-0.09	0.03	0.06
0.52	0.27	-0.08	0.10	-0.02
0.11	0.21	-0.02	-0.03	0.05
0.21	-0.22	0.03	0.04	-0.07
0.81	-0.19	0.09	0.05	-0.14
0.13	0.21	-0.06	0.02	0.04
0.04	-0.23	0.00	-0.01	0.02
0.01	0.22	-0.02	0.02	0.00
0.29	-0.20	0.07	0.00	-0.07
0.04	-0.24	0.03	0.00	-0.03
0.64	-0.20	0.12	-0.07	-0.04
0.14	0.23	-0.03	-0.01	0.04
0.67	0.23	-0.12	0.09	0.03
0.12	-0.24	0.04	0.01	-0.05
0.24	0.20	-0.07	0.05	0.03
0.26	0.20	-0.08	0.03	0.05
0.07	0.26	-0.03	0.03	0.00
0.10	0.22	-0.03	-0.01	0.04
0.06	0.22	0.00	-0.03	0.03
0.05	0.22	-0.04	0.02	0.02
0.28	-0.24	0.02	-0.07	0.05
0.22	-0.21	0.06	-0.06	0.00
0.23	-0.23	0.06	-0.05	-0.01
0.38	0.20	-0.07	-0.01	0.08
0.03	0.21	-0.03	0.03	-0.01
0.22	0.21	-0.03	-0.04	0.06
0.30	0.22	-0.04	-0.05	0.09
0.31	-0.21	0.08	-0.04	-0.04

0.47	-0.20	0.01	-0.09	0.08
0.14	0.21	-0.01	-0.04	0.05
0.02	0.21	0.00	-0.02	0.02
0.34	-0.27	-0.06	0.11	-0.05
0.10	0.29	-0.01	-0.05	0.06
0.08	-0.29	0.02	-0.05	0.03
0.02	0.32	0.00	-0.04	0.03
0.09	-0.27	-0.02	-0.04	0.06
0.69	-0.25	-0.12	0.16	-0.04
0.30	-0.28	-0.10	0.04	0.07
0.06	-0.27	-0.03	0.01	0.02
0.26	-0.28	0.04	0.06	-0.09
0.14	0.26	0.02	-0.01	0.00
0.04	-0.27	-0.01	0.03	-0.01
0.48	-0.26	0.03	0.10	-0.13
0.09	-0.29	-0.06	0.03	0.03
0.03	-0.29	-0.03	0.02	0.01
0.00	-0.27	-0.01	0.01	0.00
0.29	-0.30	-0.08	0.10	-0.02
0.66	-0.28	0.05	0.10	-0.15
0.05	0.27	-0.03	-0.02	0.05
0.00	0.28	0.01	-0.01	0.00
0.12	-0.27	0.02	0.05	-0.06
0.02	0.29	-0.02	0.01	0.01
0.52	-0.28	-0.10	-0.03	0.13
0.36	0.28	0.01	-0.10	0.09
0.08	0.28	-0.01	0.05	-0.04
0.88	0.30	0.18	-0.08	-0.11
0.27	-0.27	0.07	0.03	-0.09
0.29	0.28	0.06	-0.10	0.04
0.85	-0.25	-0.16	0.02	0.15
0.00	0.27	0.01	0.00	-0.01
0.07	-0.30	-0.07	0.05	0.02
0.21	-0.29	0.05	0.03	-0.08
0.22	0.28	0.03	-0.09	0.06
0.42	-0.25	-0.12	0.04	0.08
0.34	-0.30	-0.08	-0.04	0.12
0.18	-0.28	-0.09	0.05	0.04
0.10	-0.29	-0.04	0.06	-0.02
0.40	0.27	0.09	-0.12	0.03
0.56	0.29	0.14	-0.10	-0.04
0.02	-0.27	0.00	0.01	-0.01
0.15	0.28	-0.07	0.06	0.01
0.10	0.28	0.06	-0.03	-0.03
0.33	-0.25	-0.06	0.11	-0.05
0.11	-0.31	-0.06	0.04	0.02
0.40	0.26	0.08	-0.12	0.04
0.33	0.02	0.00	0.00	0.00
0.40	-0.02	0.00	0.00	0.00
0.53	-0.02	0.00	-0.01	0.01
0.40	0.02	0.01	0.00	0.00

0.13	-0.02	0.00	0.00	0.00
0.33	0.02	0.00	0.00	0.00
0.00	0.02	0.00	0.00	0.00
0.33	0.02	0.00	0.00	0.00
0.07	0.02	0.00	0.00	0.00
0.20	0.02	0.00	0.00	0.00
0.20	-0.02	0.00	-0.01	0.00
0.33	0.02	0.00	0.00	0.00
0.07	-0.02	0.00	0.00	0.00
0.13	-0.02	0.00	0.00	0.00
0.46	0.02	0.00	-0.01	0.00
0.46	0.02	0.00	0.00	0.00
0.00	-0.02	0.00	0.00	0.00
0.00	0.02	0.00	0.00	0.00
0.19	-0.07	-0.01	0.02	-0.02
0.06	-0.08	0.01	-0.01	0.00
0.04	-0.07	0.01	0.00	-0.01
0.25	-0.07	0.01	0.01	-0.03
0.09	0.07	-0.02	0.01	0.01
0.39	-0.08	0.01	0.03	-0.03
0.24	0.07	-0.03	0.01	0.02
0.29	0.07	-0.02	-0.01	0.03
0.14	0.07	0.02	-0.01	-0.01
0.13	0.07	0.00	-0.02	0.02
0.25	-0.08	0.02	-0.03	0.01
0.18	-0.09	0.01	0.02	-0.02
0.34	0.07	-0.03	0.01	0.02
0.01	-0.07	0.01	-0.01	0.00
0.90	0.07	-0.02	-0.04	0.05
0.18	0.07	0.02	-0.01	-0.01
0.78	0.07	0.02	-0.05	0.03
0.07	-0.08	0.01	-0.01	0.00
0.00	-0.08	0.00	0.00	0.00
0.31	0.07	-0.02	-0.02	0.03
0.17	0.07	0.01	-0.02	0.00
0.67	-0.08	0.04	0.00	-0.04
0.03	0.07	0.00	-0.01	0.01
0.08	0.07	-0.02	0.00	0.01
0.47	0.07	-0.03	0.00	0.03
0.04	-0.08	0.01	-0.01	0.00
0.05	0.10	-0.01	0.01	0.01
0.16	0.08	0.01	0.01	-0.02

Chj represent the linkage group number of the loci being tested in the EI, AAE2, AAE3 and AAE4 indicate the epistatic effects of QTL \times explained by the AA and AAE. **Bold figures indicate the same QTLs re those flanking M-QTLs identified.**

Table S5 Common single locus QTLs in comparison with the previous studies in multiple years and locations

No.	QTL	Env.	Flanking markers		BC			RIL			Reference
					LOD	Effect value	Var%	LOD	Effect value	Var%	
1	<i>qFL-Chr2-1</i>	2016E1	SWU12393	SWU11013				4.24	0.31	8.25	In the present study
	<i>qFL-Chr2-1</i>	2012E2	<u>SWU12393</u>	<u>SWU11013</u>	<u>5.72</u>	<u>0.40</u>	<u>11.06</u>				Shang et al., 2016d
	<i>qFL-Chr2-2</i>	2012E2	<u>SWU12025</u>	<u>SWU11889</u>				<u>2.38</u>	<u>0.24</u>	<u>6.92</u>	Shang et al., 2016d
2	<i>qFL-Chr5-1</i>	2015E2	NAU4034	SWU17713	3.80	0.19	7.70				In the present study
	<i>qFL-chr5-3</i>	<u>2015E1</u>	<u>Gh388</u>	<u>SWU17713</u>	<u>10.22</u>	<u>0.47</u>	<u>19.63</u>				Ma et al.,2017
		<u>2015E2</u>	<u>Gh388</u>	<u>SWU17713</u>	<u>5.39</u>	<u>0.36</u>	<u>10.65</u>				Ma et al.,2017
		<u>2015E2</u>	<u>SWU17713</u>	<u>HAU1603</u>				<u>5.62</u>	<u>0.25</u>	<u>11.52</u>	Ma et al.,2017
	<i>qFL-Chr5-4</i>	2012E1	<u>NAU4034</u>	<u>SWU17713</u>				<u>4.30</u>	<u>0.19</u>	<u>8.57</u>	Shang et al., 2016d
		2012E1	<u>NAU4034</u>	<u>SWU17713</u>	<u>8.94</u>	<u>0.37</u>	<u>16.39</u>				Shang et al., 2016d
		2012E1	NAU4034	SWU17713	6.39	0.34	11.68				Shang et al., 2016d
		2012E2	NAU4034	SWU17713	2.90	0.29	5.64				Shang et al., 2016d
3	<i>qFL-Chr5-2</i>	2016E1	HAU1603	PGML4457	3.55	0.22	7.46				In the present study
		2015E2	PGML4457	MUSS193	3.44	0.19	7.82				In the present study
	<i>qFL-chr5-4</i>	<u>2015E3</u>	<u>MUSS193</u>	<u>PGML4350</u>	<u>4.44</u>	<u>0.32</u>	<u>8.55</u>				Ma et al.,2017

No.	QTL	Env.	Flanking markers		BC			RIL			Reference
					LOD	Effect value	Var%	LOD	Effect value	Var%	
		<u>2015E2</u>	<u>PGML4350</u>	<u>SWU17781</u>				<u>3.89</u>	<u>0.22</u>	<u>8.99</u>	Ma et al.,2017
	<i>qFL-Chr5-5</i>	2012E4	<u>PGML4457</u>	<u>MUSS193</u>				<u>3.15</u>	<u>0.15</u>	<u>6.24</u>	Shang et al., 2016d
		2012E4	<u>PGML4457</u>	<u>MUSS193</u>	<u>4.18</u>	<u>0.25</u>	<u>7.92</u>				Shang et al., 2016d
		2012E4	PGML4457	MUSS193	4.40	0.27	8.97				Shang et al., 2016d
4	<i>qFL-Chr5-3</i>	2016E1	CGR5025	NBRI0694	5.57	0.26	10.49				In the present study
	<i>qFL-chr5-5</i>	<u>2015E3</u>	<u>NBRI0694</u>	<u>DPL0022</u>	<u>3.66</u>	<u>0.29</u>	<u>7.13</u>				Ma et al.,2017
	<i>qFL-Chr5-6</i>	2012E4	<u>CGR5025</u>	<u>NBRI0694</u>				<u>4.72</u>	<u>0.18</u>	<u>9.11</u>	Shang et al., 2016d
		2012E4	<u>CGR5025</u>	<u>NBRI0694</u>	<u>9.13</u>	<u>0.35</u>	<u>15.75</u>				Shang et al., 2016d
		2012E4	NBRI0694	DPL0022	4.83	0.27	9.47				Shang et al., 2016d
5	<i>qFL-Chr9-1</i>	2016E1	SWU15511	SWU15413				3.53	-0.28	6.78	In the present study
	<i>qFL-Chr9-1</i>	2012E4	<u>SWU15517</u>	<u>SWU15511</u>	<u>2.02</u>	<u>-0.15</u>	<u>3.00</u>				Shang et al., 2016d
		2012E1	<u>SWU15511</u>	<u>SWU15413</u>	<u>2.70</u>	<u>-0.19</u>	<u>4.50</u>				Shang et al., 2016d
6	<i>qFL-Chr10-2</i>	<u>2016E2</u>	<u>HAU0635</u>	<u>NAU2139</u>				<u>4.76</u>	<u>-0.52</u>	<u>17.90</u>	In the present study
	<i>qFL-Chr10-3</i>	2012E2	SWU20260	Gh144	3.89	-0.33	7.64				Shang et al., 2016d
		2012E1	Gh320	HAU0635	2.46	-0.22	5.31				Shang et al., 2016d

No.	QTL	Env.	Flanking markers		BC			RIL			Reference
					LOD	Effect value	Var%	LOD	Effect value	Var%	
7	<i>qFS-Chr21-1</i>	2012E1	<u>Gh320</u>	<u>HAU0635</u>	<u>5.45</u>	<u>-0.33</u>	<u>13.47</u>				Shang et al., 2016d
		<u>2016E2</u>	<u>SWU0189</u>	<u>DPL0050a</u>				<u>3.40</u>	<u>-0.41</u>	<u>8.42</u>	In the present study
		<u>2015E2</u>	<u>SWU15915</u>	<u>SWU0189</u>	<u>3.28</u>	<u>-0.37</u>	<u>6.35</u>				Ma et al.,2017
		2012E2	<u>SWU0189</u>	<u>DPL0050a</u>				<u>2.16</u>	<u>-0.21</u>	<u>4.72</u>	Shang et al., 2016d
		2012E2	<u>SWU0189</u>	<u>DPL0050a</u>	<u>6.65</u>	<u>-0.53</u>	<u>15.51</u>				Shang et al., 2016d
		2012E1	<u>BNL3171</u>	<u>CGR5808</u>				<u>2.89</u>	<u>-0.24</u>	<u>5.80</u>	Shang et al., 2016d
		2012E1	<u>BNL3171</u>	<u>CGR5808</u>	<u>3.98</u>	<u>-0.36</u>	<u>7.10</u>				Shang et al., 2016d
8	<i>qFS-Chr21-2</i>	2016E2	BNL3171	CGR5808				2.89	-0.35	6.27	In the present study
		<u>2016E2</u>	<u>BNL3171</u>	<u>CGR5808</u>	<u>2.97</u>	<u>-0.29</u>	<u>6.90</u>				In the present study
		<u>2016E2</u>	<u>CGR5808</u>	<u>HAU0423</u>				<u>4.24</u>	<u>-0.44</u>	<u>9.62</u>	In the present study
		2016E1	CGR5808	HAU0423				5.31	-0.46	13.37	In the present study
		2016E2	CGR5808	HAU0423				2.85	-0.42	8.92	In the present study
		2016E2	HAU0423	CGR5806	5.18	-0.34	10.14				In the present study
		<i>qFS-Chr21-4</i>	2012E2	<u>BNL3171</u>	<u>CGR5808</u>	<u>4.52</u>	<u>-0.43</u>	<u>10.60</u>			
<i>qFM-Chr4-3</i>	2012E1	<u>SWU16783</u>	<u>NAU3868</u>	<u>2.57</u>	<u>0.11</u>	<u>9.84</u>				Shang et al., 2016d	

No.	QTL	Env.	Flanking markers		BC			RIL			Reference	
					LOD	Effect value	Var%	LOD	Effect value	Var%		
9	<i>qFM-Chr15-1</i>	2012E4	NAU3868	SWU21617	2.13	0.07	3.76				Shang et al., 2016d	
		<u>2016E2</u>	<u>DC40175</u>	<u>SWU11630</u>	<u>2.57</u>	<u>0.06</u>	<u>5.46</u>				In the present study	
		2016E1	DC40175	SWU11630				6.04	0.15	12.36	In the present study	
		<i>qFM-Chr15-1</i>	2012E4	<u>DC40175</u>	<u>SWU11630</u>				<u>6.40</u>	<u>0.07</u>	<u>12.70</u>	Shang et al., 2016d
			2012E4	<u>DC40175</u>	<u>SWU11630</u>	<u>5.28</u>	<u>0.10</u>	<u>9.85</u>				Shang et al., 2016d
10	<i>qFU-Chr22-1</i>	2012E4	DC40175	SWU11630	2.80	0.08	5.26				Shang et al., 2016d	
		2015E2	SWU21635	SWU21646	4.24	0.22	8.86				In the present study	
		<i>qFM-Chr22-1</i>	2012E2	<u>SWU21586</u>	<u>PGML1712</u>				<u>3.04</u>	<u>0.06</u>	<u>6.42</u>	Shang et al., 2016d
11	<i>qFU-Chr2-1</i>	2016E1	SWU12025	SWU11889	3.91	-0.28	11.30				In the present study	
		<i>qFU-Chr2-1</i>	2012E4	<u>SWU12025</u>	<u>SWU11889</u>	<u>3.54</u>	<u>-0.23</u>	<u>9.97</u>				Shang et al., 2016d
12	<i>qFE-Chr2-1</i>	2016E1	PGML0700	SWU12016	3.62	0.02	6.90				In the present study	
		<i>qFE-Chr2-3</i>	2012E4	<u>PGML0700</u>	<u>SWU12016</u>				<u>4.43</u>	<u>0.04</u>	<u>17.31</u>	Ma et al.,2017
		<i>qFL-chr10-1</i>	<u>2015E1</u>	<u>SWU20260</u>	<u>Gh144</u>	<u>3.15</u>	<u>-0.25</u>	<u>5.61</u>				Ma et al.,2017
13	<i>qFL-Chr19-1</i>	2015E2	SWU14431b	SWU17782	3.88	0.30	17.98				In the present study	
		<u>2016E2</u>	<u>SWU17782</u>	<u>DPL0056</u>				<u>5.28</u>	<u>0.41</u>	<u>11.05</u>	In the present study	

No.	QTL	Env.	Flanking markers	BC			RIL			Reference	
				LOD	Effect value	Var%	LOD	Effect value	Var%		
		2015E2	SWU17782	DPL0056	3.16	0.24	11.35			In the present study	
	<i>qFL-chr19-1</i>	<u>2015E2</u>	<u>PGML4342</u>	<u>SWU14431b</u>				<u>2.76</u>	<u>0.25</u>	<u>11.16</u>	Ma et al.,2017

Table S6 Phenotype values of fiber quality traits of BC/M population in three field trials in this study

Number of field trial plot	Material	FL/mm	FU/%	FS(cN/tex)	FE/%	FM	FL/mm	FU/%
		2015E2	2015E2	2015E2	2015E2	2015E2	2016E1	2016E1
001	14QM003	28.9	85.5	30.2	6.9	5.0	29.6	87.3
002	14QM003H	29.6	87.3	28.9	6.9	5.0	30.3	88.2
003	P♂	28.1	86.5	29.3	6.8	4.1	29.5	88.0
004	14QM004H	29.6	85.5	30.5	7.0	4.6	29.8	87.9
005	14QM004	29.0	84.1	30.1	7.0	5.0	30.4	87.6
006	14QM005	29.3	86.3	29.8	6.9	5.2	32.3	86.0
007	14QM005H	28.6	84.3	29.8	6.8	4.6	30.3	86.1
008	P♂	29.7	86.0	29.9	6.9	4.9	29.5	88.0
009	14QM006H	31.1	86.3	31.1	6.9	4.6	31.1	86.8
010	14QM006	30.6	86.1	31.4	7.0	5.3	30.7	86.9
011	14QM007	29.5	86.2	29.2	6.9	5.0	29.8	86.3
012	14QM007H	30.7	85.2	31.1	7.0	5.2	31.6	88.5
013	P♂	29.6	85.1	30.0	6.9	4.4	29.5	88.0
014	14QM008H	30.9	84.7	30.7	7.0	4.5	30.8	87.6
015	14QM008	29.9	85.2	28.9	6.9	4.6	31.3	86.7
016	14QM009	28.1	85.4	28.4	6.8	4.1	29.9	86.0
017	14QM009H	28.7	85.4	29.0	6.8	4.8	29.0	86.7
018	P♂	27.8	84.7	27.6	6.9	5.0	29.5	88.0
019	14QM010H	30.4	86.6	30.7	7.0	4.7	30.8	87.8
020	14QM010	31.4	85.6	32.3	7.0	4.3	32.1	86.1
021	14QM011	31.5	86.0	31.9	7.0	4.9	28.9	86.4
022	14QM011H	31.2	87.5	31.2	7.0	5.1	32.1	87.5
023	P♂	30.4	87.0	30.2	6.9	4.3	29.5	88.0
024	14QM012H	30.7	87.3	31.8	7.0	5.1	30.9	85.4
025	14QM012	31.6	84.9	35.6	7.0	4.3	28.8	84.3
026	14QM013	29.6	85.2	30.3	7.1	4.9	28.7	85.9
027	14QM013H	30.3	84.9	30.4	7.0	4.5	29.0	86.1
028	P♂	29.9	86.0	29.2	6.9	4.4	29.5	88.0
029	14QM014H	32.5	86.6	31.3	7.0	4.9	30.6	87.0
030	14QM014	29.6	83.4	29.4	6.8	3.9	29.9	85.1
031	14QM015	30.3	85.5	29.6	7.0	4.8	30.0	85.6
032	14QM015H	29.2	86.1	28.3	6.8	4.6	30.5	86.9
033	P♂	28.6	85.7	31.0	6.8	3.9	29.5	88.0
034	14QM016H	30.4	85.7	30.0	6.9	5.1	29.9	87.8
035	14QM016	31.1	86.0	32.8	7.0	4.7	31.8	87.4
036	14QM017	30.5	86.1	32.6	7.0	4.2	30.7	86.5
037	14QM017H	30.3	84.8	30.8	7.2	5.0	31.1	87.5
038	P♂	29.7	85.6	29.7	6.9	4.4	29.5	88.0
039	14QM018H	29.9	84.3	30.8	6.9	4.6	30.5	86.0
040	14QM018	32.0	86.7	34.1	7.0	4.0	29.9	84.9
041	14QM019	30.7	86.2	32.4	7.0	4.7	28.8	84.1
042	14QM019H	29.7	85.3	29.1	6.8	4.8	30.2	86.6
043	P♂	29.6	84.5	27.9	7.0	4.9	29.5	88.0
044	14QM020H	30.4	86.0	30.7	7.0	4.5	30.5	86.9
045	14QM020	30.9	82.9	29.6	6.9	4.3	32.3	86.2
046	14QM021	30.3	85.2	31.2	6.9	4.7	30.9	85.1

047	14QM021H	31.0	85.8	30.8	7.0	4.7	29.9	87.3
048	P♂	29.6	84.8	28.1	6.9	4.7	29.5	88.0
049	14QM022H	30.7	86.4	32.1	7.1	4.7	30.7	87.2
050	14QM022	30.1	84.4	30.4	7.1	4.7	30.3	86.3
051	14QM023	31.9	85.2	30.5	7.0	4.5	29.9	86.0
052	14QM023H	30.8	84.8	29.1	7.0	4.8	30.0	86.7
053	14QM380	30.9	86.5	29.7	7.0	4.7	28.9	86.4
054	14QM024H	32.2	86.5	32.5	7.3	4.5	31.4	86.1
055	14QM024	33.1	86.7	33.0	7.3	4.4	30.4	86.7
056	14QM025	-	-	-	-	-	30.7	85.9
057	14QM025H	31.6	87.2	31.9	7.1	4.9	29.5	87.8
058	P♂	29.8	85.5	29.0	6.9	4.5	28.9	86.4
059	14QM026H	30.2	87.0	30.0	7.0	5.0	30.1	86.9
060	14QM026	29.6	86.2	28.1	7.1	4.9	30.3	87.3
061	14QM027	30.6	85.8	28.5	7.0	4.9	29.1	87.0
062	14QM027H	30.8	87.4	29.3	7.0	5.1	29.9	88.2
063	P♂	32.1	85.9	31.7	7.1	4.8	28.9	86.4
064	14QM028H	30.3	85.9	29.7	6.9	4.6	31.0	86.8
065	14QM028	29.8	84.9	29.6	7.0	5.0	29.7	86.1
066	14QM029	32.1	86.7	29.9	7.1	4.9	31.6	87.3
067	14QM029H	31.1	87.2	30.6	7.0	4.8	30.4	84.1
068	P♂	30.0	87.3	29.9	6.9	4.7	28.9	86.4
069	14QM030H	32.1	84.8	32.7	7.0	4.2	31.3	86.8
070	14QM030	32.6	86.2	33.8	7.2	4.1	31.7	86.8
071	14QM031	32.0	87.0	31.9	7.1	4.0	31.4	84.4
072	14QM031H	32.0	85.8	31.4	7.0	4.5	32.0	84.8
073	P♂	31.5	86.4	31.2	7.1	4.4	28.9	86.4
074	14QM032H	32.1	86.4	31.7	7.0	5.2	30.6	86.3
075	14QM032	30.6	84.0	31.9	7.1	5.1	30.2	87.5
076	14QM033	29.9	86.0	31.1	6.9	4.9	30.3	86.5
077	14QM033H	31.3	85.7	31.3	7.1	5.3	30.7	87.0
078	P♂	30.3	87.2	29.8	6.9	4.8	28.9	86.4
079	14QM034H	30.4	85.6	31.0	7.0	5.0	30.6	87.8
080	14QM034	31.4	86.0	30.7	7.1	4.6	30.8	87.1
081	14QM035	32.5	86.6	33.8	7.0	4.4	30.2	86.1
082	14QM035H	30.5	85.1	30.7	7.0	4.8	30.6	87.0
083	P♂	30.6	86.6	29.1	6.9	4.8	28.9	86.4
084	14QM036H	31.4	85.4	30.4	7.0	4.6	31.0	86.6
085	14QM036	31.4	84.9	30.8	6.9	4.1	31.1	85.8
086	14QM037	29.8	84.8	30.2	6.9	5.3	30.7	87.5
087	14QM037H	31.2	86.7	32.1	7.0	4.5	30.7	85.7
088	P♂	29.5	85.2	30.6	6.9	4.8	28.9	86.4
089	14QM038H	30.1	86.9	27.3	6.9	4.8	29.6	86.7
090	14QM038	31.4	86.1	30.5	7.0	4.7	29.2	86.5
091	14QM039	30.3	86.7	30.0	7.0	5.5	29.7	85.8
092	14QM039H	31.0	86.5	30.8	7.0	5.3	30.4	88.1
093	P♂	29.9	87.1	28.8	6.9	5.1	28.9	86.4
094	14QM040H	30.9	86.9	30.0	7.0	4.8	30.1	86.0
095	14QM040	30.5	87.2	31.0	7.0	4.8	30.0	86.9
096	14QM041	32.5	87.3	32.0	7.2	4.8	31.8	86.7

097	14QM041H	31.6	86.1	32.0	7.1	4.3	30.5	86.1
098	P♂	30.6	84.3	29.1	6.9	4.5	28.9	86.4
099	14QM042H	30.9	85.8	30.6	7.1	5.3	29.9	88.2
100	14QM042	31.2	87.0	30.2	7.1	5.1	30.2	87.3
101	14QM043	30.2	84.7	29.8	7.0	5.2	29.8	87.2
102	14QM043H	32.2	87.2	30.8	7.1	5.2	30.6	87.6
103	14QM380	29.5	86.4	29.1	6.9	5.0	28.1	83.1
104	14QM044H	30.7	86.6	29.9	7.1	5.2	29.6	86.4
105	14QM044	30.8	84.8	29.4	7.0	5.0	31.1	87.7
106	14QM045	32.4	87.1	31.6	7.1	4.7	30.7	87.3
107	14QM045H	31.9	85.9	29.0	7.0	5.0	31.5	87.1
108	P♂	30.9	86.1	30.2	7.0	4.4	28.1	83.1
109	14QM046H	29.7	86.2	29.2	7.0	4.7	29.9	88.0
110	14QM046	29.3	84.4	28.6	6.9	4.9	29.0	87.1
111	14QM047	31.5	85.4	30.7	7.0	5.1	30.9	86.1
112	14QM047H	32.2	86.3	31.6	7.0	5.1	30.3	87.1
113	P♂	30.5	86.6	30.4	7.0	5.0	28.1	83.1
114	14QM048H	31.2	84.3	31.1	7.0	4.4	30.0	87.9
115	14QM048	30.3	85.4	30.6	7.0	4.7	29.3	84.5
116	14QM049	31.1	85.1	30.6	7.1	4.1	29.5	87.5
117	14QM049H	32.0	85.4	30.5	7.1	4.6	30.7	86.8
118	P♂	31.1	85.8	31.6	7.0	5.1	28.1	83.1
119	14QM050H	29.8	86.1	28.9	6.9	4.7	31.9	86.9
120	14QM050	32.0	86.1	31.2	7.0	4.6	31.2	86.3
121	14QM051	31.7	86.5	33.2	7.0	4.6	31.2	88.3
122	14QM051H	31.6	86.2	30.9	6.9	4.4	30.2	87.5
123	P♂	28.7	85.8	28.6	6.9	4.7	28.1	83.1
124	14QM052H	30.7	85.1	30.1	7.0	4.7	30.3	87.5
125	14QM052	-	-	-	-	-	29.9	86.6
126	14QM053	33.0	85.7	34.3	7.1	3.6	30.9	86.4
127	14QM053H	31.1	85.3	31.9	7.2	4.4	31.9	87.0
128	P♂	29.4	86.5	28.9	6.9	5.0	28.1	83.1
129	14QM054H	29.9	85.7	29.9	6.9	4.8	28.6	84.8
130	14QM054	30.3	86.0	28.8	7.0	4.8	29.4	86.9
131	14QM055	29.9	85.4	31.4	6.9	5.4	30.0	88.1
132	14QM055H	31.2	85.5	30.9	6.9	4.7	28.9	85.8
133	P♂	30.4	83.8	29.7	6.9	4.3	28.1	83.1
134	14QM056H	31.4	85.4	33.1	7.0	4.4	32.0	86.4
135	14QM056	29.9	82.7	33.6	6.9	3.4	32.1	85.7
136	14QM057	29.6	84.1	30.2	6.9	3.9	29.3	85.8
137	14QM057H	30.8	83.7	31.2	7.0	4.5	28.0	85.4
138	P♂	29.4	82.9	30.6	7.0	5.0	28.1	83.1
139	14QM058H	28.9	84.6	30.7	6.9	4.8	30.2	85.5
140	14QM058	31.3	83.5	32.6	7.0	4.6	31.2	85.6
141	14QM059	28.2	85.0	28.3	6.8	4.6	31.0	86.3
142	14QM059H	30.4	85.3	29.8	7.0	4.9	30.0	88.4
143	P♂	30.8	86.5	29.4	6.9	4.7	28.1	83.1
144	14QM060H	31.1	86.4	30.4	7.0	4.6	30.3	87.7
145	14QM060	33.3	85.5	33.9	7.1	4.3	31.6	86.4
146	14QM061	29.5	86.4	30.0	6.9	5.3	29.1	85.3

147	14QM061H	30.1	84.7	29.2	6.8	5.1	28.8	86.3
148	P♂	31.1	85.5	29.9	7.0	4.5	28.1	83.1
149	14QM062H	31.7	86.7	29.9	7.0	4.6	30.6	88.5
150	14QM062	32.3	85.7	33.4	7.0	4.2	32.5	86.4
151	14QM063	31.2	86.4	31.4	7.0	5.0	29.1	86.1
152	14QM063H	31.1	86.1	32.8	7.0	4.6	30.9	87.5
153	14QM380	30.7	85.7	30.2	7.0	4.6	30.1	87.5
154	14QM064H	30.8	85.2	30.7	7.0	5.3	29.5	87.8
155	14QM064	32.3	85.6	32.2	7.1	5.1	29.9	86.4
156	14QM065	30.5	85.9	29.9	6.9	4.9	30.9	87.6
157	14QM065H	30.9	85.7	32.0	7.0	4.7	30.6	87.6
158	P♂	30.8	86.6	30.1	7.0	4.6	30.1	87.5
159	14QM066H	31.4	87.4	29.2	7.0	5.1	28.8	87.4
160	14QM066	30.9	85.6	31.5	7.0	5.0	30.5	88.1
161	14QM067	31.1	86.5	31.0	7.0	4.7	30.2	87.0
162	14QM067H	30.7	84.2	29.6	7.0	4.9	28.5	85.3
163	P♂	30.8	85.4	29.9	6.9	4.8	30.1	87.5
164	14QM068H	32.2	86.4	30.4	7.1	4.8	28.2	86.7
165	14QM068	30.7	85.2	29.8	7.0	5.5	31.1	86.8
166	14QM069	28.6	84.8	28.1	6.8	4.9	28.3	86.5
167	14QM069H	29.9	85.0	29.6	6.8	5.2	28.6	87.9
168	P♂	29.7	85.6	29.6	6.9	5.1	30.1	87.5
169	14QM070H	31.2	84.6	30.8	7.1	4.9	30.7	88.1
170	14QM070	30.8	85.0	30.4	7.0	4.6	31.7	85.7
171	14QM071	30.5	82.3	29.9	7.0	4.8	30.1	86.4
172	14QM071H	31.0	84.7	30.6	6.9	4.8	29.9	87.7
173	P♂	30.3	84.9	31.0	6.9	4.6	30.1	87.5
174	14QM072H	31.3	85.3	31.2	7.0	4.8	30.3	89.4
175	14QM072	30.6	84.8	30.0	6.9	4.9	29.0	85.3
176	14QM073	31.5	86.4	32.7	7.0	4.8	30.1	88.4
177	14QM073H	31.6	86.4	30.2	7.0	5.2	30.1	88.1
178	P♂	30.6	86.9	29.7	6.9	4.6	30.1	87.5
179	14QM074H	32.2	85.0	31.3	7.0	4.7	30.3	87.5
180	14QM074	30.9	84.2	31.4	6.9	4.5	30.2	86.7
181	14QM075	31.4	86.4	30.0	7.0	4.5	31.1	86.1
182	14QM075H	31.7	86.5	31.1	7.1	4.5	29.5	86.6
183	P♂	30.8	86.7	30.3	6.9	4.2	30.1	87.5
184	14QM076H	30.2	86.2	29.3	7.0	5.2	29.4	86.3
185	14QM076	29.1	84.9	28.1	6.9	5.4	28.2	84.2
186	14QM077	29.7	86.1	30.9	7.1	5.2	28.8	88.0
187	14QM077H	30.4	86.8	31.9	7.1	4.7	30.3	86.1
188	P♂	30.2	85.1	31.7	7.1	4.2	30.1	87.5
189	14QM078H	30.5	85.0	30.7	7.0	5.2	30.9	86.5
190	14QM078	30.1	84.9	29.6	6.9	5.1	29.0	86.3
191	14QM079	30.8	85.7	29.4	6.9	4.9	32.1	85.7
192	14QM079H	31.4	85.6	29.9	6.9	4.5	29.8	87.3
193	P♂	29.5	83.5	28.6	6.9	4.7	30.1	87.5
194	14QM080H	30.8	86.5	31.5	7.0	4.5	29.9	87.3
195	14QM080	30.2	86.1	29.4	6.9	4.5	28.8	84.1
196	14QM081	29.8	85.9	30.9	7.0	4.4	30.3	85.6

197	14QM081H	31.0	86.4	31.9	7.1	4.9	30.1	87.2
198	P♂	29.8	85.6	29.3	6.9	4.2	30.1	87.5
199	14QM082H	30.7	85.6	29.1	6.9	4.9	30.0	85.7
200	14QM082	32.8	85.2	34.5	7.0	4.0	31.5	86.0
201	14QM083	31.9	85.7	31.0	7.1	4.7	30.8	87.1
202	14QM083H	30.4	86.2	30.7	7.1	5.1	28.3	86.4
203	14QM380	29.4	86.4	28.6	6.9	4.7	30.8	87.5
204	14QM084H	30.5	87.3	28.6	7.0	5.2	31.2	87.6
205	14QM084	31.1	84.2	30.8	7.1	5.2	29.8	85.2
206	14QM085	31.3	85.7	33.0	7.1	4.5	29.9	79.3
207	14QM085H	31.7	86.7	31.1	7.1	5.0	31.1	88.0
208	P♂	30.3	86.1	30.3	7.0	4.6	30.8	87.5
209	14QM086H	30.1	86.8	30.8	7.0	4.4	29.0	86.2
210	14QM086	31.4	87.6	31.8	7.2	4.4	30.8	87.7
211	14QM087	30.8	85.0	30.9	6.9	4.4	30.5	87.1
212	14QM087H	30.2	85.2	29.9	6.9	4.8	29.0	85.7
213	P♂	31.4	85.6	30.7	7.0	4.3	30.8	87.5
214	14QM088H	32.5	86.9	33.9	7.1	4.4	32.0	85.8
215	14QM088	32.4	86.1	32.3	7.1	4.7	30.3	86.5
216	14QM089	29.5	84.6	29.4	6.9	5.5	28.9	85.9
217	14QM089H	30.4	85.3	28.2	6.9	5.1	29.8	86.2
218	P♂	30.5	84.8	30.9	7.0	4.4	30.8	87.5
219	14QM090H	32.1	84.7	30.8	7.0	3.8	33.3	86.5
220	14QM090	33.3	84.8	34.8	7.1	3.9	34.3	85.5
221	14QM091	31.5	85.3	29.9	7.0	4.8	30.0	85.4
222	14QM091H	30.7	85.4	30.5	7.0	4.5	30.2	87.0
223	P♂	30.4	87.6	31.3	7.0	4.5	30.8	87.5
224	P♂	30.0	87.3	29.4	6.9	4.9	29.5	86.0
225	F1	31.3	85.0	31.3	7.0	4.7	30.4	86.1
226	P♀	30.5	84.9	29.7	6.8	4.9	30.6	85.2
227	P♂	29.6	85.9	30.3	6.9	4.5	30.8	87.5
228	14QM092H	32.7	84.7	32.5	7.1	4.4	30.9	85.4
229	14QM092	32.3	84.8	32.5	7.0	3.8	31.4	87.2
230	14QM093	30.6	85.2	29.1	6.9	4.8	31.7	87.9
231	14QM093H	31.5	83.6	32.9	7.1	4.1	30.1	85.5
232	P♂	30.4	84.6	29.8	6.9	4.7	30.8	87.5
233	14QM094H	30.2	85.8	29.7	6.9	4.8	28.9	85.9
234	14QM094	30.5	85.1	28.5	6.9	4.7	28.5	86.1
235	14QM095	29.2	86.0	28.7	6.9	5.2	28.4	89.2
236	14QM095H	30.1	86.2	29.7	6.9	4.8	30.2	86.2
237	P♂	29.7	85.0	29.6	6.9	4.2	30.8	87.5
238	14QM096H	31.1	84.8	31.1	7.0	4.7	30.7	86.5
239	14QM096	31.7	85.8	31.4	7.1	4.3	30.7	86.8
240	14QM097	30.2	84.7	29.4	6.9	4.9	29.6	86.1
241	14QM097H	29.8	84.8	29.9	6.9	4.4	30.7	87.1
242	P♂	30.2	85.5	29.5	6.9	4.6	30.8	87.5
243	14QM098H	30.1	86.7	29.3	7.0	5.0	30.5	87.2
244	14QM098	30.7	86.0	31.3	7.0	4.5	30.1	86.4
245	14QM099	30.2	84.9	29.4	6.9	5.3	29.6	87.5
246	14QM099H	30.7	86.3	31.9	6.9	4.1	28.6	86.8

247	P♂	31.2	86.4	31.2	7.0	4.5	30.8	87.5
248	14QM100H	31.0	85.5	28.9	6.8	4.0	29.7	88.8
249	14QM100	30.0	86.6	28.9	6.9	5.1	30.6	85.4
250	14QM101	30.1	87.6	29.7	6.9	4.8	29.4	87.2
251	14QM101H	30.8	85.6	32.0	7.1	4.8	31.2	87.1
252	14QM380	30.0	84.6	27.8	6.8	4.8	30.5	86.2
253	14QM102H	31.0	84.6	29.8	7.0	4.7	30.3	85.8
254	14QM102	31.1	86.7	29.9	7.0	4.6	29.7	85.7
255	14QM103	32.8	85.8	31.2	7.0	5.0	32.4	87.4
256	14QM103H	32.3	85.8	30.3	7.0	4.7	31.4	87.3
257	P♂	29.1	84.1	28.6	6.9	4.7	30.5	86.2
258	14QM104H	32.7	86.8	31.3	7.0	5.1	30.2	86.8
259	14QM104	32.7	85.7	32.4	7.0	4.3	31.1	87.4
260	14QM105	31.2	83.8	33.4	7.1	4.5	30.2	85.7
261	14QM105H	31.5	84.9	30.0	7.0	5.0	29.9	86.0
262	P♂	29.6	84.6	28.8	6.9	4.9	30.5	86.2
263	14QM106H	32.0	85.9	29.7	7.0	5.0	30.4	86.9
264	14QM106	32.6	85.7	31.7	7.2	5.0	31.6	88.2
265	14QM107	30.0	85.1	31.0	6.9	5.1	30.4	86.3
266	14QM107H	31.8	85.9	30.3	7.0	5.4	29.6	86.8
267	P♂	32.3	85.3	30.0	7.0	4.4	30.5	86.2
268	14QM108H	31.1	86.4	29.4	7.0	5.3	30.2	87.3
269	14QM108	31.4	85.1	28.1	6.9	4.7	30.6	85.4
270	14QM109	29.5	85.3	29.2	6.9	4.4	29.1	84.1
271	14QM109H	30.8	85.0	29.1	6.9	4.8	30.7	87.4
272	P♂	31.8	86.1	30.7	7.0	4.5	30.5	86.2
273	14QM110H	31.1	86.2	31.4	7.0	5.3	30.3	86.5
274	14QM110	30.5	85.5	31.4	6.9	4.9	29.8	87.6
275	14QM111	31.4	87.1	29.3	7.1	4.6	29.7	87.8
276	14QM111H	31.0	85.7	30.1	6.9	4.6	31.3	87.6
277	P♂	31.0	85.8	30.8	6.9	4.4	30.5	86.2
278	14QM112H	31.4	85.6	29.6	7.0	5.4	31.2	86.1
279	14QM112	30.2	85.4	27.5	6.9	5.3	31.8	87.7
280	14QM113	29.8	83.5	28.8	6.8	4.9	31.8	85.9
281	14QM113H	31.4	85.8	31.5	7.0	4.0	30.6	87.0
282	P♂	30.2	86.4	29.8	7.0	4.3	30.5	86.2
283	14QM114H	31.4	86.0	28.9	6.9	4.8	30.1	85.9
284	14QM114	32.2	85.8	31.5	7.1	5.2	31.6	86.8
285	14QM115	32.0	86.1	29.8	7.0	5.1	30.4	87.1
286	14QM115H	31.9	86.2	31.9	7.0	4.7	30.6	87.0
287	P♂	29.9	84.8	28.2	6.8	4.5	30.5	86.2
288	14QM116H	31.6	87.6	29.7	7.1	5.1	30.6	86.7
289	14QM116	31.8	85.4	29.3	7.0	4.7	29.7	87.3
290	14QM117	29.4	82.9	27.3	6.8	5.3	29.5	85.7
291	14QM117H	30.8	83.6	27.0	6.9	5.3	30.1	85.2
292	P♂	29.4	85.0	27.8	6.8	4.4	30.5	86.2
293	14QM118H	30.7	86.2	29.9	6.9	4.5	31.7	86.1
294	14QM118	31.4	86.5	31.9	7.1	5.1	28.8	86.7
295	14QM119	31.1	85.5	30.4	7.0	5.0	32.1	84.6
296	14QM119H	30.7	85.9	30.3	7.0	4.6	31.1	85.9

297	P♂	29.8	85.9	28.6	6.9	4.7	30.5	86.2
298	14QM120H	31.4	87.5	29.5	7.0	5.1	30.5	86.1
299	14QM120	30.4	86.2	31.3	6.9	4.5	29.0	84.6
300	14QM121	30.5	84.9	30.5	6.9	4.4	30.5	87.4
301	14QM121H	31.0	85.7	29.8	7.0	4.7	30.8	87.0
302	14QM380	29.1	83.9	28.9	6.9	4.6	30.2	87.2
303	14QM122H	31.1	85.6	30.3	6.9	4.0	30.5	87.2
304	14QM122	31.8	87.0	33.1	7.1	4.2	31.1	86.8
305	14QM123	31.2	86.6	31.8	7.0	4.5	30.9	87.6
306	14QM123H	30.6	87.1	31.0	6.9	4.3	31.3	88.3
307	P♂	29.5	85.6	28.6	6.9	5.1	30.2	87.2
308	14QM124H	30.0	85.3	31.5	7.0	5.0	30.4	87.0
309	14QM124	31.2	86.0	29.6	7.0	5.1	30.5	87.0
310	14QM125	29.5	84.6	28.2	6.8	4.8	28.4	86.8
311	14QM125H	30.4	84.9	28.7	6.9	5.1	28.0	86.1
312	P♂	-	-	-	-	-	30.2	87.2
313	14QM126H	30.8	86.4	31.4	7.0	4.7	28.7	83.7
314	14QM126	30.7	84.5	30.9	7.0	5.4	29.8	86.9
315	14QM127	30.9	86.6	31.0	6.9	4.7	30.3	86.1
316	14QM127H	31.3	85.7	31.0	6.9	4.3	30.4	86.3
317	P♂	31.5	85.1	30.4	6.9	4.6	30.2	87.2
318	14QM128H	32.1	85.3	29.5	7.0	4.5	31.3	86.3
319	14QM128	31.3	83.5	30.6	6.9	3.7	31.3	84.6
320	14QM129	31.0	86.0	30.4	7.0	4.6	31.1	86.4
321	14QM129H	31.3	85.6	31.3	6.9	4.2	30.7	85.9
322	P♂	30.6	85.4	29.7	6.9	4.6	30.2	87.2
323	14QM130H	32.3	86.7	31.6	7.0	4.3	30.8	87.2
324	14QM130	30.9	84.3	31.6	7.0	4.2	30.8	84.9
325	14QM131	32.4	86.4	32.2	7.0	4.1	30.1	85.3
326	14QM131H	32.3	85.6	31.5	7.0	5.0	32.1	85.5
327	P♂	31.5	86.4	29.2	6.9	4.6	30.2	87.2
328	14QM132H	29.6	84.3	27.8	6.9	5.5	30.2	84.5
329	14QM132	30.2	85.4	30.1	7.0	4.4	29.7	87.2
330	14QM133	31.1	86.7	30.3	6.9	4.6	30.3	83.8
331	14QM133H	31.9	85.8	31.9	7.1	5.1	29.6	86.8
332	P♂	30.0	85.2	28.1	6.8	4.5	30.2	87.2
333	14QM134H	30.4	85.6	29.6	6.9	4.6	29.6	86.9
334	14QM134	30.9	85.2	29.9	7.0	4.9	28.9	86.0
335	14QM135	31.3	82.7	28.8	6.9	3.7	31.0	86.2
336	14QM135H	32.5	85.5	30.6	7.0	5.0	30.6	85.8
337	P♂	30.6	85.2	28.7	6.9	4.3	30.2	87.2
338	14QM136H	32.2	86.2	30.7	7.0	4.7	31.6	85.8
339	14QM136	31.5	85.8	31.2	6.9	4.9	31.3	85.3
340	14QM137	31.6	81.7	34.9	7.0	3.8	31.2	84.9
341	14QM137H	30.3	85.0	32.1	6.9	4.5	31.1	86.2
342	P♂	32.2	84.4	35.3	7.1	4.1	30.2	87.2
343	14QM138H	31.1	86.1	31.2	6.9	4.6	29.6	83.7
344	14QM138	31.4	86.0	31.0	6.9	4.3	29.7	86.0
345	14QM139	30.9	86.1	29.9	7.0	4.7	28.5	85.4
346	14QM139H	31.5	87.4	31.3	7.0	4.3	31.4	85.7

347	P♂	31.2	85.8	29.7	7.0	4.8	30.2	87.2
348	14QM140H	31.8	85.8	31.8	7.0	4.9	33.1	86.9
349	14QM140	31.4	84.7	31.6	6.9	4.3	30.8	86.4
350	14QM141	30.3	86.7	30.2	7.0	5.2	30.9	85.8
351	14QM141H	31.3	86.3	31.4	7.0	4.7	30.3	85.9
352	14QM380	31.4	86.9	30.0	7.0	4.3	29.3	87.2
353	14QM142H	32.3	86.8	30.2	7.0	4.6	30.3	86.9
354	14QM142	31.5	86.1	32.1	7.0	4.1	31.3	84.7
355	14QM143	31.8	86.7	34.5	7.1	4.6	29.5	86.6
356	14QM143H	31.2	86.4	33.2	6.9	3.9	29.6	86.3
357	P♂	31.0	86.3	29.2	6.9	4.7	29.3	87.2
358	14QM144H	31.7	86.5	31.3	7.0	4.6	29.7	85.4
359	14QM144	-	-	-	-	-	27.3	82.7
360	14QM145	31.0	86.2	28.4	6.9	4.4	29.7	87.4
361	14QM145H	31.6	86.1	31.2	7.0	4.7	29.9	86.5
362	P♂	29.9	85.8	29.1	6.8	4.4	29.3	87.2
363	14QM146H	30.3	87.8	30.6	6.9	4.8	31.1	87.6
364	14QM146	29.8	86.7	29.7	6.9	4.2	31.5	86.7
365	14QM147	32.7	88.3	30.4	7.2	4.4	31.6	84.8
366	14QM147H	32.6	86.6	30.4	7.0	4.4	32.1	85.3
367	P♂	31.1	86.2	31.0	6.9	4.7	29.3	87.2
368	14QM148H	32.2	87.5	32.2	7.0	4.1	31.5	87.5
369	14QM148	31.9	86.6	32.6	7.0	4.2	31.4	86.4
370	14QM149	31.9	86.7	32.0	7.0	4.2	31.9	86.0
371	14QM149H	31.3	85.6	30.9	6.9	3.9	32.2	84.6
372	P♂	30.3	85.4	30.2	6.9	4.5	29.3	87.2
373	14QM150H	31.9	86.9	30.3	7.0	4.7	30.6	85.4
374	14QM150	31.8	87.8	33.5	7.1	4.6	30.9	86.3
375	14QM151	30.7	87.8	31.3	6.9	4.5	30.7	86.3
376	14QM151H	31.3	87.4	33.5	7.0	4.2	30.3	86.6
377	P♂	28.2	85.7	26.7	6.8	4.8	29.3	87.2
378	14QM152H	31.4	87.0	31.7	7.0	4.2	30.4	85.7
379	14QM152	31.2	86.6	31.9	6.9	4.3	30.2	87.5
380	14QM153	29.9	87.2	31.0	6.9	4.7	30.0	86.8
381	14QM153H	31.2	87.4	31.4	7.0	5.1	30.5	85.6
382	P♂	31.3	86.8	29.7	6.9	4.5	29.3	87.2
383	14QM154H	31.3	85.9	30.3	7.0	4.5	29.7	85.3
384	14QM154	31.4	86.6	29.8	6.9	4.7	31.9	85.3
385	14QM155	31.4	87.7	34.2	7.1	4.8	30.6	85.4
386	14QM155H	31.0	86.6	29.9	6.9	4.8	29.3	87.6
387	P♂	30.4	88.2	31.2	6.9	4.1	29.3	87.2
388	14QM156H	31.6	86.0	30.3	7.0	4.7	31.3	83.5
389	14QM156	30.8	85.0	31.1	7.0	4.4	30.4	86.7
390	14QM157	32.5	85.0	30.4	7.0	4.6	31.0	86.4
391	14QM157H	31.9	86.3	30.0	7.0	4.4	31.6	85.0
392	P♂	31.7	86.7	31.4	7.0	4.2	29.3	87.2
393	14QM158H	30.2	86.0	29.2	6.9	4.8	28.2	84.7
394	14QM158	29.2	86.3	28.4	6.9	5.1	24.4	82.7
395	14QM159	32.9	87.8	29.7	7.1	4.7	32.5	86.3
396	14QM159H	32.8	86.9	31.4	7.2	4.6	31.0	86.3

397	P♂	31.6	86.4	30.9	6.9	4.6	29.3	87.2
398	14QM160H	31.3	87.3	31.3	7.0	4.7	31.2	85.6
399	14QM160	31.9	86.2	31.3	6.9	4.6	30.9	86.2
400	14QM161	31.3	85.4	29.4	6.9	4.6	29.6	85.9
401	14QM161H	30.8	86.1	29.2	7.0	5.1	30.5	87.1
402	14QM380	29.9	85.7	29.4	6.9	4.8	29.7	87.5
403	14QM162H	31.0	86.7	31.0	7.1	4.8	29.4	85.5
404	14QM162	30.3	87.5	30.2	7.0	5.5	28.7	86.4
405	14QM163	32.4	87.0	32.4	7.1	4.5	31.3	86.1
406	14QM163H	31.3	87.9	32.0	7.0	4.7	31.3	85.7
407	P♂	30.1	86.4	30.5	7.0	5.1	29.7	87.5
408	14QM164H	31.3	87.5	33.7	7.1	4.1	29.4	85.1
409	14QM164	30.3	87.9	30.2	7.0	4.6	28.4	87.0
410	14QM165	31.4	84.0	33.5	6.9	4.2	29.2	85.0
411	14QM165H	31.9	87.1	32.5	6.9	4.2	31.5	86.5
412	P♂	30.7	87.6	28.7	7.0	4.8	29.7	87.5
413	14QM166H	33.4	86.9	32.2	7.0	4.5	30.4	85.6
414	14QM166	33.4	86.8	32.8	7.0	4.2	31.4	87.6
415	14QM167	32.2	85.8	32.8	7.0	4.0	31.4	85.6
416	14QM167H	32.4	86.8	33.5	7.0	4.3	31.1	83.5
417	P♂	30.4	86.5	30.2	6.9	4.7	29.7	87.5
418	14QM168H	31.3	86.8	30.7	7.0	4.6	29.9	85.0
419	14QM168	30.0	85.9	27.7	6.8	5.1	29.2	85.0
420	14QM169	30.0	85.3	29.1	6.9	5.2	28.7	86.9
421	14QM169H	29.8	87.5	28.3	6.9	5.3	28.7	86.0
422	P♂	30.7	88.0	30.3	7.0	4.6	29.7	87.5
423	14QM170H	29.8	85.6	28.7	6.9	4.8	29.6	86.0
424	14QM170	30.1	86.7	29.2	7.1	4.9	29.7	86.2
425	14QM171	30.7	86.7	31.8	7.0	5.1	29.3	86.7
426	14QM171H	30.2	86.4	29.2	6.9	4.8	30.2	85.5
427	P♂	31.4	86.2	29.9	7.0	5.1	29.7	87.5
428	14QM172H	31.5	84.4	31.7	7.0	4.3	30.7	84.9
429	14QM172	32.0	86.6	30.7	7.1	5.0	29.5	85.5
430	14QM173	31.3	85.2	30.8	7.1	4.8	31.0	85.3
431	14QM173H	30.8	85.8	30.7	7.0	4.8	30.4	84.2
432	P♂	29.9	86.6	30.2	7.0	4.4	29.7	87.5
433	14QM174H	30.6	85.7	30.8	6.9	4.4	26.8	84.2
434	14QM174	30.5	84.9	31.3	6.9	4.3	25.2	84.2
435	14QM175	30.8	86.3	30.5	7.0	5.3	27.5	83.0
436	14QM175H	31.6	86.9	31.3	7.1	5.0	31.1	86.3
437	P♂	30.2	85.5	29.3	6.9	5.0	29.7	87.5
438	14QM176H	32.4	85.4	32.9	7.0	4.5	31.4	85.0
439	14QM176	32.5	85.0	33.3	7.0	4.5	31.4	84.2
440	14QM177	29.7	85.7	29.5	7.1	5.2	30.1	85.5
441	14QM177H	30.3	87.0	29.3	6.9	4.9	29.3	87.3
442	P♂	31.0	87.1	29.3	6.9	5.0	29.7	87.5
443	14QM178H	31.9	87.4	32.6	7.1	5.1	29.2	84.2
444	14QM178	30.7	85.6	31.2	7.0	4.5	31.6	85.6
445	14QM179	31.7	85.9	31.5	7.1	5.0	31.0	85.6
446	14QM179H	31.0	86.1	29.2	7.0	5.2	31.5	86.2

447	P♂	31.6	85.5	32.8	7.1	4.2	29.7	87.5
448	P♂	31.9	85.9	30.9	6.9	4.4	29.2	86.7
449	F1	31.4	85.7	31.8	7.0	4.3	31.4	86.2
450	P♀	30.6	85.8	31.2	7.0	5.4	31.8	85.4
451	14QM003	29.7	85.6	30.7	7.0	5.2	29.4	85.2
452	14QM003H	30.1	85.8	29.7	7.0	5.4	29.2	84.0
453	14QM380	30.1	86.2	28.8	7.0	5.0	29.7	86.0
454	14QM004H	30.4	85.3	31.2	6.9	5.1	31.0	86.1
455	14QM004	30.2	85.6	29.3	6.9	5.0	30.9	86.6
456	14QM005	32.1	83.8	32.3	7.0	5.0	32.0	85.0
457	14QM005H	30.9	85.9	31.9	7.0	5.3	30.6	85.7
458	P♂	31.2	86.6	30.6	7.0	5.0	29.7	86.0
459	14QM006H	31.3	87.2	31.7	7.1	5.3	30.3	85.0
460	14QM006	32.1	86.2	33.5	7.0	5.2	31.5	86.0
461	14QM007	30.9	86.9	30.1	7.1	5.1	29.5	84.3
462	14QM007H	30.8	86.8	29.7	7.0	5.2	29.6	87.2
463	P♂	30.0	84.9	29.3	6.9	4.5	29.7	86.0
464	14QM008H	32.1	85.4	31.5	7.0	4.1	31.4	85.3
465	14QM008	30.9	84.9	31.5	7.0	4.0	30.6	85.8
466	14QM009	29.1	85.8	28.6	6.9	4.9	29.1	87.2
467	14QM009H	31.7	85.9	31.4	7.0	5.0	29.7	87.8
468	P♂	29.7	86.8	29.8	6.9	4.1	29.7	86.0
469	14QM010H	31.2	84.9	32.9	7.0	4.3	31.4	84.9
470	14QM010	30.8	82.1	33.1	7.0	4.3	31.6	87.8
471	14QM011	31.4	86.4	32.1	7.0	5.3	30.0	86.0
472	14QM011H	32.0	87.4	29.9	7.0	4.9	31.1	85.6
473	P♂	31.1	84.0	30.9	6.9	4.7	29.7	86.0
474	14QM012H	32.3	86.4	34.1	7.1	4.6	30.3	85.4
475	14QM012	31.3	84.5	32.9	6.9	4.3	30.0	86.6
476	14QM013	30.4	85.7	29.1	7.0	4.9	29.5	84.1
477	14QM013H	30.9	86.1	30.4	7.0	4.5	28.8	87.3
478	P♂	31.0	86.2	31.3	7.0	4.6	29.7	86.0
479	14QM014H	30.1	85.4	29.5	6.9	4.7	29.7	87.0
480	14QM014	30.5	85.8	28.5	6.9	4.4	30.2	85.3
481	14QM015	30.7	86.9	29.3	7.1	4.7	29.3	85.1
482	14QM015H	30.2	85.4	28.0	6.9	5.2	28.7	87.6
483	P♂	31.3	86.3	30.8	7.0	4.8	29.7	86.0
484	14QM016H	31.7	86.3	31.0	7.0	5.0	30.1	85.8
485	14QM016	31.7	85.2	32.2	7.0	4.5	30.1	86.3
486	14QM017	32.1	85.3	31.4	7.2	4.3	31.0	86.6
487	14QM017H	31.1	85.6	33.0	7.1	4.0	30.4	85.6
488	P♂	30.1	86.9	31.7	6.9	4.3	29.7	86.0
489	14QM018H	32.1	85.6	32.5	7.0	4.0	31.5	84.9
490	14QM018	32.2	85.8	34.4	7.0	4.1	30.8	84.8
491	14QM019	31.2	85.5	33.1	7.1	4.3	30.0	85.9
492	14QM019H	29.9	85.9	31.7	7.1	4.8	31.0	85.3
493	P♂	30.7	85.9	30.4	7.0	5.0	29.7	86.0
494	14QM020H	31.9	86.0	31.9	7.1	4.9	30.2	86.2
495	14QM020	31.1	84.9	31.4	6.9	4.2	30.6	83.2
496	14QM021	30.0	85.0	30.9	7.0	4.9	31.2	85.0

497	14QM021H	29.9	85.4	29.9	7.0	4.9	30.2	86.2
498	P♂	-	-	-	-	-	29.7	86.0
499	14QM022H	31.5	85.9	31.0	7.0	4.5	31.3	86.4
500	14QM022	31.2	85.4	30.6	6.9	3.9	32.1	86.7
501	14QM023	31.8	85.6	31.2	7.1	4.2	31.8	84.6
502	14QM023H	30.8	85.9	30.8	7.0	4.5	31.0	85.5
503	14QM380	30.6	86.4	30.0	6.9	4.9	29.4	85.9
504	14QM024H	31.9	86.2	31.9	7.1	4.6	31.7	87.6
505	14QM024	32.2	86.1	32.8	7.2	4.4	32.1	86.3
506	14QM025	-	-	-	-	-	30.5	87.2
507	14QM025H	31.5	87.2	33.1	7.0	4.3	30.4	86.7
508	P♂	30.5	86.2	30.2	7.0	4.7	29.4	85.9
509	14QM026H	30.5	88.2	28.6	7.0	5.1	30.8	87.7
510	14QM026	31.5	87.1	30.1	7.1	4.9	31.2	86.5
511	14QM027	30.4	86.3	30.1	7.1	4.7	30.2	87.0
512	14QM027H	30.8	88.4	29.7	7.2	5.2	29.5	88.4
513	P♂	29.9	87.0	29.6	6.9	4.4	29.4	85.9
514	14QM028H	31.4	86.8	30.3	7.0	5.0	29.4	86.6
515	14QM028	30.6	86.6	31.9	7.1	4.6	29.7	88.9
516	14QM029	31.3	86.7	30.4	7.2	4.6	32.3	86.5
517	14QM029H	31.5	86.5	30.3	7.0	4.7	31.0	86.5
518	P♂	30.2	86.4	29.1	7.0	4.6	29.4	85.9
519	14QM030H	31.8	85.6	31.9	7.1	4.1	31.3	85.4
520	14QM030	31.8	86.4	31.0	7.1	4.1	30.8	85.8
521	14QM031	32.2	85.6	31.2	7.3	4.5	31.7	86.3
522	14QM031H	32.0	86.4	31.7	7.1	4.1	31.2	85.6
523	P♂	31.7	86.7	30.8	6.9	4.7	29.4	85.9
524	14QM032H	31.3	86.5	33.0	7.0	4.3	30.2	86.4
525	14QM032	31.4	86.0	31.6	7.1	5.0	30.6	85.7
526	14QM033	30.4	86.7	31.0	7.0	5.6	28.1	88.0
527	14QM033H	30.6	87.2	30.3	7.1	5.4	29.4	85.6
528	P♂	29.8	81.8	29.1	7.0	5.2	29.4	85.9
529	14QM034H	31.4	86.0	30.5	7.1	5.3	30.0	87.6
530	14QM034	31.1	86.7	33.0	7.1	5.1	31.1	87.2
531	14QM035	31.6	85.9	31.9	6.9	4.5	29.6	85.8
532	14QM035H	31.7	85.2	31.5	7.0	4.5	31.4	86.5
533	P♂	30.6	86.6	30.1	7.0	4.7	29.4	85.9
534	14QM036H	31.3	85.8	30.4	7.0	5.0	29.8	87.3
535	14QM036	31.8	85.1	30.6	7.1	4.4	29.4	86.4
536	14QM037	30.3	86.1	29.4	6.9	5.2	31.0	87.2
537	14QM037H	31.3	86.7	30.2	6.9	5.2	30.2	86.9
538	P♂	30.6	85.7	29.8	6.9	5.0	29.4	85.9
539	14QM038H	31.1	85.8	29.6	7.0	5.1	30.1	87.7
540	14QM038	29.4	85.8	27.7	6.9	4.6	28.2	85.8
541	14QM039	30.1	87.3	30.6	7.0	5.1	29.4	86.5
542	14QM039H	31.0	84.9	31.3	7.0	4.9	30.2	85.9
543	P♂	30.7	84.7	29.9	6.9	4.9	29.4	85.9
544	14QM040H	30.1	84.7	30.5	7.0	5.1	29.5	85.8
545	14QM040	29.8	85.6	28.7	6.9	5.1	29.0	86.0
546	14QM041	30.6	84.6	29.3	6.9	4.8	31.4	86.6

547	14QM041H	30.6	85.3	31.4	7.0	4.4	30.1	86.0
548	P♂	28.8	87.2	28.2	6.9	5.0	29.4	85.9
549	14QM042H	30.0	86.8	28.4	7.0	5.2	28.3	85.6
550	14QM042	30.0	85.8	28.7	7.0	5.1	27.1	84.2
551	14QM043	29.6	85.4	28.0	6.9	5.5	28.0	85.2
552	14QM043H	30.1	85.5	28.2	6.9	5.3	30.3	85.8
553	14QM380	30.3	85.8	29.1	6.8	5.0	28.4	83.5
554	14QM044H	31.3	85.8	30.5	7.0	4.8	29.2	86.4
555	14QM044	30.4	85.8	29.6	7.0	5.0	30.3	86.5
556	14QM045	31.3	87.3	31.6	6.9	4.6	30.8	85.8
557	14QM045H	31.6	85.9	29.2	7.0	5.1	31.0	86.4
558	P♂	30.0	84.3	30.6	6.9	5.0	28.4	83.5
559	14QM046H	30.1	87.2	30.4	7.0	4.9	30.4	86.7
560	14QM046	29.8	86.3	28.3	6.9	5.0	29.5	87.0
561	14QM047	31.1	85.5	31.1	7.0	5.6	31.1	86.0
562	14QM047H	31.9	85.5	32.3	7.2	5.1	30.9	86.8
563	P♂	29.0	85.5	28.0	6.8	4.6	28.4	83.5
564	14QM048H	29.3	85.8	29.2	7.0	5.1	30.4	85.7
565	14QM048	30.6	86.4	30.8	7.0	4.8	28.9	86.5
566	14QM049	30.6	86.4	30.7	7.0	4.7	29.1	87.3
567	14QM049H	30.4	85.6	30.1	6.9	4.9	29.2	87.6
568	P♂	-	-	-	-	-	28.4	83.5
569	14QM050H	31.2	86.0	30.8	7.0	5.1	30.0	86.7
570	14QM050	33.5	85.1	32.4	7.1	5.1	31.5	85.4
571	14QM051	31.8	85.3	30.0	6.9	4.8	31.5	87.8
572	14QM051H	31.8	85.9	30.9	7.1	5.0	32.0	85.6
573	P♂	31.3	86.5	31.1	7.0	4.9	28.4	83.5
574	14QM052H	31.5	86.4	31.1	7.0	4.7	31.0	86.4
575	14QM052	30.7	85.1	29.6	6.9	4.5	31.1	85.8
576	14QM053	33.1	85.3	32.0	7.1	3.7	33.1	85.8
577	14QM053H	30.3	84.5	30.0	6.9	4.2	31.6	85.6
578	P♂	30.4	85.4	29.1	6.9	4.6	28.4	83.5
579	14QM054H	30.1	86.7	28.8	6.9	4.7	30.0	86.2
580	14QM054	29.7	84.7	29.0	7.0	4.9	28.2	85.4
581	14QM055	29.8	86.4	30.6	6.9	5.4	28.5	86.8
582	14QM055H	30.9	86.4	29.8	7.0	5.1	29.1	86.9
583	P♂	31.0	85.2	29.8	7.0	4.5	28.4	83.5
584	14QM056H	32.7	85.4	34.1	7.1	4.4	30.9	85.6
585	14QM056	32.5	84.9	31.6	7.0	4.6	31.1	85.0
586	14QM057	30.0	86.8	30.8	7.0	3.5	27.8	84.8
587	14QM057H	29.3	83.7	27.4	6.8	4.4	29.5	86.5
588	P♂	30.7	86.3	29.5	6.9	4.8	28.4	83.5
589	14QM058H	29.8	85.1	29.8	6.9	5.1	30.2	86.1
590	14QM058	31.3	86.3	30.8	7.0	4.9	31.5	83.2
591	14QM059	30.4	80.4	30.1	7.0	4.9	31.3	85.6
592	14QM059H	29.7	86.4	29.5	7.0	4.8	28.4	85.8
593	P♂	30.1	85.9	28.5	6.9	4.6	28.4	83.5
594	14QM060H	32.1	85.7	31.9	7.1	4.7	30.3	86.6
595	14QM060	32.1	85.7	30.5	7.0	4.9	30.8	84.5
596	14QM061	29.6	84.7	29.5	6.9	4.4	30.4	84.7

597	14QM061H	30.4	85.7	30.6	7.1	4.9	29.9	84.9
598	P♂	30.0	85.5	29.3	6.9	4.2	28.4	83.5
599	14QM062H	31.1	84.5	31.2	7.0	4.2	31.2	87.3
600	14QM062	33.2	86.8	33.0	7.2	4.2	31.0	84.9
601	14QM063	28.7	85.0	30.1	6.9	4.5	29.2	86.2
602	14QM063H	30.9	85.6	31.5	7.0	4.5	30.2	85.6
603	14QM380	30.1	84.9	31.8	7.0	4.5	31.0	86.2
604	14QM064H	31.3	86.3	29.3	6.9	5.0	30.1	86.9
605	14QM064	31.3	85.4	31.0	7.0	5.1	30.6	87.2
606	14QM065	31.8	85.7	31.1	7.1	5.0	30.0	85.8
607	14QM065H	30.7	85.7	30.2	6.9	4.3	30.1	86.2
608	P♂	30.6	86.8	29.6	7.0	4.6	31.0	86.2
609	14QM066H	31.7	87.1	31.0	7.1	4.8	31.6	85.3
610	14QM066	31.7	85.3	31.2	7.0	4.5	31.3	85.5
611	14QM067	30.5	86.0	29.8	6.9	4.4	30.7	86.2
612	14QM067H	30.8	86.2	30.2	7.0	4.4	29.7	86.8
613	P♂	30.7	86.0	28.9	6.9	5.2	31.0	86.2
614	14QM068H	31.2	85.9	32.3	7.1	4.8	30.1	86.3
615	14QM068	30.1	87.6	29.0	7.0	5.2	30.2	86.6
616	14QM069	29.4	85.4	29.1	6.9	5.1	27.3	86.7
617	14QM069H	30.5	87.8	29.9	7.0	5.0	29.5	86.0
618	P♂	29.9	87.0	29.9	7.0	4.6	31.0	86.2
619	14QM070H	31.6	86.4	31.7	6.9	4.6	31.6	85.9
620	14QM070	31.1	86.9	30.8	7.0	4.7	32.0	86.6
621	14QM071	31.1	85.8	29.8	6.9	4.5	30.0	84.8
622	14QM071H	31.0	87.7	32.0	7.0	4.3	30.0	85.1
623	P♂	29.4	85.3	29.4	6.9	4.5	31.0	86.2
624	14QM072H	30.5	86.1	29.4	6.9	4.8	30.2	86.8
625	14QM072	29.6	85.9	28.6	6.8	5.0	29.8	85.7
626	14QM073	31.1	87.1	31.6	6.9	4.5	30.6	86.0
627	14QM073H	31.6	86.7	30.2	6.9	4.6	29.7	86.5
628	P♂	31.3	85.9	28.7	7.0	4.5	31.0	86.2
629	14QM074H	31.3	84.5	32.2	7.0	5.0	30.5	86.2
630	14QM074	30.9	86.8	31.2	6.9	4.5	30.6	85.0
631	14QM075	30.4	85.3	29.9	6.9	4.0	31.8	85.5
632	14QM075H	31.5	87.2	30.0	7.0	4.3	29.9	86.0
633	P♂	31.6	85.7	30.2	7.0	5.2	31.0	86.2
634	14QM076H	31.6	87.1	31.7	7.2	5.1	29.0	84.2
635	14QM076	30.5	85.0	27.6	7.0	5.5	30.8	86.1
636	14QM077	29.1	87.0	29.2	7.0	5.3	28.9	87.1
637	14QM077H	29.6	87.1	28.1	6.8	4.8	30.5	86.1
638	P♂	31.3	88.2	31.4	7.0	4.8	31.0	86.2
639	14QM078H	30.5	85.9	28.1	7.0	5.3	31.0	85.2
640	14QM078	29.2	84.5	26.7	6.9	5.0	29.1	85.5
641	14QM079	30.3	86.3	31.5	6.9	5.1	30.9	86.3
642	14QM079H	31.8	85.7	30.8	6.9	5.0	31.2	85.2
643	P♂	30.1	87.0	28.5	6.9	5.3	31.0	86.2
644	14QM080H	30.3	86.3	30.5	7.0	4.6	30.0	87.5
645	14QM080	30.4	86.7	28.6	6.9	4.9	29.2	85.8
646	14QM081	30.0	84.7	29.7	6.9	4.6	30.1	86.5

647	14QM081H	31.1	86.2	31.6	7.0	4.2	30.6	86.2
648	P♂	29.7	83.6	29.1	6.9	4.7	31.0	86.2
649	14QM082H	30.8	86.7	31.0	6.9	4.3	31.3	86.0
650	14QM082	32.6	86.1	34.1	7.1	4.5	31.3	84.6
651	14QM083	32.1	87.8	29.6	7.0	4.8	30.4	86.1
652	14QM083H	31.5	86.3	31.0	7.0	4.7	30.2	87.2
653	14QM380	30.9	86.3	29.5	7.0	4.9	30.5	86.8
654	14QM084H	30.6	87.5	29.2	6.9	5.3	31.2	86.5
655	14QM084	31.4	87.4	29.1	7.0	5.0	29.9	87.7
656	14QM085	31.7	87.6	31.8	7.1	4.9	31.1	86.4
657	14QM085H	31.5	86.8	29.8	7.0	4.7	29.5	85.1
658	P♂	30.3	87.4	27.4	6.9	5.3	30.5	86.8
659	14QM086H	30.8	86.7	29.1	7.0	5.1	31.0	86.0
660	14QM086	29.6	89.1	30.6	7.1	5.5	29.0	86.9
661	14QM087	31.7	86.5	31.8	7.0	5.0	31.0	86.5
662	14QM087H	31.8	86.5	30.7	7.1	5.4	29.7	87.3
663	P♂	31.2	87.9	29.7	6.9	4.9	30.5	86.8
664	14QM088H	30.9	86.6	28.8	6.9	5.0	29.9	86.5
665	14QM088	31.3	86.9	33.1	6.9	3.8	29.0	84.2
666	14QM089	31.0	86.6	30.0	7.0	5.2	29.6	86.4
667	14QM089H	31.4	86.0	29.4	7.0	4.8	30.5	85.8
668	P♂	30.0	86.2	28.6	6.9	4.9	30.5	86.8
669	14QM090H	33.0	85.8	30.6	7.0	4.5	32.6	84.9
670	14QM090	33.1	87.3	33.4	7.0	4.7	33.2	86.5
671	14QM091	30.3	86.4	29.8	7.0	4.8	28.0	84.0
672	14QM091H	31.6	88.0	31.7	7.1	4.4	30.3	84.2
673	P♂	29.7	87.0	29.4	7.0	4.4	30.5	86.8
674	P♂	31.0	84.6	30.5	6.9	4.2	30.3	86.5
675	F1	29.9	87.6	29.1	6.9	4.7	31.0	85.8
676	P♀	30.2	86.1	29.6	6.9	5.1	29.0	84.0
677	P♂	30.2	88.4	29.0	6.9	4.8	30.5	86.8
678	14QM092H	31.5	85.6	30.7	7.0	4.9	31.6	85.7
679	14QM092	31.9	85.9	31.3	7.0	4.0	32.2	86.7
680	14QM093	31.2	86.2	29.5	7.0	4.8	30.5	85.7
681	14QM093H	31.9	85.3	30.8	7.0	4.9	30.0	85.2
682	P♂	29.7	85.4	29.0	6.9	4.7	30.5	86.8
683	14QM094H	31.1	85.9	29.4	6.9	4.8	30.0	87.0
684	14QM094	29.3	85.1	29.2	6.9	4.9	29.4	86.3
685	14QM095	30.8	87.2	33.8	7.1	4.5	29.7	86.4
686	14QM095H	29.7	87.3	28.8	6.9	4.6	28.9	86.4
687	P♂	30.4	86.5	29.1	6.9	4.5	30.5	86.8
688	14QM096H	32.1	87.1	30.9	7.1	4.7	30.9	85.2
689	14QM096	32.7	86.2	32.1	7.1	4.7	31.1	86.5
690	14QM097	30.0	84.5	29.5	7.0	4.5	28.9	86.0
691	14QM097H	31.1	86.1	31.1	7.0	4.4	29.5	85.9
692	P♂	30.4	86.2	30.9	6.9	4.7	30.5	86.8
693	14QM098H	31.6	86.3	29.3	7.0	4.1	29.7	86.5
694	14QM098	30.6	86.5	28.6	6.9	4.8	28.6	85.5
695	14QM099	30.9	86.1	31.8	6.9	4.2	29.5	84.9
696	14QM099H	30.8	84.0	30.9	7.0	4.5	28.3	85.5

697	P♂	31.7	85.3	29.8	7.0	4.4	30.5	86.8
698	14QM100H	31.6	88.1	31.0	7.1	4.8	29.7	85.9
699	14QM100	29.4	84.8	27.4	6.8	4.7	29.2	85.3
700	14QM101	29.6	86.6	29.6	6.9	4.6	29.9	86.7
701	14QM101H	30.6	87.1	29.0	6.9	4.8	29.7	87.9
702	14QM380	31.4	85.3	31.9	7.0	4.5	29.2	86.9
703	14QM102H	31.3	85.8	30.8	7.1	5.0	31.4	86.0
704	14QM102	32.5	84.9	31.3	7.0	4.6	30.6	84.6
705	14QM103	32.9	85.2	33.2	7.2	4.4	32.6	86.6
706	14QM103H	31.5	84.4	30.9	7.0	4.8	31.7	85.1
707	P♂	29.7	85.4	28.0	6.9	4.4	29.2	86.9
708	14QM104H	31.4	86.9	29.9	7.1	4.7	30.6	86.0
709	14QM104	31.2	86.7	31.0	7.1	4.8	31.1	84.9
710	14QM105	31.6	84.4	31.2	7.1	4.7	31.4	84.7
711	14QM105H	31.6	86.6	29.8	7.0	4.7	29.5	86.7
712	P♂	31.1	84.7	30.9	7.0	4.3	29.2	86.9
713	14QM106H	-	-	-	-	-	31.1	86.6
714	14QM106	32.5	85.5	30.4	7.1	4.6	30.7	86.0
715	14QM107	30.9	85.7	31.6	7.0	5.0	28.9	82.7
716	14QM107H	31.2	86.2	30.8	7.0	5.2	30.8	86.2
717	P♂	29.7	85.9	28.5	7.0	5.1	29.2	86.9
718	14QM108H	30.5	86.4	28.9	7.0	5.3	30.0	84.3
719	14QM108	32.0	85.8	28.5	7.0	5.0	30.6	84.9
720	14QM109	29.5	85.9	28.2	6.9	4.7	30.7	85.5
721	14QM109H	30.1	84.3	28.8	6.8	4.1	29.4	86.9
722	P♂	29.0	85.6	27.7	6.9	5.1	29.2	86.9
723	14QM110H	30.9	86.6	31.4	6.9	4.7	30.0	85.9
724	14QM110	30.2	86.8	30.9	7.0	5.2	30.1	85.8
725	14QM111	31.5	86.4	32.2	7.0	4.0	30.6	86.4
726	14QM111H	32.0	86.3	30.4	7.0	4.9	31.1	85.8
727	P♂	31.4	85.9	32.2	7.0	4.0	29.2	86.9
728	14QM112H	30.6	87.3	31.2	7.0	4.8	31.4	85.9
729	14QM112	29.6	86.2	27.9	6.9	5.0	30.8	85.7
730	14QM113	-	-	-	-	-	31.1	85.5
731	14QM113H	32.1	86.7	30.0	7.0	5.3	31.6	85.5
732	P♂	30.5	87.0	28.6	6.9	4.6	29.2	86.9
733	14QM114H	32.6	86.4	29.7	7.0	5.2	29.7	85.6
734	14QM114	31.5	86.9	30.5	7.0	5.0	31.2	86.6
735	14QM115	31.9	87.0	33.0	7.0	4.2	31.4	84.4
736	14QM115H	30.6	84.7	30.1	7.0	5.3	31.9	86.2
737	P♂	29.9	86.6	27.6	6.9	4.6	29.2	86.9
738	14QM116H	30.2	85.4	29.4	7.0	4.9	30.3	85.3
739	14QM116	30.7	86.1	29.5	6.9	4.9	28.6	85.7
740	14QM117	31.8	85.9	30.4	7.0	4.9	31.3	85.3
741	14QM117H	31.9	84.6	31.6	7.0	4.4	31.1	82.3
742	P♂	29.8	86.1	27.9	6.8	4.6	29.2	86.9
743	14QM118H	31.3	87.1	31.7	7.1	4.6	32.4	85.3
744	14QM118	31.7	84.9	30.8	7.0	4.9	30.5	86.4
745	14QM119	32.4	85.0	32.3	7.0	4.5	31.3	84.7
746	14QM119H	31.5	86.2	30.6	7.0	4.8	31.3	86.5

747	P♂	30.4	86.1	28.6	6.9	5.0	29.2	86.9
748	14QM120H	31.0	85.5	32.3	7.0	4.5	30.4	86.6
749	14QM120	30.3	85.8	30.7	6.9	4.1	29.9	87.0
750	14QM121	31.3	85.3	30.9	7.0	5.0	30.6	86.2
751	14QM121H	32.1	86.8	30.6	7.0	5.2	30.5	86.5
752	14QM380	30.2	86.2	28.9	6.9	4.9	30.1	85.2
753	14QM122H	32.1	86.0	30.8	7.0	5.2	30.5	86.0
754	14QM122	32.2	86.7	31.2	7.2	5.3	31.3	85.5
755	14QM123	31.8	86.8	31.7	6.9	4.5	29.3	86.3
756	14QM123H	31.2	85.8	28.8	7.0	5.4	30.2	86.5
757	P♂	30.1	85.2	28.7	6.9	5.7	30.1	85.2
758	14QM124H	30.8	86.1	29.3	6.9	5.3	29.9	85.7
759	14QM124	29.8	83.7	29.5	7.0	5.4	30.3	84.1
760	14QM125	29.8	86.4	28.2	6.9	5.3	28.6	82.9
761	14QM125H	29.4	85.9	29.1	6.9	5.1	29.9	87.0
762	P♂	29.3	86.4	28.1	6.9	5.1	30.1	85.2
763	14QM126H	29.2	84.3	28.9	7.0	5.3	29.3	86.3
764	14QM126	30.4	87.0	30.7	7.2	5.9	29.7	86.5
765	14QM127	30.4	85.4	31.9	6.9	4.2	29.9	84.3
766	14QM127H	31.0	86.5	30.6	6.9	4.7	30.2	85.7
767	P♂	30.6	86.8	29.0	7.0	5.0	30.1	85.2
768	14QM128H	31.7	87.1	30.2	7.0	4.9	31.1	86.3
769	14QM128	31.4	85.9	29.8	7.0	4.5	31.9	85.3
770	14QM129	31.7	86.7	29.7	7.0	5.3	31.1	84.9
771	14QM129H	32.2	86.2	31.5	7.0	4.8	29.7	87.6
772	P♂	30.8	86.4	30.2	7.0	4.7	30.1	85.2
773	14QM130H	31.6	86.7	30.2	7.0	5.1	31.8	85.2
774	14QM130	33.2	86.1	32.8	7.2	4.0	31.4	84.5
775	14QM131	32.7	86.9	32.5	7.2	4.6	31.2	86.0
776	14QM131H	32.0	86.6	29.9	7.0	4.9	32.5	85.8
777	P♂	30.5	86.6	29.0	6.9	5.1	30.1	85.2
778	14QM132H	30.3	86.0	29.4	7.0	5.3	30.0	86.6
779	14QM132	29.4	85.0	28.8	6.8	4.5	29.6	85.1
780	14QM133	32.0	87.2	31.9	7.1	5.0	32.1	86.4
781	14QM133H	32.5	87.0	31.3	7.1	5.2	31.2	83.2
782	P♂	30.7	85.5	29.3	6.9	4.9	30.1	85.2
783	14QM134H	29.9	85.9	28.6	6.9	4.7	29.9	87.1
784	14QM134	-	-	-	-	-	28.9	86.8
785	14QM135	32.1	85.2	33.1	7.1	4.6	30.3	84.7
786	14QM135H	30.6	85.8	29.5	7.0	4.6	31.1	84.7
787	P♂	30.7	85.6	29.9	7.1	4.7	30.1	85.2
788	14QM136H	31.3	84.7	31.0	7.0	4.8	31.3	85.0
789	14QM136	-	-	-	-	-	32.8	85.1
790	14QM137	30.5	84.5	29.5	6.8	4.6	32.2	84.1
791	14QM137H	31.7	85.3	33.0	7.1	4.6	31.4	85.8
792	P♂	31.4	85.4	30.1	7.0	4.5	30.1	85.2
793	14QM138H	31.9	85.9	31.0	7.0	4.7	30.0	85.6
794	14QM138	30.6	85.2	29.8	6.9	4.1	29.3	84.6
795	14QM139	29.6	85.6	28.4	6.9	4.7	30.4	86.0
796	14QM139H	30.7	85.7	30.4	7.0	4.5	30.6	85.7

797	P♂	29.5	85.2	28.4	6.8	4.7	30.1	85.2
798	14QM140H	-	-	-	-	-	31.9	86.2
799	14QM140	32.4	86.3	31.8	7.0	4.5	31.0	86.2
800	14QM141	31.3	87.5	32.1	7.1	4.9	30.5	86.5
801	14QM141H	31.5	86.2	31.1	7.0	4.6	30.9	86.1
802	14QM380	30.4	87.3	30.3	7.0	4.8	29.9	85.0
803	14QM142H	31.0	87.7	31.3	7.0	4.5	28.0	84.2
804	14QM142	30.8	86.7	31.9	7.1	4.5	31.1	85.2
805	14QM143	31.1	86.6	32.8	7.0	5.0	30.4	87.1
806	14QM143H	30.8	85.1	30.9	6.9	4.5	29.8	87.0
807	P♂	30.7	86.5	31.6	7.0	4.5	29.9	85.0
808	14QM144H	31.0	87.1	32.1	7.0	4.9	31.0	86.0
809	14QM144	31.4	86.4	32.1	7.0	5.1	30.0	86.3
810	14QM145	29.8	86.3	29.1	6.8	4.4	31.7	86.4
811	14QM145H	30.6	86.6	30.4	7.0	4.4	30.2	86.0
812	P♂	30.5	85.6	32.5	7.0	4.7	29.9	85.0
813	14QM146H	29.3	86.2	29.6	6.9	4.8	29.1	87.4
814	14QM146	30.6	86.9	32.3	7.0	4.1	31.5	86.2
815	14QM147	32.4	86.3	31.3	7.2	4.3	32.7	84.2
816	14QM147H	32.4	87.4	29.5	7.1	4.6	29.2	84.2
817	P♂	29.6	86.6	28.2	6.9	4.7	29.9	85.0
818	14QM148H	31.5	84.6	32.0	7.1	4.9	31.0	85.8
819	14QM148	31.9	86.7	33.1	7.1	4.3	32.0	86.5
820	14QM149	30.5	85.4	31.6	6.9	4.2	32.2	85.4
821	14QM149H	31.7	85.6	30.0	7.0	4.9	32.3	85.8
822	P♂	30.3	86.4	30.6	7.0	4.1	29.9	85.0
823	14QM150H	30.2	87.6	30.3	7.0	4.3	31.3	85.5
824	14QM150	31.7	87.6	31.5	7.0	4.4	31.5	86.1
825	14QM151	30.3	85.3	29.3	6.9	4.6	29.9	87.1
826	14QM151H	31.2	85.8	31.0	7.0	4.1	31.3	85.7
827	P♂	29.6	85.8	28.3	7.0	4.6	29.9	85.0
828	14QM152H	29.8	84.9	29.3	6.9	4.9	29.8	85.8
829	14QM152	30.1	85.4	30.8	6.9	4.9	29.6	86.8
830	14QM153	29.5	86.0	30.4	6.9	5.3	29.2	87.5
831	14QM153H	30.8	87.2	30.3	7.0	4.8	31.5	86.4
832	P♂	29.6	87.5	29.3	6.9	5.3	29.9	85.0
833	14QM154H	30.4	84.7	31.5	6.9	4.7	30.3	86.1
834	14QM154	32.1	87.2	32.6	7.0	4.7	31.7	86.1
835	14QM155	31.0	84.8	32.7	7.0	4.9	30.4	86.0
836	14QM155H	31.5	86.0	30.5	7.1	5.0	31.2	86.8
837	P♂	30.7	86.5	31.2	6.9	4.4	29.9	85.0
838	14QM156H	31.4	86.8	30.6	7.1	4.9	30.7	86.1
839	14QM156	30.1	87.1	30.8	7.1	5.1	30.0	85.2
840	14QM157	30.7	85.6	31.7	7.2	4.9	31.6	86.2
841	14QM157H	31.3	87.8	32.3	7.1	4.4	30.0	86.6
842	P♂	30.7	86.3	31.9	7.0	4.6	29.9	85.0
843	14QM158H	28.7	86.5	27.1	6.8	5.4	27.8	85.7
844	14QM158	28.2	84.2	26.6	6.8	4.8	28.3	85.9
845	14QM159	32.2	86.1	30.5	7.0	4.2	31.9	86.3
846	14QM159H	33.2	87.3	31.2	7.2	4.7	30.9	86.8

847	P♂	30.4	86.7	30.0	6.9	4.4	29.9	85.0
848	14QM160H	29.9	84.3	32.2	7.0	5.0	29.1	86.1
849	14QM160	31.6	86.7	31.7	7.1	4.7	30.5	85.2
850	14QM161	30.8	86.0	31.3	7.0	4.8	30.5	85.9
851	14QM161H	30.7	85.8	30.7	6.9	4.2	31.0	85.4
852	14QM380	29.5	84.7	30.5	6.9	3.9	29.3	85.5
853	14QM162H	30.5	87.0	30.3	7.0	5.2	31.1	85.8
854	14QM162	29.2	87.2	31.8	7.1	5.4	30.1	84.6
855	14QM163	32.2	87.2	32.6	7.2	4.7	31.4	85.7
856	14QM163H	31.6	87.0	32.3	7.0	4.5	31.1	85.2
857	P♂	30.4	87.5	30.8	7.0	4.4	29.3	85.5
858	14QM164H	31.2	86.7	32.9	7.2	5.1	29.7	87.9
859	14QM164	29.4	84.9	29.5	6.9	5.2	28.7	86.3
860	14QM165	29.8	87.3	32.8	6.9	4.3	31.4	84.0
861	14QM165H	32.1	87.0	32.5	7.0	4.5	32.2	85.3
862	P♂	30.2	85.9	30.3	6.9	4.6	29.3	85.5
863	14QM166H	32.5	88.1	31.9	7.1	4.6	31.3	85.2
864	14QM166	32.5	86.9	34.0	7.0	4.2	31.1	85.0
865	14QM167	31.8	86.8	32.0	7.0	4.6	31.2	84.3
866	14QM167H	31.5	87.0	31.4	7.1	4.6	29.9	85.3
867	P♂	30.1	87.3	30.2	6.9	5.1	29.3	85.5
868	14QM168H	31.3	86.3	32.7	7.0	4.5	30.8	85.7
869	14QM168	29.2	85.2	29.3	6.8	5.0	28.7	86.1
870	14QM169	28.9	85.2	26.9	6.8	4.9	28.0	85.0
871	14QM169H	28.6	85.5	28.3	6.9	4.7	29.4	87.4
872	P♂	29.4	84.6	31.6	7.1	4.5	29.3	85.5
873	14QM170H	30.6	87.5	31.5	7.0	4.9	30.5	86.6
874	14QM170	29.9	84.5	29.2	7.0	5.5	30.1	86.4
875	14QM171	30.2	86.5	30.1	6.9	5.1	31.2	84.9
876	14QM171H	30.7	85.1	31.2	6.9	4.1	30.4	85.4
877	P♂	31.0	85.8	28.7	7.0	5.2	29.3	85.5
878	14QM172H	31.2	85.3	31.2	7.0	4.7	29.8	83.5
879	14QM172	31.1	85.2	32.5	7.0	4.4	30.4	85.3
880	14QM173	32.1	85.4	32.3	7.1	4.7	30.4	85.0
881	14QM173H	31.0	85.6	31.4	7.0	5.0	30.7	86.1
882	P♂	30.3	86.6	29.8	6.9	4.6	29.3	85.5
883	14QM174H	28.7	85.3	30.1	7.0	4.8	28.6	86.3
884	14QM174	30.2	86.7	30.6	7.0	4.9	30.8	87.2
885	14QM175	30.4	85.3	32.0	7.1	4.8	31.0	84.4
886	14QM175H	31.4	86.3	31.0	6.9	4.5	30.0	86.1
887	P♂	30.5	84.5	31.3	6.9	4.4	29.3	85.5
888	14QM176H	31.6	87.0	30.4	6.9	4.6	31.9	86.2
889	14QM176	33.1	86.5	32.1	7.0	4.4	32.8	85.1
890	14QM177	29.9	85.9	30.4	6.9	4.2	29.0	84.5
891	14QM177H	31.6	84.9	32.0	7.0	4.1	31.2	88.1
892	P♂	30.4	85.2	30.0	7.0	4.4	29.3	85.5
893	14QM178H	31.0	83.8	32.3	7.0	4.7	30.1	84.8
894	14QM178	32.4	85.2	31.7	7.0	4.7	32.6	84.7
895	14QM179	31.2	85.3	30.9	7.0	4.7	30.6	85.6
896	14QM179H	31.0	85.8	30.5	7.1	5.4	30.6	85.6

897	P♂	29.7	83.6	29.3	6.9	4.6	29.3	85.5
898	P♂	30.0	85.3	30.1	6.9	4.5	30.8	86.3
899	F1	31.3	86.0	30.9	7.1	5.1	31.4	86.4
900	P♀	30.3	84.9	30.0	6.9	5.0	31.3	85.8

4QM003H- 14QM179H refer to 177 F₁₄BC progenies in BC/P population.

FS(cN/tex)	FE/%	FM	FL/mm	FU/%	FS(cN/tex)	FE/%	FM
2016E1	2016E1	2016E1	2016E2	2016E2	2016E2	2016E2	2016E2
28.1	6.7	5.5	29.3	86.2	28.9	6.8	5.0
29.0	6.8	5.1	30.7	86.3	31.9	6.9	4.8
26.3	6.8	5.5	28.4	84.9	29.2	6.6	4.9
27.5	6.8	5.0	30.1	87.2	30.2	6.8	4.9
27.0	6.7	5.1	30.5	86.0	29.6	6.8	4.9
31.8	6.8	4.9	29.3	82.9	31.1	6.7	4.8
28.0	6.7	4.3	30.8	85.3	30.6	6.7	4.3
26.3	6.8	5.5	28.4	84.9	29.2	6.6	4.9
27.6	6.7	5.2	29.9	85.7	28.6	6.7	5.1
31.1	6.9	4.8	30.3	85.6	30.5	6.7	4.8
27.2	6.8	5.5	29.5	85.0	28.2	6.8	5.6
27.2	6.9	5.5	29.8	86.3	29.0	6.8	5.3
26.3	6.8	5.5	28.4	84.9	29.2	6.6	4.9
28.7	6.8	4.5	29.3	84.1	29.0	6.7	4.7
29.6	6.8	4.5	27.8	84.6	28.8	6.6	4.8
28.6	6.7	4.2	28.6	85.3	26.7	6.7	5.7
25.9	6.6	5.3	28.9	85.0	28.4	6.7	5.4
26.3	6.8	5.5	28.4	84.9	29.2	6.6	4.9
28.1	6.9	4.4	29.9	86.8	28.5	6.8	5.1
30.8	6.8	4.7	29.0	86.7	28.9	6.7	4.9
27.0	6.6	5.6	30.6	87.5	29.4	6.8	5.6
29.3	6.9	5.3	31.4	87.2	29.3	6.8	4.8
26.3	6.8	5.5	28.4	84.9	29.2	6.6	4.9
31.0	6.9	4.5	30.3	85.6	30.9	6.8	4.9
29.5	6.8	5.2	29.8	85.2	29.8	6.7	5.1
27.0	6.7	5.5	29.1	86.3	27.7	6.8	5.7
28.2	6.7	3.8	29.5	85.2	27.3	6.7	5.3
26.3	6.8	5.5	28.4	84.9	29.2	6.6	4.9
30.5	6.8	4.4	30.3	87.1	27.7	6.7	5.3
26.8	6.7	4.9	29.4	86.0	27.9	6.7	5.0
27.7	6.8	4.5	30.6	86.7	28.4	6.9	4.8
27.4	6.8	5.1	29.9	84.1	29.0	6.8	5.0
26.3	6.8	5.5	28.4	84.9	29.2	6.6	4.9
27.8	6.8	5.1	29.9	87.0	28.7	6.8	5.3
28.9	6.8	5.2	29.0	85.2	27.8	6.7	5.4
29.8	6.9	4.4	29.7	86.8	30.1	6.7	4.6
28.6	6.9	4.7	30.3	85.5	29.5	6.8	5.1
26.3	6.8	5.5	28.4	84.9	29.2	6.6	4.9
28.9	6.8	4.7	28.9	85.2	29.4	6.7	5.0
31.9	6.9	4.3	30.7	86.4	30.2	6.8	4.5
28.0	6.7	4.6	28.5	85.7	29.1	6.7	5.6
31.4	6.8	4.3	28.9	85.3	29.1	6.8	5.6
26.3	6.8	5.5	28.4	84.9	29.2	6.6	4.9
28.4	6.8	4.5	30.4	85.6	30.1	6.8	5.1
29.3	6.9	4.6	30.6	83.4	30.5	6.8	4.8
29.2	6.8	4.6	28.4	84.3	28.6	6.7	5.7

27.6	6.8	4.8	29.5	85.4	28.4	6.8	5.4
26.3	6.8	5.5	28.4	84.9	29.2	6.6	4.9
28.5	6.8	4.6	29.9	87.2	28.9	6.8	5.4
28.5	6.8	4.6	30.7	87.4	32.4	7.0	4.9
28.9	6.7	4.4	28.0	85.1	27.4	6.6	5.0
29.5	6.8	4.5	29.0	85.2	27.8	6.7	5.3
26.4	6.7	4.4	28.6	84.8	27.1	6.8	5.9
30.1	6.9	4.5	29.5	84.1	29.7	6.8	4.5
28.9	6.8	4.5	27.6	85.2	29.8	6.7	4.3
30.7	6.7	3.8	29.3	85.6	28.7	6.8	4.9
28.7	6.9	5.7	28.2	86.6	26.3	6.6	5.0
26.4	6.7	4.4	28.6	84.8	27.1	6.8	5.9
28.0	6.8	4.9	30.2	86.6	28.0	6.8	4.9
28.6	6.9	5.3	29.4	86.6	27.8	6.8	5.4
27.4	6.8	4.7	29.3	85.1	28.1	6.7	5.0
27.8	6.8	4.7	28.7	84.9	28.0	6.7	5.4
26.4	6.7	4.4	28.6	84.8	27.1	6.8	5.9
27.9	6.8	5.1	28.7	86.2	28.1	6.7	5.4
27.9	6.8	5.3	26.5	84.0	26.8	6.6	5.6
28.8	6.9	4.5	30.4	86.8	29.5	6.8	4.7
28.2	6.8	4.1	30.5	85.6	29.5	6.8	5.1
26.4	6.7	4.4	28.6	84.8	27.1	6.8	5.9
29.1	6.9	3.9	29.9	87.8	27.7	6.7	4.7
29.1	6.8	4.1	30.2	84.5	28.7	6.8	4.7
27.8	6.7	3.5	29.9	86.9	28.9	6.7	4.8
30.2	6.9	4.0	29.5	86.0	28.4	6.8	4.7
26.4	6.7	4.4	28.6	84.8	27.1	6.8	5.9
28.3	6.8	5.3	29.7	83.9	28.2	6.7	5.3
29.7	6.9	5.4	25.9	83.0	26.2	6.6	5.8
28.0	6.8	5.6	30.0	87.0	29.8	6.8	4.9
27.8	6.8	5.7	29.4	85.3	28.5	6.7	5.1
26.4	6.7	4.4	28.6	84.8	27.1	6.8	5.9
28.1	6.8	5.5	26.6	83.5	26.2	6.6	5.4
29.2	6.8	5.4	29.1	84.5	29.8	6.7	4.6
29.1	6.7	4.6	30.1	85.4	28.2	6.7	4.8
29.1	6.7	4.6	29.8	84.8	29.3	6.7	4.6
26.4	6.7	4.4	28.6	84.8	27.1	6.8	5.9
27.8	6.8	5.1	29.3	87.0	29.1	6.7	4.9
27.4	6.9	4.8	29.7	87.4	28.9	6.8	5.3
29.5	6.7	4.7	30.0	87.1	31.2	6.7	4.2
27.7	6.7	4.9	29.8	85.2	29.4	6.7	4.6
26.4	6.7	4.4	28.6	84.8	27.1	6.8	5.9
27.3	6.7	4.9	28.3	84.4	28.8	6.7	5.0
26.4	6.6	4.9	30.1	85.5	29.2	6.8	5.1
27.8	6.8	5.6	28.7	85.4	27.7	6.7	5.5
28.0	6.8	5.4	29.8	86.4	28.8	6.8	5.4
26.4	6.7	4.4	28.6	84.8	27.1	6.8	5.9
28.5	6.7	4.4	30.0	87.8	28.1	6.8	5.4
29.3	6.8	5.0	27.5	82.2	27.5	6.6	5.1
30.3	6.9	4.9	29.1	83.6	28.4	6.7	4.6

29.6	6.7	3.9	27.9	84.6	28.8	6.7	4.5
26.4	6.7	4.4	28.6	84.8	27.1	6.8	5.9
27.9	6.9	5.4	29.9	86.0	28.1	6.7	5.1
28.8	6.9	5.3	30.9	85.6	28.9	6.9	5.8
26.7	6.8	5.3	28.2	86.2	28.3	6.7	4.9
29.0	6.9	4.7	28.7	85.1	27.4	6.7	5.0
28.0	6.8	3.9	27.6	84.1	27.0	6.6	5.0
27.7	6.8	5.1	29.6	85.3	31.1	6.8	5.1
27.2	6.8	5.0	27.6	82.1	26.8	6.6	5.7
29.7	6.8	5.1	28.1	83.9	28.8	6.7	4.8
31.0	7.0	4.8	30.2	87.4	29.2	6.8	4.7
28.0	6.8	3.9	27.6	84.1	27.0	6.6	5.0
28.8	6.8	4.6	29.8	86.0	26.8	6.7	5.4
27.1	6.7	5.2	29.9	86.6	28.3	6.7	4.9
29.4	6.8	5.3	29.2	86.2	29.3	6.7	5.1
27.6	6.8	5.7	29.7	87.2	28.3	6.7	4.9
28.0	6.8	3.9	27.6	84.1	27.0	6.6	5.0
28.0	6.7	4.4	28.5	85.6	28.6	6.7	4.5
27.7	6.6	4.3	28.9	86.6	28.2	6.7	4.6
29.6	6.8	4.5	28.4	86.9	29.5	6.7	4.2
28.3	6.8	4.8	30.4	88.2	28.6	6.8	4.8
28.0	6.8	3.9	27.6	84.1	27.0	6.6	5.0
28.4	6.8	4.7	30.4	86.5	29.6	6.8	5.1
31.4	6.8	4.8	28.9	84.9	29.2	6.7	5.3
28.9	6.8	5.1	28.0	85.5	28.3	6.6	5.3
29.0	6.7	4.7	29.1	85.3	28.9	6.7	5.7
28.0	6.8	3.9	27.6	84.1	27.0	6.6	5.0
29.1	6.8	4.9	28.5	84.7	28.0	6.7	5.1
28.1	6.7	5.1	28.8	86.9	29.6	6.7	5.0
29.8	6.7	4.8	30.5	84.7	30.9	6.7	4.5
30.6	6.9	4.8	31.0	86.8	31.3	6.8	4.6
28.0	6.8	3.9	27.6	84.1	27.0	6.6	5.0
26.0	6.6	5.0	29.5	85.3	28.8	6.8	4.7
27.1	6.7	4.6	29.2	86.0	29.7	6.8	4.9
27.0	6.6	4.9	26.2	83.4	28.9	6.5	5.0
28.9	6.7	4.6	29.5	86.5	28.9	6.7	5.4
28.0	6.8	3.9	27.6	84.1	27.0	6.6	5.0
29.9	6.8	4.7	30.2	86.7	29.1	6.8	4.8
30.9	6.8	4.7	28.9	84.6	29.6	6.7	4.6
27.1	6.8	4.8	26.6	81.6	26.5	6.6	5.0
26.3	6.7	4.9	27.4	83.9	26.7	6.6	4.9
28.0	6.8	3.9	27.6	84.1	27.0	6.6	5.0
27.6	6.8	4.7	29.2	86.5	30.6	6.8	4.6
31.2	6.9	4.6	29.4	85.8	31.8	6.7	4.2
28.9	6.7	4.5	25.5	82.8	25.5	6.5	5.2
30.1	6.9	5.0	28.1	86.2	27.2	6.6	5.1
28.0	6.8	3.9	27.6	84.1	27.0	6.6	5.0
27.5	6.8	5.3	29.2	86.4	29.0	6.7	4.9
29.2	6.9	5.5	29.8	86.2	31.9	6.8	4.6
28.0	6.8	5.6	27.0	84.7	28.9	6.6	5.0

26.5	6.7	5.4	29.2	86.5	29.7	6.7	4.9
28.0	6.8	3.9	27.6	84.1	27.0	6.6	5.0
28.1	6.9	5.3	28.7	84.1	31.9	6.7	4.2
30.2	6.9	5.0	26.9	81.0	29.6	6.6	4.5
27.7	6.7	4.9	29.0	86.5	31.0	6.7	4.8
29.4	6.9	5.0	27.7	84.5	29.0	6.6	4.6
27.8	6.8	5.2	30.0	87.3	30.4	6.8	4.6
29.2	6.8	4.8	27.9	84.2	29.6	6.7	5.2
27.3	6.7	5.2	30.2	86.4	31.1	6.8	5.4
30.1	6.8	4.4	30.4	87.2	29.8	6.7	5.0
28.6	6.8	5.1	30.3	86.3	30.0	6.7	4.5
27.8	6.8	5.2	30.0	87.3	30.4	6.8	4.6
27.1	6.6	5.0	28.9	83.2	29.2	6.7	5.3
27.0	6.7	5.2	28.4	83.2	27.5	6.7	5.1
29.1	6.7	4.6	29.0	85.5	27.7	6.7	5.4
28.5	6.7	3.5	28.8	86.3	28.4	6.7	5.0
27.8	6.8	5.2	30.0	87.3	30.4	6.8	4.6
27.0	6.7	5.0	30.5	86.7	29.3	6.8	5.0
28.2	6.8	5.3	30.2	84.8	30.5	6.8	4.7
26.6	6.7	5.8	27.5	84.7	26.9	6.6	5.6
27.4	6.8	5.6	28.7	85.6	28.1	6.7	5.2
27.8	6.8	5.2	30.0	87.3	30.4	6.8	4.6
26.9	6.8	5.0	28.7	85.2	28.8	6.6	4.4
29.2	6.8	5.4	30.1	86.1	28.9	6.7	4.8
28.6	6.8	4.5	29.7	87.1	30.8	6.8	4.5
26.4	6.8	5.6	29.2	85.5	29.5	6.7	4.6
27.8	6.8	5.2	30.0	87.3	30.4	6.8	4.6
29.2	6.8	4.6	29.3	85.1	30.2	6.7	4.3
28.5	6.7	5.0	28.9	83.5	28.7	6.6	4.8
31.9	6.9	5.0	30.7	85.2	31.7	6.8	4.7
28.2	6.8	5.0	29.8	87.2	30.5	6.8	4.8
27.8	6.8	5.2	30.0	87.3	30.4	6.8	4.6
31.0	6.9	4.8	29.5	86.0	30.2	6.8	5.1
30.9	6.8	4.7	27.2	83.2	26.2	6.5	5.1
27.6	6.9	4.2	30.0	84.5	27.4	6.7	4.3
27.9	6.7	3.9	30.3	85.6	28.7	6.8	4.7
27.8	6.8	5.2	30.0	87.3	30.4	6.8	4.6
26.3	6.7	4.9	29.4	85.0	28.1	6.7	4.6
25.8	6.7	5.3	28.5	84.9	27.1	6.7	4.9
27.6	6.7	4.9	28.6	85.5	27.4	6.7	5.2
28.1	6.8	4.3	28.7	85.1	29.2	6.8	5.1
27.8	6.8	5.2	30.0	87.3	30.4	6.8	4.6
29.2	6.8	4.4	31.1	86.8	28.6	6.8	4.6
27.0	6.7	5.1	29.1	85.4	28.8	6.7	4.7
30.3	6.8	4.7	30.8	85.9	29.5	6.7	5.1
29.0	6.7	4.7	30.0	85.9	29.8	6.7	5.1
27.8	6.8	5.2	30.0	87.3	30.4	6.8	4.6
29.0	6.8	4.7	27.5	84.6	27.9	6.6	4.6
28.7	6.7	4.3	27.0	82.4	26.5	6.6	4.9
29.5	6.8	4.8	30.2	87.1	29.6	6.7	4.8

28.6	6.7	4.6	29.5	85.6	28.1	6.7	4.9
27.8	6.8	5.2	30.0	87.3	30.4	6.8	4.6
28.0	6.7	4.4	27.4	84.0	27.7	6.6	4.9
31.4	6.8	4.8	29.9	86.2	30.2	6.8	4.9
28.8	6.9	5.1	29.4	85.0	29.0	6.8	5.5
28.6	6.7	4.6	27.1	84.3	26.4	6.6	5.3
29.9	6.9	5.3	28.9	86.2	27.0	6.7	5.1
31.1	6.9	4.5	30.1	87.1	28.3	6.7	4.9
27.1	6.8	5.6	29.1	85.9	30.5	6.8	5.4
31.4	6.8	4.3	30.4	85.6	31.2	6.8	4.9
29.4	6.9	4.8	30.1	86.0	28.5	6.7	5.1
29.9	6.9	5.3	28.9	86.2	27.0	6.7	5.1
27.4	6.8	5.2	30.9	87.1	29.7	6.9	5.7
27.6	6.8	5.4	29.4	86.0	27.4	6.8	6.0
29.1	6.9	5.2	28.6	83.8	30.2	6.8	5.6
27.8	6.7	4.9	28.0	84.5	28.1	6.7	5.0
29.9	6.9	5.3	28.9	86.2	27.0	6.7	5.1
28.3	6.9	5.2	28.7	84.6	27.9	6.6	4.3
28.6	6.9	5.8	28.3	85.3	28.6	6.7	5.7
28.2	6.7	5.7	27.2	84.4	27.6	6.7	5.9
26.9	6.8	5.4	28.5	84.0	28.7	6.7	5.1
29.9	6.9	5.3	28.9	86.2	27.0	6.7	5.1
28.4	6.9	5.2	30.2	85.7	27.9	6.7	5.3
31.0	6.9	4.5	30.9	85.9	31.8	6.8	4.2
29.4	6.8	4.9	28.1	84.0	27.0	6.6	5.0
28.0	6.8	5.1	27.9	82.7	27.4	6.6	4.8
29.9	6.9	5.3	28.9	86.2	27.0	6.7	5.1
29.4	6.8	5.1	27.8	85.4	26.7	6.6	5.5
28.2	6.8	5.7	29.8	86.7	30.0	6.7	5.1
29.8	6.8	5.3	29.8	86.4	29.1	6.7	5.7
29.9	6.9	5.3	28.9	86.2	27.0	6.7	5.1
28.1	6.8	5.0	29.4	86.2	29.9	6.8	5.5
27.4	6.8	4.8	31.3	87.2	30.1	6.8	5.1
27.9	6.8	4.8	29.0	84.4	28.4	6.7	4.9
29.4	6.8	4.6	28.7	84.3	27.5	6.7	5.1
29.9	6.9	5.3	28.9	86.2	27.0	6.7	5.1
28.7	6.7	5.1	28.6	85.6	28.0	6.7	4.8
26.1	6.6	5.6	28.8	84.3	27.9	6.7	5.4
29.1	6.8	5.4	27.6	83.7	27.4	6.7	5.5
29.9	6.8	4.8	30.1	86.0	27.6	6.7	4.9
29.9	6.9	5.3	28.9	86.2	27.0	6.7	5.1
27.6	6.8	5.1	29.0	84.1	27.6	6.7	4.6
28.4	6.8	4.6	31.4	84.4	29.6	6.8	4.5
28.5	6.8	5.3	27.7	82.7	27.0	6.6	5.0
30.0	6.8	4.5	29.0	85.7	27.0	6.7	4.9
29.9	6.9	5.3	28.9	86.2	27.0	6.7	5.1
28.5	6.9	5.3	29.9	84.2	29.8	6.8	4.2
28.4	6.8	4.6	28.0	83.2	27.5	6.7	5.0
27.4	6.7	4.7	29.6	87.0	29.8	6.8	5.2
25.9	6.6	5.3	28.3	82.7	28.9	6.7	5.1

29.9	6.9	5.3	28.9	86.2	27.0	6.7	5.1
27.3	6.8	5.6	29.3	83.2	31.4	6.8	4.1
27.6	6.8	5.5	29.3	86.2	28.9	6.8	5.4
29.3	6.8	5.2	28.7	86.6	29.3	6.7	5.2
29.0	6.8	5.5	29.4	86.0	29.8	6.8	5.0
29.6	6.9	5.4	27.7	84.9	27.2	6.6	4.6
28.9	6.8	4.4	29.1	86.2	28.6	6.7	4.6
26.5	6.8	5.1	28.9	85.5	28.0	6.7	4.8
30.8	6.9	4.5	30.6	84.5	31.7	6.9	4.6
27.2	6.8	4.9	31.6	87.2	31.9	6.9	4.5
29.6	6.9	5.4	27.7	84.9	27.2	6.6	4.6
27.5	6.8	4.9	29.3	84.8	28.5	6.7	4.5
29.3	6.9	4.6	29.5	87.8	30.1	6.8	4.6
28.8	6.8	4.9	29.6	87.8	29.5	6.8	4.7
30.5	6.8	4.3	29.5	86.9	30.8	6.7	4.3
29.6	6.9	5.4	27.7	84.9	27.2	6.6	4.6
28.4	6.8	4.3	29.4	86.4	29.8	6.8	4.7
29.9	6.9	4.9	31.5	86.8	31.4	6.8	4.6
29.1	6.8	5.6	29.2	85.7	30.7	6.7	4.9
28.8	6.9	5.6	29.2	86.7	27.8	6.7	5.1
29.6	6.9	5.4	27.7	84.9	27.2	6.6	4.6
28.2	6.8	5.3	28.8	84.6	28.0	6.7	5.1
27.3	6.8	4.8	27.5	82.8	26.6	6.6	5.2
26.9	6.7	4.2	28.6	86.3	28.9	6.7	4.7
28.8	6.8	4.4	29.1	84.4	30.2	6.8	4.6
29.6	6.9	5.4	27.7	84.9	27.2	6.6	4.6
29.1	6.7	4.8	29.7	85.3	31.9	6.8	4.2
28.9	6.7	5.4	28.5	84.0	30.3	6.7	5.1
27.1	6.8	5.1	29.4	84.6	31.7	6.8	4.6
31.4	6.9	3.9	29.7	85.6	30.9	6.8	4.3
29.6	6.9	5.4	27.7	84.9	27.2	6.6	4.6
29.8	6.8	4.4	30.2	87.4	31.9	6.9	4.5
29.4	7.0	5.4	29.1	85.9	29.8	6.8	4.8
29.1	6.9	4.9	28.1	85.3	28.8	6.7	5.4
29.4	6.9	4.6	29.3	84.1	32.0	6.9	5.2
29.6	6.9	5.4	27.7	84.9	27.2	6.6	4.6
28.0	6.8	4.9	29.4	84.0	30.3	6.8	4.7
29.5	6.9	5.0	27.9	84.0	30.3	6.7	5.0
29.0	7.0	5.6	29.9	84.5	30.5	6.9	5.5
27.2	7.0	5.5	29.9	86.5	29.4	6.7	5.1
29.6	6.9	5.4	27.7	84.9	27.2	6.6	4.6
28.2	6.9	5.1	27.8	82.3	29.2	6.7	4.8
26.9	6.8	4.8	30.2	86.9	31.3	6.9	4.6
27.4	6.9	5.5	26.6	84.3	26.5	6.6	5.2
28.1	6.8	4.5	29.6	85.2	29.1	6.7	4.7
29.6	6.9	5.4	27.7	84.9	27.2	6.6	4.6
30.2	6.9	4.9	29.6	85.0	31.2	6.8	4.7
27.0	6.6	5.0	27.2	82.7	26.9	6.6	5.5
30.6	6.8	4.4	29.1	84.6	31.3	6.7	4.3
29.5	6.8	5.1	29.4	86.4	30.5	6.8	4.8

29.6	6.9	5.4	27.7	84.9	27.2	6.6	4.6
28.3	6.7	4.9	28.6	85.3	27.5	6.7	5.2
28.3	6.7	4.8	28.0	82.8	27.0	6.6	5.4
28.0	6.8	5.3	28.7	84.3	28.6	6.6	5.0
30.5	6.9	4.7	29.4	86.4	30.1	6.8	4.5
29.6	6.9	4.7	29.6	85.7	29.4	6.8	4.8
29.4	6.8	4.9	28.8	84.8	28.6	6.7	4.6
28.8	6.8	4.7	30.4	86.2	31.1	6.9	5.0
30.1	6.9	5.4	28.5	84.4	28.7	6.6	4.5
28.5	6.8	5.0	29.4	86.4	31.9	6.8	5.3
29.6	6.9	4.7	29.6	85.7	29.4	6.8	4.8
27.6	6.8	5.6	29.2	84.6	30.3	6.7	4.7
29.5	6.9	5.6	27.6	82.9	27.2	6.6	5.6
25.1	6.6	5.8	28.0	84.8	28.3	6.7	5.1
27.3	6.7	4.9	29.4	87.3	29.0	6.8	5.1
29.6	6.9	4.7	29.6	85.7	29.4	6.8	4.8
27.0	6.7	5.6	28.5	85.2	29.6	6.8	5.1
29.9	6.9	5.5	29.1	84.7	30.6	6.8	4.9
28.7	6.7	4.8	30.0	85.2	31.5	6.7	4.1
30.6	6.8	4.9	29.9	85.0	30.6	6.7	4.8
29.6	6.9	4.7	29.6	85.7	29.4	6.8	4.8
29.9	6.9	4.6	30.1	83.0	29.5	6.8	4.5
28.0	6.8	4.5	30.2	86.6	30.0	6.8	4.8
28.7	6.9	4.9	30.5	83.9	30.0	6.8	4.7
26.9	6.8	4.5	30.2	83.0	32.5	6.9	4.7
29.6	6.9	4.7	29.6	85.7	29.4	6.8	4.8
30.1	6.9	4.5	30.9	86.6	30.7	6.8	4.8
30.6	6.9	4.6	29.4	83.6	30.7	6.7	3.9
27.5	6.7	3.9	30.4	83.3	30.4	6.8	4.2
30.1	6.8	4.8	30.5	86.2	30.3	6.8	4.3
29.6	6.9	4.7	29.6	85.7	29.4	6.8	4.8
28.5	6.8	4.1	28.5	84.3	28.7	6.8	5.3
28.9	6.8	4.9	28.8	85.3	27.2	6.7	5.1
29.7	6.8	4.7	30.6	86.7	31.7	6.9	5.4
30.2	6.8	4.6	30.4	84.6	31.2	6.8	5.0
29.6	6.9	4.7	29.6	85.7	29.4	6.8	4.8
27.5	6.8	4.7	28.0	82.3	28.6	6.7	4.9
29.4	6.8	5.1	27.9	84.8	27.4	6.6	5.2
29.7	6.8	5.0	30.8	85.4	30.4	6.8	4.7
30.1	6.8	3.5	29.6	83.6	27.9	6.7	5.0
29.6	6.9	4.7	29.6	85.7	29.4	6.8	4.8
29.3	6.9	5.4	30.5	84.9	29.2	6.8	5.0
29.4	6.8	5.3	30.8	86.2	30.2	6.8	4.8
28.5	6.7	5.2	31.5	83.8	31.3	6.8	4.5
30.0	6.8	4.7	28.0	77.9	29.4	6.7	4.8
29.6	6.9	4.7	29.6	85.7	29.4	6.8	4.8
27.1	6.8	5.0	29.5	85.8	28.5	6.7	5.0
28.0	6.8	5.4	29.5	84.2	28.9	6.7	4.6
28.6	6.6	4.3	29.1	84.8	28.6	6.7	5.0
28.3	6.9	4.8	30.5	87.0	30.9	6.8	4.5

29.6	6.9	4.7	29.6	85.7	29.4	6.8	4.8
31.9	6.9	4.9	30.5	86.3	29.2	6.8	5.2
28.4	6.9	5.5	30.0	84.9	29.4	6.7	5.3
30.9	6.8	5.0	30.3	87.9	30.4	6.8	4.5
28.9	6.7	5.2	31.6	84.6	30.3	6.9	4.4
27.5	6.7	4.8	29.9	83.8	27.7	6.7	5.0
26.9	6.8	4.9	29.4	84.9	28.4	6.7	4.8
30.3	6.9	5.4	28.2	82.3	28.2	6.7	4.7
28.3	6.7	4.6	28.8	82.7	30.0	6.7	4.4
29.4	6.7	4.9	29.8	83.5	28.9	6.8	5.1
27.5	6.7	4.8	29.9	83.8	27.7	6.7	5.0
29.1	6.8	5.2	30.0	85.0	28.9	6.8	4.8
25.2	6.6	2.9	30.7	85.9	28.8	6.8	5.4
28.5	6.8	4.7	29.5	84.9	27.3	6.7	4.5
30.5	6.8	4.0	29.7	85.7	30.1	6.8	4.4
27.5	6.7	4.8	29.9	83.8	27.7	6.7	5.0
29.5	6.8	5.0	28.2	84.6	28.5	6.7	4.7
27.2	6.8	4.7	28.7	82.6	27.0	6.7	4.8
28.0	6.8	5.2	28.6	84.2	28.5	6.7	4.5
28.1	7.0	5.3	29.8	82.0	29.7	6.8	5.1
27.5	6.7	4.8	29.9	83.8	27.7	6.7	5.0
28.1	6.9	5.4	28.2	85.2	28.1	6.7	4.9
31.0	6.9	4.4	29.8	86.3	27.8	6.7	5.2
29.8	6.9	4.3	29.5	87.1	28.3	6.7	5.2
28.7	6.8	4.9	27.8	82.3	28.0	6.7	5.4
27.5	6.7	4.8	29.9	83.8	27.7	6.7	5.0
27.7	6.7	4.0	28.6	85.2	28.3	6.7	5.4
30.0	6.8	4.3	27.9	81.5	27.6	6.7	5.0
29.2	6.9	5.4	29.3	85.0	28.5	6.7	5.7
28.5	6.8	4.5	29.7	83.6	29.7	6.8	5.1
27.5	6.7	4.8	29.9	83.8	27.7	6.7	5.0
29.3	6.8	5.0	28.7	85.2	29.9	6.7	5.1
27.7	6.8	5.1	27.6	83.9	27.4	6.6	5.2
28.8	6.8	5.3	27.6	85.1	27.6	6.6	5.7
31.5	6.9	4.2	27.9	83.1	27.0	6.6	5.9
27.5	6.7	4.8	29.9	83.8	27.7	6.7	5.0
30.4	6.7	4.2	28.8	83.8	28.2	6.7	5.3
30.8	6.8	4.5	29.5	87.6	28.7	6.7	5.2
30.5	6.8	5.0	27.9	83.5	28.2	6.6	5.1
28.4	6.8	5.4	29.2	80.8	28.9	6.7	5.4
27.5	6.7	4.8	29.9	83.8	27.7	6.7	5.0
28.4	6.7	4.8	29.9	87.8	30.0	6.8	5.0
28.4	6.8	4.7	29.0	82.7	28.9	6.7	4.8
28.3	6.8	4.5	30.9	84.8	29.2	6.8	4.5
30.7	6.8	4.1	31.3	87.2	30.8	6.9	4.6
27.5	6.7	4.8	29.9	83.8	27.7	6.7	5.0
27.0	6.7	4.9	29.9	83.9	28.3	6.7	4.8
22.9	6.4	4.4	28.1	84.7	28.2	6.7	4.7
30.1	6.9	4.6	29.8	82.5	30.1	6.8	4.9
29.9	6.8	4.1	30.1	83.5	30.2	6.8	4.8

27.5	6.7	4.8	29.9	83.8	27.7	6.7	5.0
29.7	6.8	4.5	30.4	86.1	30.2	6.8	4.4
32.1	6.8	4.2	30.1	84.0	30.2	6.8	5.1
28.5	6.8	4.9	29.6	82.1	30.2	6.8	4.9
28.2	6.7	5.1	31.1	83.7	32.6	6.9	4.7
28.4	6.8	5.1	29.1	83.9	28.9	6.7	4.7
27.3	6.7	5.8	28.5	85.4	29.7	6.7	4.8
28.3	6.7	5.8	27.7	84.0	27.4	6.7	5.6
29.7	6.8	4.3	30.5	87.8	29.4	6.8	4.8
29.9	6.8	4.4	31.1	86.4	30.2	6.9	5.4
28.4	6.8	5.1	29.1	83.9	28.9	6.7	4.7
29.2	6.7	5.3	29.1	84.8	32.8	6.8	4.9
29.3	6.7	5.2	27.6	83.5	29.4	6.7	4.9
31.0	6.7	4.5	32.1	85.5	32.8	6.8	4.5
29.7	6.7	4.4	28.5	79.5	30.7	6.7	4.8
28.4	6.8	5.1	29.1	83.9	28.9	6.7	4.7
27.7	6.7	5.1	29.5	81.9	30.5	6.8	5.0
29.7	6.8	4.5	29.9	85.7	33.3	6.8	3.8
29.1	6.8	4.7	30.1	85.2	30.1	6.7	4.9
30.7	6.8	4.3	30.9	83.8	29.9	6.8	5.1
28.4	6.8	5.1	29.1	83.9	28.9	6.7	4.7
27.8	6.8	4.4	29.2	86.1	28.7	6.7	4.6
26.8	6.7	5.9	26.6	82.3	26.0	6.5	5.7
27.9	6.7	5.2	28.1	85.5	28.3	6.6	4.9
27.9	6.7	5.1	26.9	86.0	26.8	6.5	4.9
28.4	6.8	5.1	29.1	83.9	28.9	6.7	4.7
29.3	6.8	4.1	30.1	86.7	28.8	6.8	4.6
29.9	6.8	4.0	29.1	84.9	28.3	6.8	5.2
28.2	6.6	4.8	28.3	83.3	30.3	6.7	4.3
28.9	6.8	4.9	29.0	86.8	31.1	6.7	4.7
28.4	6.8	5.1	29.1	83.9	28.9	6.7	4.7
29.7	6.7	4.6	30.1	85.9	30.9	6.8	4.6
26.6	6.7	4.8	29.6	83.1	28.4	6.7	4.4
31.3	6.8	4.2	28.1	81.6	29.3	6.7	4.5
29.3	6.7	3.9	29.2	86.5	27.6	6.7	4.7
28.4	6.8	5.1	29.1	83.9	28.9	6.7	4.7
26.5	6.7	4.5	30.2	85.0	28.8	6.7	4.5
24.4	6.4	4.3	28.0	84.4	27.7	6.7	5.3
27.3	6.7	4.9	28.2	85.5	29.4	6.6	4.3
30.0	6.9	4.5	30.1	84.4	29.4	6.8	4.8
28.4	6.8	5.1	29.1	83.9	28.9	6.7	4.7
29.4	6.9	5.1	30.3	86.3	30.8	6.8	4.9
29.8	6.8	4.8	31.8	85.6	31.0	6.7	4.5
28.1	6.8	4.8	27.9	83.4	28.6	6.7	4.3
28.4	6.7	4.6	30.0	85.9	31.1	6.8	4.2
28.4	6.8	5.1	29.1	83.9	28.9	6.7	4.7
29.4	6.7	4.0	30.9	85.9	28.9	6.7	4.8
31.0	6.8	4.3	29.3	84.6	30.4	6.7	4.6
29.4	6.9	5.2	30.5	86.7	28.9	6.8	5.3
28.9	6.8	4.9	30.9	87.3	30.6	6.8	5.2

28.4	6.8	5.1	29.1	83.9	28.9	6.7	4.7
27.3	6.7	4.8	28.8	83.2	27.7	6.6	4.6
27.9	6.9	5.3	30.7	85.4	31.8	6.8	4.5
29.6	6.8	4.6	29.8	85.8	30.0	6.7	5.1
28.7	6.7	5.2	28.4	85.6	28.2	6.6	5.3
28.1	6.7	3.9	29.3	86.1	28.0	6.7	5.5
28.1	6.7	4.7	28.6	86.1	26.8	6.7	5.5
29.8	6.8	4.8	28.2	83.9	27.6	6.7	4.8
29.4	6.8	5.0	28.7	85.7	27.0	6.7	5.8
29.7	6.8	5.1	29.6	85.3	29.5	6.7	5.6
30.5	6.9	5.0	28.4	85.4	27.8	6.6	5.6
28.1	6.7	4.7	28.6	86.1	26.8	6.7	5.5
28.4	6.8	4.7	29.0	85.9	28.3	6.7	5.3
28.7	6.9	5.1	29.1	84.5	28.1	6.6	4.8
27.0	6.8	5.2	27.5	82.2	27.9	6.7	5.7
27.6	6.8	4.9	27.2	84.3	25.9	6.6	5.1
28.1	6.7	4.7	28.6	86.1	26.8	6.7	5.5
29.8	6.9	4.5	29.2	88.0	27.0	6.7	5.4
27.8	6.9	5.1	27.4	86.0	26.2	6.6	5.1
28.5	6.9	5.5	29.8	85.4	29.7	6.8	4.8
28.7	6.8	5.1	28.1	85.5	27.4	6.6	5.4
28.1	6.7	4.7	28.6	86.1	26.8	6.7	5.5
27.6	6.8	4.8	30.2	86.3	29.7	6.8	5.0
29.5	7.0	5.2	30.1	85.5	29.7	6.8	5.7
29.4	6.8	4.6	28.7	85.1	27.0	6.6	5.6
30.6	6.9	5.0	29.1	84.5	28.8	6.7	5.5
28.1	6.7	4.7	28.6	86.1	26.8	6.7	5.5
29.8	6.8	4.4	30.2	85.7	30.6	6.8	4.5
29.7	6.8	4.6	29.0	85.5	31.5	6.8	4.8
29.4	6.8	4.3	28.9	85.2	27.0	6.7	5.2
28.0	6.9	5.2	27.8	83.8	28.1	6.7	4.9
28.1	6.7	4.7	28.6	86.1	26.8	6.7	5.5
28.3	6.8	4.7	29.5	85.6	29.2	6.7	4.8
30.1	6.8	4.3	29.1	83.7	27.9	6.7	4.5
27.7	6.8	4.6	27.0	84.3	25.3	6.6	5.0
26.7	6.7	5.3	26.5	84.4	25.7	6.6	5.1
28.1	6.7	4.7	28.6	86.1	26.8	6.7	5.5
27.4	6.8	5.1	28.9	85.0	28.5	6.7	4.9
30.3	6.8	5.4	29.4	85.2	29.3	6.8	5.1
31.4	7.0	4.5	31.5	85.9	32.0	6.9	4.7
28.8	6.8	4.7	30.3	86.9	28.4	6.8	4.8
28.1	6.7	4.7	28.6	86.1	26.8	6.7	5.5
30.7	6.8	4.5	30.8	85.4	29.9	6.8	5.0
32.6	6.9	4.0	29.4	84.0	32.3	6.7	3.9
30.1	6.8	4.8	27.3	83.0	29.2	6.7	4.9
30.3	6.9	4.7	28.0	82.0	28.9	6.7	4.6
28.1	6.7	4.7	28.6	86.1	26.8	6.7	5.5
30.7	6.9	4.5	28.1	82.9	29.9	6.6	3.7
29.6	6.8	3.2	29.4	83.4	29.1	6.7	4.7
30.5	6.8	4.5	29.1	84.6	32.1	6.8	5.0

29.7	6.8	3.8	29.5	85.8	31.0	6.8	4.8
28.1	6.7	4.7	28.6	86.1	26.8	6.7	5.5
31.4	7.0	4.4	28.5	81.3	28.9	6.7	4.6
31.0	6.9	4.2	30.7	86.4	35.4	7.0	4.1
29.6	6.7	3.5	29.4	86.0	29.3	6.8	4.6
30.3	6.9	4.3	28.4	84.9	27.7	6.7	5.0
29.3	6.8	5.0	28.4	85.7	27.8	6.7	4.9
29.6	6.9	4.8	28.4	85.0	28.4	6.7	5.0
31.4	7.0	4.9	29.8	87.6	30.7	6.8	4.8
30.2	6.9	5.0	30.3	87.0	29.8	6.8	5.0
29.7	6.8	4.6	29.5	85.8	31.0	6.8	4.6
29.3	6.8	5.0	28.4	85.7	27.8	6.7	4.9
28.0	6.9	5.1	28.2	84.1	28.2	6.7	4.7
29.1	6.8	5.0	28.8	84.6	28.8	6.8	5.1
27.4	6.9	5.0	28.4	84.4	28.0	6.7	4.7
29.1	6.8	5.3	29.2	84.4	28.0	6.7	5.0
29.3	6.8	5.0	28.4	85.7	27.8	6.7	4.9
28.9	6.8	4.9	26.7	81.6	26.9	6.6	4.9
29.1	6.9	5.3	29.0	85.1	30.0	6.8	4.8
28.7	6.9	4.6	30.5	85.9	29.6	6.8	4.6
28.7	6.9	4.6	27.2	83.6	28.1	6.6	4.4
29.3	6.8	5.0	28.4	85.7	27.8	6.7	4.9
28.8	6.9	4.5	29.6	84.0	30.3	6.8	4.5
29.8	6.9	4.3	29.2	83.7	28.8	6.7	4.2
29.0	6.9	4.6	29.0	85.5	30.0	6.7	4.8
30.4	6.8	4.0	28.7	86.2	28.3	6.7	4.8
29.3	6.8	5.0	28.4	85.7	27.8	6.7	4.9
28.3	6.9	5.3	28.4	85.7	27.8	6.7	5.1
30.1	6.8	4.8	26.1	85.1	27.1	6.6	5.6
27.0	6.6	5.9	24.2	82.8	23.9	6.3	5.9
27.5	6.7	5.7	29.2	86.9	28.4	6.7	5.0
29.3	6.8	5.0	28.4	85.7	27.8	6.7	4.9
28.8	6.8	4.9	30.3	87.1	28.8	6.8	5.4
29.9	7.0	5.3	28.3	83.5	29.0	6.7	5.5
30.0	6.6	4.5	28.8	84.0	29.7	6.6	4.5
30.5	6.8	4.9	30.0	86.4	29.3	6.7	4.9
29.3	6.8	5.0	28.4	85.7	27.8	6.7	4.9
29.4	6.7	4.6	28.8	86.1	27.7	6.7	4.8
27.0	6.7	4.6	25.0	80.1	24.7	6.5	5.4
29.9	6.8	4.6	28.8	83.7	28.7	6.6	5.1
29.7	6.8	4.8	28.0	85.4	28.3	6.7	5.2
29.3	6.8	5.0	28.4	85.7	27.8	6.7	4.9
28.3	6.9	5.0	29.2	87.3	27.0	6.7	5.6
26.9	6.7	4.9	29.2	84.5	30.0	6.7	5.2
27.4	6.8	5.3	25.7	82.9	25.5	6.5	5.7
26.5	6.8	5.2	26.9	84.9	28.0	6.6	5.6
29.3	6.8	5.0	28.4	85.7	27.8	6.7	4.9
28.0	6.7	4.9	28.1	85.1	28.2	6.7	4.8
29.1	6.8	5.1	28.7	85.9	29.3	6.7	4.6
29.7	6.9	4.7	30.3	85.3	29.9	6.8	4.9

29.7	6.8	4.1	29.2	85.1	28.4	6.7	5.0
29.3	6.8	5.0	28.4	85.7	27.8	6.7	4.9
28.0	6.8	4.9	28.9	86.5	27.7	6.8	5.5
27.5	6.7	5.3	28.1	84.8	26.6	6.7	5.5
28.4	6.7	4.6	27.3	84.7	26.2	6.6	5.7
30.4	6.7	4.5	28.4	85.8	27.5	6.7	5.3
25.8	6.6	4.1	28.5	86.2	27.1	6.7	5.0
28.6	6.8	5.0	29.1	87.6	28.4	6.7	4.9
27.1	6.9	5.9	28.9	87.6	27.2	6.8	5.7
30.2	6.9	5.0	30.6	87.5	29.3	6.8	5.0
30.5	6.9	4.6	30.2	86.3	28.5	6.7	5.2
25.8	6.6	4.1	28.5	86.2	27.1	6.7	5.0
28.7	6.7	4.9	29.6	85.5	28.4	6.7	4.5
27.8	6.7	5.0	26.8	84.2	25.7	6.6	5.1
33.6	6.9	5.1	29.3	85.3	29.2	6.7	5.7
31.2	6.8	4.8	29.7	86.1	29.3	6.7	5.1
25.8	6.6	4.1	28.5	86.2	27.1	6.7	5.0
31.5	6.8	4.5	27.8	82.9	27.3	6.6	5.0
30.1	6.8	3.3	25.8	82.3	24.1	6.5	4.9
30.2	6.8	3.6	27.1	84.4	27.5	6.6	4.7
29.3	6.8	4.3	29.5	86.6	28.1	6.7	4.5
25.8	6.6	4.1	28.5	86.2	27.1	6.7	5.0
29.4	6.8	5.3	28.5	85.6	29.0	6.7	5.0
31.3	6.8	5.2	30.3	86.9	29.4	6.8	4.8
31.7	6.8	5.1	29.2	85.3	28.6	6.7	5.3
31.6	6.9	4.5	28.5	85.3	28.2	6.6	4.7
25.8	6.6	4.1	28.5	86.2	27.1	6.7	5.0
30.3	6.9	5.0	29.4	85.7	28.1	6.7	4.8
30.1	6.9	4.8	29.2	84.4	28.4	6.7	4.6
30.6	7.0	4.8	30.4	85.2	29.7	6.7	4.4
31.0	7.0	5.1	28.3	83.8	28.5	6.6	4.9
25.8	6.6	4.1	28.5	86.2	27.1	6.7	5.0
29.1	6.9	4.9	28.9	84.7	27.0	6.7	5.0
27.5	6.8	4.7	28.7	84.8	28.3	6.7	4.8
28.7	6.7	5.4	28.4	85.4	28.0	6.6	5.3
29.5	6.8	5.1	29.6	87.9	28.0	6.7	5.4
25.8	6.6	4.1	28.5	86.2	27.1	6.7	5.0
30.4	6.9	4.9	30.0	86.3	30.3	6.8	4.9
30.1	6.8	5.0	29.9	81.4	29.8	6.8	5.3
27.0	6.7	4.3	26.3	84.3	25.8	6.6	4.8
27.9	6.9	5.1	28.1	86.7	27.1	6.7	5.0
25.8	6.6	4.1	28.5	86.2	27.1	6.7	5.0
28.6	6.8	5.4	28.9	85.3	29.7	6.8	5.2
31.4	6.8	3.3	29.4	85.4	28.2	6.7	5.1
31.7	6.9	4.5	30.4	87.3	28.9	6.7	5.1
26.9	6.7	5.1	29.1	86.6	28.6	6.7	4.7
25.8	6.6	4.1	28.5	86.2	27.1	6.7	5.0
28.9	6.8	4.0	30.1	86.2	28.0	6.7	5.0
31.5	6.8	3.8	31.5	86.8	29.0	6.8	5.5
30.9	6.8	4.5	26.7	83.2	25.6	6.5	4.9

29.4	6.7	4.6	28.5	85.7	28.3	6.7	4.9
25.8	6.6	4.1	28.5	86.2	27.1	6.7	5.0
28.1	6.9	4.7	28.1	84.3	27.7	6.7	5.0
29.9	6.8	4.5	29.6	81.7	30.7	6.7	4.5
29.2	6.8	4.9	29.1	86.4	29.6	6.7	4.4
30.3	6.9	4.2	28.2	82.6	31.2	6.8	4.4
29.9	6.9	5.3	28.0	85.0	27.0	6.6	4.3
29.3	6.8	5.0	28.4	84.7	28.9	6.7	4.9
28.3	6.7	4.7	28.1	83.3	28.1	6.7	5.5
29.7	6.8	5.2	28.7	83.8	29.4	6.7	4.7
30.5	6.9	4.8	29.6	86.0	27.5	6.7	4.9
29.9	6.9	5.3	28.0	85.0	27.0	6.6	4.3
30.2	6.9	5.1	27.2	85.3	27.0	6.6	5.5
29.3	6.8	5.4	26.2	85.4	26.2	6.5	5.5
28.7	6.8	5.3	29.4	85.9	29.3	6.7	5.8
28.2	6.9	5.5	28.8	86.4	28.7	6.7	5.1
29.9	6.9	5.3	28.0	85.0	27.0	6.6	4.3
28.4	6.8	5.0	28.8	86.6	30.0	6.8	5.2
28.0	6.8	5.5	29.1	86.5	28.0	6.7	5.2
26.2	6.6	5.2	28.8	87.0	28.2	6.7	5.8
29.1	6.8	5.0	28.2	86.3	27.9	6.7	5.4
29.9	6.9	5.3	28.0	85.0	27.0	6.6	4.3
28.3	6.8	5.0	29.7	86.0	29.8	6.7	4.5
29.7	6.9	5.4	29.2	83.7	31.2	6.7	4.4
27.9	6.7	4.7	29.1	83.0	31.1	6.7	4.2
27.8	6.7	5.0	29.0	85.4	29.8	6.7	4.1
29.9	6.9	5.3	28.0	85.0	27.0	6.6	4.3
27.7	6.7	4.9	29.8	86.0	29.3	6.7	4.8
30.3	6.7	5.0	29.2	84.2	30.2	6.7	4.5
28.4	6.7	5.0	29.3	86.1	29.7	6.8	5.2
28.3	6.8	5.1	29.5	85.7	29.8	6.7	5.5
29.9	6.9	5.3	28.0	85.0	27.0	6.6	4.3
29.4	6.9	5.7	29.5	86.9	31.4	6.7	4.3
30.7	6.8	5.3	29.9	85.9	28.8	6.7	5.4
29.3	6.8	4.1	30.8	84.5	28.7	6.7	4.4
29.2	6.8	4.0	29.6	85.8	30.6	6.8	4.1
29.9	6.9	5.3	28.0	85.0	27.0	6.6	4.3
28.5	6.8	4.9	29.9	85.6	30.1	6.8	4.9
28.8	6.9	5.3	28.7	84.3	26.6	6.7	5.4
28.5	6.8	4.9	28.8	84.3	29.7	6.7	3.4
29.6	6.8	3.9	29.3	86.2	29.0	6.8	5.0
29.9	6.9	5.3	28.0	85.0	27.0	6.6	4.3
30.2	6.8	3.7	29.3	82.5	29.1	6.7	4.6
27.3	6.7	5.0	29.7	84.9	29.2	6.7	4.9
28.8	6.6	4.6	29.8	84.6	31.0	6.7	4.5
29.1	6.8	4.7	29.8	85.3	30.3	6.7	4.8
29.9	6.9	5.3	28.0	85.0	27.0	6.6	4.3
28.3	6.8	4.9	30.0	85.4	29.5	6.8	5.3
27.5	6.7	4.1	28.8	85.8	28.7	6.7	4.7
28.3	6.8	4.7	29.5	85.7	29.7	6.7	4.6

28.8	6.8	4.6	29.1	84.3	28.3	6.7	5.1
29.9	6.9	5.3	28.0	85.0	27.0	6.6	4.3
29.1	6.7	4.8	29.8	85.4	31.9	6.8	4.1
30.9	6.9	4.8	29.1	84.4	29.7	6.7	5.1
29.6	6.8	3.2	26.5	83.7	26.5	6.6	5.9
27.9	6.8	5.5	28.7	85.3	28.2	6.7	4.9
29.4	6.9	4.9	28.4	85.3	28.6	6.7	4.7
29.3	6.9	5.3	29.5	87.0	29.3	6.7	5.0
28.5	6.9	5.8	29.6	85.6	29.3	6.8	5.0
30.2	6.9	5.2	31.3	85.9	31.1	6.8	5.1
28.8	6.8	5.1	30.0	85.5	30.1	6.8	5.1
29.4	6.9	4.9	28.4	85.3	28.6	6.7	4.7
29.3	6.9	5.0	29.4	85.6	28.6	6.8	5.7
27.9	6.9	5.6	27.1	82.4	27.6	6.6	5.3
30.5	6.9	5.4	30.0	84.7	29.1	6.8	5.5
28.4	6.9	5.4	30.3	85.9	31.9	6.8	4.2
29.4	6.9	4.9	28.4	85.3	28.6	6.7	4.7
30.6	6.8	4.9	29.1	82.9	28.6	6.8	5.8
28.5	6.9	5.7	27.0	83.0	27.0	6.6	5.5
29.6	6.8	5.4	29.3	85.3	29.1	6.8	5.9
30.2	6.8	5.0	29.3	85.8	27.4	6.6	4.5
29.4	6.9	4.9	28.4	85.3	28.6	6.7	4.7
31.5	6.9	4.6	31.1	86.5	32.0	6.8	4.8
33.6	6.9	4.1	32.3	85.1	33.2	6.8	4.1
27.4	6.7	4.9	28.3	82.6	27.7	6.7	5.3
31.1	6.9	4.6	28.1	82.7	25.5	6.6	4.7
29.4	6.9	4.9	28.4	85.3	28.6	6.7	4.7
29.0	6.8	5.3	29.1	85.9	28.6	6.7	4.3
29.1	6.8	5.1	31.2	85.5	29.7	6.8	5.0
28.2	6.7	4.8	28.4	82.8	27.7	6.7	5.5
29.4	6.9	4.9	28.4	85.3	28.6	6.7	4.7
29.0	6.8	4.5	30.1	86.0	31.1	6.7	4.3
31.7	6.8	4.6	31.4	85.4	30.2	6.8	5.3
27.6	6.9	5.3	30.1	84.3	29.0	6.7	4.1
29.4	6.7	3.8	28.3	82.9	26.4	6.6	4.5
29.4	6.9	4.9	28.4	85.3	28.6	6.7	4.7
29.6	6.8	4.8	30.1	87.0	29.7	6.8	4.8
27.8	6.8	5.5	28.6	86.2	27.7	6.7	4.8
30.9	6.9	4.7	28.4	85.0	31.3	6.8	5.1
27.0	6.7	5.4	30.0	87.2	29.6	6.8	5.5
29.4	6.9	4.9	28.4	85.3	28.6	6.7	4.7
28.5	6.9	5.2	29.2	85.3	28.1	6.7	4.9
31.9	7.0	4.7	28.6	82.0	29.1	6.7	4.5
29.6	6.7	4.6	27.7	82.1	26.8	6.6	5.1
27.3	6.7	4.7	30.2	86.0	28.6	6.7	5.0
29.4	6.9	4.9	28.4	85.3	28.6	6.7	4.7
28.2	6.8	4.7	29.2	85.1	26.9	6.6	5.1
28.0	6.7	4.2	29.9	86.4	27.5	6.7	5.6
30.0	6.8	4.7	27.1	82.7	28.8	6.6	5.1
27.0	6.5	4.3	28.2	84.1	27.6	6.6	4.8

29.4	6.9	4.9	28.4	85.3	28.6	6.7	4.7
27.7	6.8	5.4	27.8	83.6	27.6	6.6	4.9
28.2	6.8	4.3	28.8	84.7	27.3	6.6	5.5
28.2	6.8	4.7	28.9	84.3	28.6	6.7	5.4
27.4	6.8	5.3	30.5	86.9	30.9	6.9	5.4
29.8	6.7	3.8	27.6	84.8	28.0	6.6	5.3
30.9	6.8	4.2	31.0	85.9	31.2	6.8	4.4
30.2	6.9	5.4	30.6	86.9	29.7	6.8	5.2
31.2	6.9	5.4	32.3	86.8	31.1	6.9	5.0
31.7	6.9	4.2	31.3	86.5	29.8	6.9	4.8
29.8	6.7	3.8	27.6	84.8	28.0	6.6	5.3
30.2	6.8	4.8	31.1	85.6	29.3	6.8	4.9
32.5	6.9	3.5	31.0	86.0	32.3	7.0	4.7
30.8	6.8	4.2	30.4	86.3	32.2	6.8	4.6
29.3	6.8	5.4	29.7	85.3	29.2	6.8	4.7
29.8	6.7	3.8	27.6	84.8	28.0	6.6	5.3
28.0	6.8	4.8	31.0	85.2	28.9	6.8	5.1
29.4	6.8	4.7	30.5	87.3	30.4	6.8	5.2
31.0	6.7	4.8	27.7	84.9	30.0	6.7	5.7
28.8	6.8	4.7	29.6	85.2	29.5	6.8	5.2
29.8	6.7	3.8	27.6	84.8	28.0	6.6	5.3
30.5	6.7	3.7	31.1	86.4	30.2	6.9	4.9
27.6	6.8	5.2	30.2	84.6	30.0	6.8	4.6
30.2	6.9	4.6	30.1	86.5	29.2	6.7	4.4
30.2	6.8	4.2	29.3	86.3	29.5	6.8	5.0
29.8	6.7	3.8	27.6	84.8	28.0	6.6	5.3
27.6	6.8	5.3	29.9	86.7	29.2	6.8	5.2
31.1	6.8	5.1	27.6	84.3	29.0	6.7	5.6
28.4	6.9	5.0	30.0	86.5	31.4	6.8	4.5
29.5	6.8	4.0	30.0	85.9	31.0	6.9	5.0
29.8	6.7	3.8	27.6	84.8	28.0	6.6	5.3
27.9	6.8	5.0	29.0	84.0	28.5	6.7	5.0
29.9	6.9	4.7	28.7	85.4	31.0	6.9	5.0
28.3	6.8	5.3	28.7	83.7	29.5	6.7	4.9
29.4	6.9	4.8	28.4	83.9	28.3	6.7	5.4
29.8	6.7	3.8	27.6	84.8	28.0	6.6	5.3
28.5	6.8	5.2	28.6	84.3	29.5	6.8	5.2
30.3	6.8	4.6	30.5	85.4	28.9	6.8	5.1
30.1	6.9	4.6	29.8	83.7	29.1	6.8	4.9
30.4	7.0	4.7	29.9	85.0	30.4	6.8	4.6
29.8	6.7	3.8	27.6	84.8	28.0	6.6	5.3
29.4	6.8	3.9	30.0	85.5	28.6	6.8	5.1
28.1	6.6	4.2	29.8	85.2	28.9	6.8	4.9
27.7	6.9	5.3	28.9	85.3	27.4	6.7	5.3
27.8	6.8	4.8	29.9	84.5	28.5	6.8	5.1
29.8	6.7	3.8	27.6	84.8	28.0	6.6	5.3
30.6	6.9	4.7	29.8	85.0	29.9	6.8	5.1
30.9	6.8	4.6	28.3	84.9	27.0	6.6	5.4
30.9	6.8	4.4	30.9	85.7	31.3	6.8	4.2
28.4	6.8	4.9	30.5	86.2	29.7	6.8	4.9

29.8	6.7	3.8	27.6	84.8	28.0	6.6	5.3
30.4	6.8	4.6	29.7	84.1	31.9	6.8	4.6
26.1	6.6	5.2	29.0	85.2	28.8	6.7	4.8
28.5	6.8	4.8	30.2	87.3	30.7	6.8	4.7
27.9	6.8	5.2	30.3	88.0	29.2	6.8	4.7
29.4	6.7	3.5	29.4	85.8	28.8	6.7	5.3
29.6	6.8	4.8	30.9	87.4	29.9	6.8	5.1
31.4	6.9	4.7	29.0	83.7	29.0	6.7	5.5
26.3	6.6	5.1	29.4	85.6	28.0	6.7	5.5
29.2	6.9	5.4	30.3	85.3	29.8	6.8	5.1
29.4	6.7	3.5	29.4	85.8	28.8	6.7	5.3
29.1	6.9	5.2	29.6	83.7	29.4	6.8	5.4
29.1	6.7	4.0	27.1	80.9	26.4	6.6	5.6
27.6	6.7	5.1	28.7	84.7	27.3	6.7	5.3
27.9	6.8	5.4	29.4	84.9	28.4	6.7	4.8
29.4	6.7	3.5	29.4	85.8	28.8	6.7	5.3
28.5	6.9	5.3	29.9	85.6	29.0	6.8	5.4
29.7	6.9	5.3	29.4	85.2	30.6	6.8	5.1
28.4	6.7	4.0	30.3	86.3	29.6	6.8	4.5
28.9	6.8	4.7	29.5	85.4	29.8	6.8	4.7
29.4	6.7	3.5	29.4	85.8	28.8	6.7	5.3
28.9	6.9	4.7	30.5	85.8	31.2	6.8	4.4
29.2	6.9	4.9	30.9	85.7	29.1	6.7	4.5
29.5	6.8	4.5	29.4	85.9	29.3	6.8	5.2
27.2	6.8	4.8	30.5	85.1	30.6	6.8	5.4
29.4	6.7	3.5	29.4	85.8	28.8	6.7	5.3
30.0	6.9	4.1	29.1	82.7	28.2	6.8	5.4
28.2	6.9	4.6	31.6	88.3	30.0	6.9	4.7
29.1	6.9	4.5	29.4	83.1	29.9	6.7	4.0
29.4	6.8	3.8	30.2	84.9	29.8	6.7	4.3
29.4	6.7	3.5	29.4	85.8	28.8	6.7	5.3
28.4	6.9	5.4	29.8	85.4	29.9	6.8	5.0
27.5	6.9	4.7	27.9	84.3	28.8	6.7	4.8
32.5	7.0	4.9	31.0	86.2	30.8	6.9	5.6
30.7	6.9	4.5	32.4	84.5	33.7	6.9	5.0
29.4	6.7	3.5	29.4	85.8	28.8	6.7	5.3
29.2	6.8	5.1	29.6	86.5	28.2	6.7	5.0
27.8	6.8	5.6	29.2	85.3	29.6	6.8	5.3
29.1	6.9	4.9	31.0	85.9	31.5	6.8	4.9
29.0	6.8	4.5	30.6	85.8	29.6	6.7	4.8
29.4	6.7	3.5	29.4	85.8	28.8	6.7	5.3
28.6	6.8	4.5	29.3	84.1	28.7	6.7	5.5
29.7	6.9	5.2	29.9	86.1	28.7	6.6	5.0
29.0	6.7	4.3	30.8	86.4	29.3	6.7	4.9
29.1	6.9	5.0	31.3	86.4	28.9	6.7	4.4
29.4	6.7	3.5	29.4	85.8	28.8	6.7	5.3
27.9	6.8	4.8	29.8	86.4	27.0	6.7	5.2
28.0	6.7	5.1	30.1	85.9	29.3	6.8	5.0
30.3	6.9	4.7	30.9	86.6	28.5	6.8	4.6
29.3	6.8	5.0	29.3	86.5	27.3	6.7	5.3

29.4	6.7	3.5	29.4	85.8	28.8	6.7	5.3
29.1	6.9	5.2	30.1	86.1	29.5	6.8	5.3
29.0	6.8	5.4	30.9	86.0	30.1	6.8	5.3
29.2	6.9	5.6	29.5	82.5	28.9	6.8	5.1
29.0	6.9	4.9	30.2	84.6	27.0	6.7	5.1
29.9	6.8	3.9	30.1	86.6	30.1	6.8	4.6
26.3	6.6	3.8	28.0	82.7	28.4	6.6	4.6
28.0	6.8	5.2	31.9	86.4	31.2	6.9	4.6
28.9	6.8	5.2	29.3	84.4	29.7	6.7	5.3
28.3	6.8	5.4	30.6	83.7	31.4	6.9	4.7
29.9	6.8	3.9	30.1	86.6	30.1	6.8	4.6
28.6	6.8	4.4	30.7	86.2	30.3	6.9	4.9
27.6	6.8	5.3	29.7	84.9	28.2	6.7	5.4
28.9	6.8	4.4	28.7	85.0	27.1	6.6	4.8
28.1	6.8	4.8	28.0	84.3	28.0	6.6	4.8
29.9	6.8	3.9	30.1	86.6	30.1	6.8	4.6
25.9	6.7	5.4	25.1	81.5	24.9	6.5	5.0
28.0	6.9	5.1	26.5	79.1	26.8	6.5	4.4
29.0	6.9	4.6	30.5	83.7	28.8	6.8	5.1
28.2	6.8	4.3	32.0	85.8	29.0	6.9	4.8
29.9	6.8	3.9	30.1	86.6	30.1	6.8	4.6
28.5	6.8	4.7	30.0	86.2	28.0	6.7	4.6
28.4	6.8	4.7	31.0	82.9	30.4	6.8	4.1
28.9	6.9	5.1	31.3	84.4	28.6	6.7	5.0
30.1	6.9	4.9	30.6	85.1	30.2	6.8	4.4
29.9	6.8	3.9	30.1	86.6	30.1	6.8	4.6
28.4	6.9	4.6	30.8	85.7	30.2	6.8	4.7
28.3	6.7	3.9	31.3	87.1	29.8	6.8	5.0
28.2	6.7	5.3	30.0	86.2	29.2	6.8	5.3
28.4	6.8	4.8	29.4	86.2	28.5	6.7	4.6
29.9	6.8	3.9	30.1	86.6	30.1	6.8	4.6
27.0	6.7	4.6	28.7	83.1	31.7	6.7	5.0
28.7	6.8	5.5	28.7	86.3	29.7	6.7	5.5
27.8	6.8	5.6	30.8	86.0	31.0	6.9	5.2
29.8	6.9	5.0	31.7	86.0	31.2	7.0	5.1
29.9	6.8	3.9	30.1	86.6	30.1	6.8	4.6
29.0	6.8	4.6	31.2	82.5	30.6	6.8	5.1
30.4	6.8	4.8	30.5	84.3	30.8	6.8	4.9
31.3	6.8	4.7	30.9	85.8	31.7	6.8	4.6
27.2	6.9	5.5	30.8	86.6	30.9	6.8	4.8
29.9	6.8	3.9	30.1	86.6	30.1	6.8	4.6
28.1	6.9	5.3	30.1	84.8	29.4	6.8	5.5
31.2	6.7	4.0	28.9	84.9	26.5	6.7	5.2
29.8	6.9	4.8	30.6	85.8	30.3	6.9	5.1
29.5	6.8	4.6	30.4	86.3	29.4	6.8	5.1
29.9	6.8	3.9	30.1	86.6	30.1	6.8	4.6
25.1	6.6	5.5	29.6	86.0	27.8	6.6	5.0
26.4	6.7	5.3	28.0	84.6	26.9	6.7	5.3
29.0	7.0	5.2	28.9	81.7	27.8	6.7	4.7
30.2	6.9	4.8	30.7	86.6	30.8	6.9	4.7

29.9	6.8	3.9	30.1	86.6	30.1	6.8	4.6
28.7	6.8	5.2	31.3	87.2	30.6	6.8	4.9
30.7	6.8	4.7	30.6	86.5	30.9	6.7	4.4
28.7	6.8	5.4	30.5	85.2	31.8	6.8	4.3
28.9	6.9	5.3	30.5	85.4	28.8	6.8	4.6
27.0	6.7	4.8	29.1	87.2	28.8	6.7	4.8
28.7	6.9	5.3	29.7	86.4	28.3	6.7	5.4
28.6	6.8	5.4	27.7	84.0	27.7	6.6	5.2
31.5	6.9	4.0	30.0	85.4	30.1	6.8	4.8
29.0	6.9	4.8	29.8	84.9	30.5	6.8	4.4
27.0	6.7	4.8	29.1	87.2	28.8	6.7	4.8
29.4	6.8	5.2	27.8	81.6	29.3	6.7	5.3
29.2	6.7	4.5	28.2	85.9	29.9	6.7	5.1
29.7	6.7	4.8	28.1	85.1	31.9	6.7	4.8
30.2	6.8	4.9	29.2	84.0	29.3	6.6	4.7
27.0	6.7	4.8	29.1	87.2	28.8	6.7	4.8
29.9	6.8	4.0	29.6	86.4	31.4	6.8	4.4
30.1	6.9	4.5	30.7	86.3	29.5	6.7	4.7
29.2	6.7	4.4	31.1	85.4	30.8	6.8	4.5
29.4	6.8	4.6	30.2	83.7	29.3	6.8	5.4
27.0	6.7	4.8	29.1	87.2	28.8	6.7	4.8
28.3	6.8	4.4	27.8	85.4	27.0	6.6	5.7
25.8	6.6	5.6	25.5	83.4	25.2	6.5	5.7
27.5	6.6	5.2	26.3	83.2	26.8	6.5	4.7
27.4	6.8	5.1	27.4	83.2	27.5	6.6	5.2
27.0	6.7	4.8	29.1	87.2	28.8	6.7	4.8
29.1	6.9	5.2	27.7	84.5	27.0	6.6	5.4
28.4	6.9	5.1	29.0	85.9	27.8	6.8	5.2
29.1	6.7	5.0	28.6	86.4	28.7	6.7	5.2
29.7	6.8	4.4	29.5	84.6	30.5	6.8	5.3
27.0	6.7	4.8	29.1	87.2	28.8	6.7	4.8
28.2	6.8	4.9	30.6	85.0	29.4	6.8	5.2
29.0	6.8	4.5	29.8	82.3	30.2	6.8	4.8
28.7	6.7	3.7	31.0	85.0	30.7	6.8	4.3
27.9	6.8	4.6	31.0	85.4	30.8	6.8	4.5
27.0	6.7	4.8	29.1	87.2	28.8	6.7	4.8
26.4	6.6	4.3	29.0	84.9	29.1	6.7	4.8
28.8	6.9	5.1	29.3	86.5	28.5	6.7	5.2
29.5	6.8	3.4	28.8	85.1	27.6	6.6	5.1
28.0	6.8	4.9	31.2	86.1	30.4	6.8	5.0
27.0	6.7	4.8	29.1	87.2	28.8	6.7	4.8
29.6	6.8	5.2	30.2	86.8	28.3	6.7	5.1
31.7	7.0	4.8	30.5	85.2	30.1	6.7	5.0
27.9	6.7	4.7	26.5	82.7	26.7	6.6	4.9
28.3	6.8	5.2	28.0	83.0	28.2	6.7	5.2
27.0	6.7	4.8	29.1	87.2	28.8	6.7	4.8
29.1	6.7	5.0	29.1	85.2	28.4	6.7	5.0
30.6	6.9	4.6	31.6	86.1	30.0	6.7	4.5
27.7	6.9	5.7	27.3	84.0	27.1	6.6	4.9
28.3	6.8	5.4	31.2	85.7	30.2	6.9	4.9

27.0	6.7	4.8	29.1	87.2	28.8	6.7	4.8
29.4	6.8	5.2	28.5	84.8	28.8	6.7	4.8
27.4	6.8	5.3	29.7	84.2	29.2	6.7	5.3
29.0	6.8	5.5	28.9	84.0	29.8	6.7	5.6

Table S7 Phenotype values of fiber quality traits in field trial of BC/P population in this study

Number of field trial plot	Material	FL/mm	FU/%	FS(cN/tex)	FE/%	FM
		2016E2	2016E2	2016E2	2016E2	2016E2
001	14QM003	29.4	85.7	30.4	6.8	4.8
002	14QM003H	30.0	86.5	31.0	6.8	5.0
003	P♀	28.4	82.9	30.6	6.8	5.4
004	14QM004H	29.8	83.5	30.3	6.8	5.2
005	14QM004	30.7	85.8	30.3	6.8	4.7
006	14QM005	29.3	84.8	33.0	6.8	5.2
007	14QM005H	29.1	85.4	30.8	6.7	5.4
008	P♀	28.4	82.9	30.6	6.8	5.4
009	14QM006H	29.9	85.4	30.9	6.8	5.0
010	14QM006	30.9	86.0	31.5	6.7	4.6
011	14QM007	29.1	85.2	28.3	6.8	5.2
012	14QM007H	29.3	83.2	29.7	6.8	5.2
013	P♀	28.4	82.9	30.6	6.8	5.4
014	14QM008H	29.5	85.3	29.6	6.7	4.9
015	14QM008	31.3	84.4	30.6	6.9	4.4
016	14QM009	26.3	80.8	25.6	6.5	5.1
017	14QM009H	28.3	83.1	29.0	6.7	5.2
018	P♀	28.4	82.9	30.6	6.8	5.4
019	14QM010H	30.0	84.8	28.9	6.8	5.3
020	14QM010	30.1	82.9	31.8	6.8	5.4
021	14QM011	29.9	86.2	29.9	6.8	5.3
022	14QM011H	30.3	84.9	30.5	6.8	5.3
023	P♀	28.4	82.9	30.6	6.8	5.4
024	14QM012H	29.8	82.1	32.1	6.8	5.2
025	14QM012	30.1	84.5	32.0	6.9	5.3
026	14QM013	27.6	84.6	27.2	6.7	5.6
027	14QM013H	28.9	86.2	27.9	6.7	5.4
028	P♀	28.4	82.9	30.6	6.8	5.4
029	14QM014H	30.0	84.3	29.8	6.7	4.9
030	14QM014	28.4	85.2	27.9	6.7	4.7
031	14QM015	28.9	86.3	27.8	6.7	4.7
032	14QM015H	28.1	83.2	28.5	6.7	5.1
033	P♀	28.4	82.9	30.6	6.8	5.4
034	14QM016H	27.1	84.7	27.7	6.6	5.4
035	14QM016	30.9	85.8	32.0	6.9	5.1
036	14QM017	30.4	85.1	30.8	6.8	4.3
037	14QM017H	28.4	84.6	31.0	6.7	4.9
038	P♀	28.4	82.9	30.6	6.8	5.4
039	14QM018H	30.3	85.3	30.2	6.8	4.7
040	14QM018	30.0	85.5	29.7	6.7	4.7
041	14QM019	27.9	84.3	29.9	6.7	5.0
042	14QM019H	30.1	83.4	31.1	6.8	4.9
043	P♀	28.4	82.9	30.6	6.8	5.4
044	14QM020H	28.7	85.4	28.1	6.6	5.2
045	14QM020	29.5	84.9	29.6	6.7	4.5
046	14QM021	28.7	84.1	28.1	6.7	5.2
047	14QM021H	29.8	85.3	29.8	6.7	5.0
048	P♀	28.4	82.9	30.6	6.8	5.4
049	14QM022H	29.5	86.0	29.7	6.7	5.1
050	14QM022	30.2	86.1	31.1	6.8	4.6
051	14QM023	28.5	85.2	28.0	6.7	4.8
052	14QM023H	30.4	84.2	30.7	6.8	5.1
053	P♀	30.2	84.9	30.4	6.8	5.4
054	14QM024H	30.5	83.5	30.2	6.8	4.9
055	14QM024	30.9	86.2	30.1	6.8	4.4
056	14QM025	29.8	81.4	28.6	6.7	5.4

057	14QM025H	28.9	84.4	29.8	6.7	5.4
058	P♀	30.2	84.9	30.4	6.8	5.4
059	14QM026H	28.6	84.1	28.2	6.7	5.2
060	14QM026	28.7	85.2	27.3	6.7	5.1
061	14QM027	27.8	82.3	26.9	6.7	5.6
062	14QM027H	27.8	84.5	27.2	6.7	5.2
063	P♀	30.2	84.9	30.4	6.8	5.4
064	14QM028H	30.4	86.4	30.2	6.8	5.2
065	14QM028	29.0	86.8	27.5	6.7	5.3
066	14QM029	30.9	86.2	28.9	6.7	4.9
067	14QM029H	32.4	87.8	30.3	6.9	4.7
068	P♀	30.2	84.9	30.4	6.8	5.4
069	14QM030H	30.0	81.8	29.7	6.8	4.5
070	14QM030	31.6	84.3	30.7	6.8	3.8
071	14QM031	32.7	86.7	30.9	6.9	4.1
072	14QM031H	30.0	83.1	30.2	6.7	4.6
073	P♀	30.2	84.9	30.4	6.8	5.4
074	14QM032H	26.8	84.1	28.4	6.6	5.6
075	14QM032	31.9	87.6	31.9	6.9	4.7
076	14QM033	25.3	84.2	25.1	6.5	6.0
077	14QM033H	26.0	84.7	25.3	6.5	5.4
078	P♀	30.2	84.9	30.4	6.8	5.4
079	14QM034H	30.8	87.5	29.7	6.8	5.4
080	14QM034	27.4	82.9	28.1	6.6	5.1
081	14QM035	27.6	83.1	28.9	6.6	4.3
082	14QM035H	27.4	83.2	28.7	6.6	5.2
083	P♀	30.2	84.9	30.4	6.8	5.4
084	14QM036H	28.0	84.7	29.2	6.7	4.9
085	14QM036	28.6	85.5	26.5	6.7	5.6
086	14QM037	26.3	83.1	26.3	6.5	4.7
087	14QM037H	30.7	86.7	30.6	6.8	5.2
088	P♀	30.2	84.9	30.4	6.8	5.4
089	14QM038H	29.0	84.5	30.1	6.7	5.2
090	14QM038	27.2	82.3	28.7	6.7	5.4
091	14QM039	26.3	84.4	26.2	6.5	5.2
092	14QM039H	30.3	85.5	28.4	6.8	5.7
093	P♀	30.2	84.9	30.4	6.8	5.4
094	14QM040H	30.7	86.3	31.3	6.8	4.8
095	14QM040	25.8	84.1	25.9	6.5	4.9
096	14QM041	29.2	84.7	28.7	6.7	4.6
097	14QM041H	28.4	85.3	30.3	6.7	5.0
098	P♀	30.2	84.9	30.4	6.8	5.4
099	14QM042H	29.8	86.1	29.7	6.8	5.3
100	14QM042	27.3	82.5	27.1	6.6	5.4
101	14QM043	28.4	85.0	28.5	6.7	5.1
102	14QM043H	28.7	84.1	28.6	6.7	5.5
103	P♀	29.2	87.2	30.6	6.7	4.7
104	14QM044H	29.6	85.9	29.0	6.8	5.5
105	14QM044	29.4	83.1	28.6	6.7	5.0
106	14QM045	30.5	85.5	30.5	6.8	4.8
107	14QM045H	30.3	86.6	30.8	6.8	4.7
108	P♀	29.2	87.2	30.6	6.7	4.7
109	14QM046H	28.0	84.4	29.9	6.7	4.6
110	14QM046	27.8	84.6	28.3	6.7	5.2
111	14QM047	29.4	85.7	30.5	6.7	4.8
112	14QM047H	28.9	86.2	30.7	6.7	4.8
113	P♀	29.2	87.2	30.6	6.7	4.7
114	14QM048H	28.5	84.4	27.7	6.7	5.4
115	14QM048	28.7	85.6	28.3	6.7	4.6

116	14QM049	28.9	86.8	29.7	6.7	4.2
117	14QM049H	28.1	84.8	27.1	6.6	5.2
118	P♀	29.2	87.2	30.6	6.7	4.7
119	14QM050H	28.5	84.9	28.0	6.6	5.3
120	14QM050	31.1	84.7	30.4	6.8	4.8
121	14QM051	29.2	82.8	28.8	6.7	4.5
122	14QM051H	28.6	86.2	28.0	6.6	5.4
123	P♀	29.2	87.2	30.6	6.7	4.7
124	14QM052H	27.5	83.8	28.0	6.6	5.6
125	14QM052	28.0	84.0	28.4	6.7	4.7
126	14QM053	31.1	85.6	30.5	6.7	4.9
127	14QM053H	29.3	83.7	29.8	6.7	4.8
128	P♀	29.2	87.2	30.6	6.7	4.7
129	14QM054H	27.7	84.6	27.0	6.6	5.4
130	14QM054	27.6	84.7	26.6	6.6	5.2
131	14QM055	27.0	84.4	27.1	6.5	5.6
132	14QM055H	28.4	85.9	29.1	6.6	5.0
133	P♀	29.2	87.2	30.6	6.7	4.7
134	14QM056H	30.1	85.7	30.1	6.7	5.1
135	14QM056	28.6	84.8	30.8	6.7	4.9
136	14QM057	28.0	83.8	27.7	6.7	5.3
137	14QM057H	28.6	85.2	28.2	6.7	5.2
138	P♀	29.2	87.2	30.6	6.7	4.7
139	14QM058H	27.9	85.7	29.9	6.7	5.3
140	14QM058	27.8	81.8	29.0	6.7	5.0
141	14QM059	26.3	84.1	27.2	6.6	5.1
142	14QM059H	26.9	84.4	28.9	6.7	5.3
143	P♀	29.2	87.2	30.6	6.7	4.7
144	14QM060H	31.1	85.2	32.0	6.8	4.9
145	14QM060	31.2	85.6	30.8	6.8	4.7
146	14QM061	26.9	82.6	29.3	6.7	5.5
147	14QM061H	28.4	85.0	28.4	6.7	5.4
148	P♀	29.2	87.2	30.6	6.7	4.7
149	14QM062H	31.0	84.1	31.9	6.8	4.7
150	14QM062	30.3	86.4	29.8	6.8	5.0
151	14QM063	28.9	84.7	30.2	6.8	4.9
152	14QM063H	29.6	86.0	29.9	6.7	4.2
153	P♀	28.2	83.3	27.1	6.6	5.2
154	14QM064H	30.2	84.2	29.2	6.7	4.9
155	14QM064	28.7	85.4	29.7	6.7	5.6
156	14QM065	28.8	84.2	29.1	6.7	4.8
157	14QM065H	29.1	86.1	29.2	6.7	5.1
158	P♀	28.2	83.3	27.1	6.6	5.2
159	14QM066H	30.3	86.1	28.9	6.7	5.0
160	14QM066	29.0	82.7	27.4	6.6	5.1
161	14QM067	30.0	87.0	28.8	6.7	5.2
162	14QM067H	28.9	85.7	29.3	6.8	5.1
163	P♀	28.2	83.3	27.1	6.6	5.2
164	14QM068H	30.3	86.1	29.9	6.7	4.7
165	14QM068	26.9	82.1	28.5	6.6	5.4
166	14QM069					
167	14QM069H	27.9	84.2	29.1	6.7	5.4
168	P♀	28.2	83.3	27.1	6.6	5.2
169	14QM070H	28.9	85.0	29.1	6.7	5.6
170	14QM070	29.2	85.7	28.3	6.7	5.4
171	14QM071	28.2	84.6	28.2	6.6	4.8
172	14QM071H	29.9	85.7	30.4	6.8	5.4
173	P♀	28.2	83.3	27.1	6.6	5.2
174	14QM072H	31.0	86.0	31.0	6.9	5.0

175	14QM072	28.5	83.3	31.5	6.8	5.3
176	14QM073	28.4	84.2	31.9	6.7	4.4
177	14QM073H	26.9	82.6	28.2	6.6	5.1
178	P♀	28.2	83.3	27.1	6.6	5.2
179	14QM074H	30.2	85.5	29.7	6.7	4.9
180	14QM074	29.5	83.7	29.4	6.7	5.6
181	14QM075	26.1	79.2	26.4	6.6	5.0
182	14QM075H	30.7	86.8	29.1	6.8	4.7
183	P♀	28.2	83.3	27.1	6.6	5.2
184	14QM076H	29.8	83.8	29.6	6.8	5.4
185	14QM076	28.9	84.4	29.8	6.7	4.5
186	14QM077	28.5	84.9	30.8	6.7	4.5
187	14QM077H	28.9	84.2	29.2	6.7	4.9
188	P♀	28.2	83.3	27.1	6.6	5.2
189	14QM078H	29.2	86.3	31.0	6.7	4.7
190	14QM078	29.4	85.2	28.5	6.7	4.8
191	14QM079	30.2	85.2	30.5	6.7	4.9
192	14QM079H	28.8	84.9	31.6	6.7	5.0
193	P♀	28.2	83.3	27.1	6.6	5.2
194	14QM080H	26.8	84.7	27.1	6.5	4.9
195	14QM080	28.5	83.2	28.2	6.7	5.1
196	14QM081	27.8	83.6	29.4	6.7	4.9
197	14QM081H	29.9	86.4	29.6	6.8	4.8
198	P♀	28.2	83.3	27.1	6.6	5.2
199	14QM082H	29.2	84.5	31.0	6.7	4.9
200	14QM082	30.2	83.7	31.9	6.9	5.2
201	14QM083	29.0	85.8	28.9	6.7	5.1
202	14QM083H	26.2	84.6	27.3	6.6	5.4
203	P♀	29.0	85.1	28.9	6.7	5.0
204	14QM084H	28.5	85.6	27.9	6.7	5.3
205	14QM084	29.0	85.9	28.9	6.8	5.6
206	14QM085	28.7	82.2	28.2	6.7	5.3
207	14QM085H	29.6	85.4	31.0	6.8	5.3
208	P♀	29.0	85.1	28.9	6.7	5.0
209	14QM086H	26.4	84.3	26.3	6.6	5.5
210	14QM086	28.7	86.7	27.8	6.7	5.6
211	14QM087	28.6	85.9	28.2	6.7	5.0
212	14QM087H	29.9	86.0	29.4	6.8	5.3
213	P♀	29.0	85.1	28.9	6.7	5.0
214	14QM088H	29.5	84.7	30.1	6.8	5.5
215	14QM088	28.5	84.3	28.1	6.8	5.8
216	14QM089	25.6	83.1	24.7	6.5	5.9
217	14QM089H	29.5	86.0	30.2	6.8	5.4
218	P♀	29.0	85.1	28.9	6.7	5.0
219	14QM090H	30.0	85.5	28.5	6.7	4.7
220	14QM090	32.5	87.2	30.5	6.8	4.8
221	14QM091	30.7	87.1	29.7	6.8	5.2
222	14QM091H	28.3	83.8	28.0	6.6	5.0
223	P♀	29.0	85.1	28.9	6.7	5.0
224	P♂	28.6	85.3	27.2	6.6	5.1
225	F1	29.9	85.7	29.4	6.7	5.0
226	P♀	28.4	85.7	28.1	6.7	4.9
227	P♀	29.0	85.1	28.9	6.7	5.0
228	14QM092H	28.6	84.2	28.9	6.6	4.3
229	14QM092	31.9	86.1	31.8	6.8	4.4
230	14QM093	28.1	84.6	28.1	6.7	4.7
231	14QM093H	29.7	85.0	27.4	6.7	5.1
232	P♀	29.0	85.1	28.9	6.7	5.0
233	14QM094H	28.0	85.5	28.6	6.7	5.1

234	14QM094	29.1	85.9	27.7	6.7	5.5
235	14QM095	29.7	87.5	28.8	6.8	5.7
236	14QM095H	28.9	83.9	27.9	6.7	5.2
237	P♀	29.0	85.1	28.9	6.7	5.0
238	14QM096H	30.0	85.2	30.3	6.8	4.9
239	14QM096	31.0	86.6	27.8	6.7	4.7
240	14QM097	27.9	82.2	26.7	6.5	4.9
241	14QM097H	29.2	84.9	27.9	6.7	5.2
242	P♀	29.0	85.1	28.9	6.7	5.0
243	14QM098H	29.6	84.8	28.4	6.6	4.6
244	14QM098	28.6	84.4	27.4	6.7	4.6
245	14QM099	30.3	83.5	30.0	6.8	5.1
246	14QM099H	27.7	81.7	26.4	6.6	4.9
247	P♀	29.0	85.1	28.9	6.7	5.0
248	14QM100H	30.2	83.7	29.4	6.7	5.2
249	14QM100	29.7	83.4	28.0	6.7	4.9
250	14QM101	29.3	85.0	29.7	6.7	5.2
251	14QM101H	29.8	85.5	31.4	6.8	5.3
252	P♀	30.2	84.6	29.5	6.7	5.3
253	14QM102H	29.4	84.9	29.6	6.7	4.9
254	14QM102	29.4	82.8	29.7	6.8	5.3
255	14QM103	31.5	83.3	31.0	6.8	5.4
256	14QM103H	31.1	86.3	30.6	6.8	5.4
257	P♀	30.2	84.6	29.5	6.7	5.3
258	14QM104H	31.4	87.3	30.7	6.9	5.1
259	14QM104	30.8	86.8	31.7	6.8	5.0
260	14QM105	28.4	82.4	28.9	6.8	5.3
261	14QM105H	29.9	84.9	29.8	6.8	5.3
262	P♀	30.2	84.6	29.5	6.7	5.3
263	14QM106H	31.2	86.1	30.0	6.9	5.2
264	14QM106	31.3	84.1	31.2	6.8	4.7
265	14QM107	29.6	86.1	33.8	6.8	4.8
266	14QM107H	28.7	83.9	32.3	6.8	4.8
267	P♀	30.2	84.6	29.5	6.7	5.3
268	14QM108H	28.6	83.4	28.5	6.7	5.8
269	14QM108	30.1	84.6	30.3	6.8	4.7
270	14QM109	29.2	85.1	28.7	6.7	4.3
271	14QM109H	28.8	84.4	27.0	6.7	5.3
272	P♀	30.2	84.6	29.5	6.7	5.3
273	14QM110H	29.8	85.3	30.6	6.7	5.0
274	14QM110	28.4	83.2	29.2	6.6	4.8
275	14QM111	28.7	83.9	31.2	6.7	4.0
276	14QM111H	29.3	86.7	29.3	6.7	4.7
277	P♀	30.2	84.6	29.5	6.7	5.3
278	14QM112H	29.0	85.4	29.2	6.7	5.4
279	14QM112	28.2	82.5	27.6	6.6	5.2
280	14QM113	29.7	85.6	29.1	6.7	5.1
281	14QM113H	29.2	85.6	27.8	6.6	4.6
282	P♀	30.2	84.6	29.5	6.7	5.3
283	14QM114H	30.5	84.6	30.3	6.7	5.1
284	14QM114	30.2	84.5	29.6	6.7	4.7
285	14QM115	30.4	85.9	30.1	6.9	5.4
286	14QM115H	29.6	86.1	28.4	6.8	5.7
287	P♀	30.2	84.6	29.5	6.7	5.3
288	14QM116H	28.5	83.9	30.6	6.7	5.0
289	14QM116	28.6	84.2	28.7	6.7	5.3
290	14QM117	29.5	83.6	28.1	6.7	5.3
291	14QM117H	28.2	84.5	27.4	6.6	5.4
292	P♀	30.2	84.6	29.5	6.7	5.3

293	14QM118H	28.9	85.8	28.4	6.7	5.3
294	14QM118	28.0	83.6	28.2	6.6	4.8
295	14QM119	30.1	85.4	30.0	6.7	4.7
296	14QM119H	28.9	84.4	31.6	6.7	4.6
297	P♀	30.2	84.6	29.5	6.7	5.3
298	14QM120H	29.0	85.3	28.1	6.6	5.2
299	14QM120	27.8	85.0	27.9	6.7	5.1
300	14QM121	27.6	83.8	28.9	6.6	5.2
301	14QM121H	28.3	85.1	28.8	6.7	5.0
302	P♀	28.6	82.8	31.0	6.7	4.7
303	14QM122H	28.6	83.7	30.3	6.8	4.9
304	14QM122	28.1	83.5	28.7	6.8	4.6
305	14QM123	29.9	84.1	31.9	6.8	5.1
306	14QM123H	30.3	86.2	30.7	6.8	5.3
307	P♀	28.6	82.8	31.0	6.7	4.7
308	14QM124H	27.5	85.5	29.4	6.7	5.2
309	14QM124	29.2	85.2	27.9	6.7	5.5
310	14QM125	27.5	85.7	27.8	6.6	4.9
311	14QM125H	27.7	84.1	28.0	6.6	5.4
312	P♀	28.6	82.8	31.0	6.7	4.7
313	14QM126H	27.7	83.2	28.7	6.6	5.0
314	14QM126	26.6	83.5	27.2	6.5	5.5
315	14QM127	29.6	84.8	31.4	6.7	4.7
316	14QM127H	29.4	84.1	29.7	6.7	5.4
317	P♀	28.6	82.8	31.0	6.7	4.7
318	14QM128H	29.8	83.7	30.3	6.7	5.1
319	14QM128	28.9	80.4	31.6	6.7	4.5
320	14QM129	30.5	84.6	31.2	6.9	5.0
321	14QM129H	29.7	85.2	30.8	6.8	5.1
322	P♀	28.6	82.8	31.0	6.7	4.7
323	14QM130H	28.2	80.9	29.5	6.7	5.0
324	14QM130	30.5	84.7	31.2	6.8	4.2
325	14QM131	30.3	85.8	30.2	6.7	3.7
326	14QM131H	29.0	82.7	30.2	6.8	4.9
327	P♀	28.6	82.8	31.0	6.7	4.7
328	14QM132H	27.6	83.3	31.2	6.7	4.5
329	14QM132	28.6	85.6	28.2	6.7	5.2
330	14QM133	29.0	85.5	30.2	6.8	5.5
331	14QM133H	30.2	83.6	31.4	6.8	5.3
332	P♀	28.6	82.8	31.0	6.7	4.7
333	14QM134H	30.0	86.3	31.1	6.8	5.4
334	14QM134	27.9	83.3	28.7	6.7	5.4
335	14QM135	29.9	85.9	32.6	6.8	4.6
336	14QM135H	30.9	85.7	31.3	6.8	5.1
337	P♀	28.6	82.8	31.0	6.7	4.7
338	14QM136H	29.8	83.2	31.1	6.8	5.0
339	14QM136	29.9	83.6	30.5	6.8	4.9
340	14QM137	31.5	85.7	32.1	6.8	4.9
341	14QM137H	30.9	84.0	30.6	6.8	4.9
342	P♀	28.6	82.8	31.0	6.7	4.7
343	14QM138H	30.1	84.5	30.4	6.8	5.0
344	14QM138	29.4	84.9	29.1	6.7	4.7
345	14QM139	28.7	82.5	30.4	6.7	5.0
346	14QM139H	30.6	87.2	33.6	6.9	4.9
347	P♀	28.6	82.8	31.0	6.7	4.7
348	14QM140H	30.6	84.6	31.5	6.8	4.9
349	14QM140	32.2	86.0	31.3	6.9	5.1
350	14QM141	31.4	84.4	28.9	6.8	5.4
351	14QM141H	29.0	85.0	33.0	6.9	5.2

352	P♀	29.1	84.7	29.6	6.7	5.2
353	14QM142H	30.4	86.1	31.1	6.8	4.7
354	14QM142	29.4	86.0	31.9	6.8	4.3
355	14QM143	29.2	84.5	30.0	6.7	4.8
356	14QM143H	30.4	86.4	30.5	6.8	5.6
357	P♀	29.1	84.7	29.6	6.7	5.2
358	14QM144H	28.4	85.0	28.1	6.6	4.7
359	14QM144	27.1	82.1	27.3	6.6	5.4
360	14QM145	28.5	80.4	28.6	6.7	4.7
361	14QM145H	29.4	86.3	28.0	6.7	5.1
362	P♀	29.1	84.7	29.6	6.7	5.2
363	14QM146H	27.4	82.3	28.2	6.7	5.2
364	14QM146	29.6	84.0	28.7	6.8	4.5
365	14QM147	29.3	85.6	28.8	6.7	4.5
366	14QM147H	30.6	85.3	30.8	6.8	5.0
367	P♀	29.1	84.7	29.6	6.7	5.2
368	14QM148H	28.1	86.0	28.3	6.7	5.2
369	14QM148	30.8	86.4	29.5	6.9	4.8
370	14QM149	30.1	86.7	29.5	6.7	5.2
371	14QM149H	27.0	84.0	28.5	6.6	5.5
372	P♀	29.1	84.7	29.6	6.7	5.2
373	14QM150H	28.8	86.6	28.8	6.7	5.4
374	14QM150	28.8	86.7	28.1	6.7	5.2
375	14QM151	28.0	86.5	27.0	6.6	5.7
376	14QM151H	26.9	84.3	27.1	6.5	5.2
377	P♀	29.1	84.7	29.6	6.7	5.2
378	14QM152H	29.0	88.3	30.5	6.8	5.5
379	14QM152	28.1	85.0	28.2	6.6	5.1
380	14QM153	28.4	85.0	27.3	6.6	5.4
381	14QM153H	29.0	85.3	29.1	6.7	5.1
382	P♀	29.1	84.7	29.6	6.7	5.2
383	14QM154H	28.2	82.8	30.7	6.7	5.4
384	14QM154	28.7	82.8	28.8	6.7	4.8
385	14QM155	28.7	86.8	29.2	6.7	5.7
386	14QM155H	27.9	83.6	29.4	6.7	5.6
387	P♀	29.1	84.7	29.6	6.7	5.2
388	14QM156H	28.4	85.1	27.8	6.7	5.6
389	14QM156	28.9	85.8	29.1	6.7	5.3
390	14QM157	28.9	85.2	28.0	6.7	5.3
391	14QM157H	29.4	86.0	28.3	6.7	5.6
392	P♀	29.1	84.7	29.6	6.7	5.2
393	14QM158H	27.0	82.1	27.6	6.6	5.7
394	14QM158	26.2	83.3	25.9	6.6	5.5
395	14QM159	29.8	83.9	29.4	6.8	5.0
396	14QM159H	28.7	85.9	29.6	6.8	5.6
397	P♀	29.1	84.7	29.6	6.7	5.2
398	14QM160H	29.1	86.3	29.9	6.7	5.0
399	14QM160	28.9	87.7	32.1	6.8	5.2
400	14QM161	29.5	83.0	28.4	6.7	5.4
401	14QM161H	27.2	83.1	28.1	6.6	5.4
402	P♀	27.1	83.8	27.0	6.6	5.9
403	14QM162H	28.1	85.9	28.9	6.7	5.6
404	14QM162	28.1	84.2	26.7	6.6	5.7
405	14QM163	27.9	84.5	27.5	6.7	5.2
406	14QM163H	29.1	84.1	30.7	6.8	4.5
407	P♀	27.1	83.8	27.0	6.6	5.9
408	14QM164H	29.9	85.2	28.4	6.7	5.5
409	14QM164	28.4	87.2	28.6	6.7	5.0
410	14QM165	30.5	86.5	31.7	6.7	4.6

411	14QM165H	30.8	86.9	31.2	6.8	5.2
412	P♀	27.1	83.8	27.0	6.6	5.9
413	14QM166H	31.3	87.1	30.5	6.8	5.3
414	14QM166	31.8	87.7	30.4	6.9	5.0
415	14QM167	27.8	85.2	27.5	6.6	4.9
416	14QM167H	31.0	84.0	31.8	6.8	5.4
417	P♀	27.1	83.8	27.0	6.6	5.9
418	14QM168H	27.5	83.1	27.1	6.6	5.7
419	14QM168	26.6	83.4	25.8	6.5	5.6
420	14QM169	28.6	82.2	28.0	6.7	5.4
421	14QM169H	29.5	84.2	28.8	6.7	5.2
422	P♀	27.1	83.8	27.0	6.6	5.9
423	14QM170H	29.4	84.6	27.6	6.7	5.4
424	14QM170	30.0	85.6	28.9	6.8	5.1
425	14QM171	29.0	86.2	29.0	6.7	5.0
426	14QM171H	29.4	84.8	30.6	6.7	5.4
427	P♀	27.1	83.8	27.0	6.6	5.9
428	14QM172H	31.2	86.6	29.7	6.8	5.4
429	14QM172	30.3	85.6	32.0	6.9	4.5
430	14QM173	31.2	85.1	30.1	6.8	4.6
431	14QM173H	29.9	84.4	30.7	6.8	4.8
432	P♀	27.1	83.8	27.0	6.6	5.9
433	14QM174H	29.9	86.6	30.1	6.8	5.1
434	14QM174	30.0	86.3	29.0	6.8	4.8
435	14QM175	29.2	85.4	29.7	6.8	5.3
436	14QM175H	31.6	85.0	29.4	6.8	5.3
437	P♀	27.1	83.8	27.0	6.6	5.9
438	14QM176H	29.9	85.8	29.9	6.8	5.3
439	14QM176	32.7	85.3	31.1	6.8	4.8
440	14QM177	27.6	86.4	27.4	6.6	4.9
441	14QM177H	30.0	86.3	29.4	6.8	5.6
442	P♀	27.1	83.8	27.0	6.6	5.9
443	14QM178H	31.5	85.8	33.0	7.0	4.9
444	14QM178	31.7	84.3	31.9	6.8	4.5
445	14QM179	29.6	85.4	30.8	6.8	4.6
446	14QM179H	30.7	85.9	32.5	6.9	5.2
447	P♀	27.1	83.8	27.0	6.6	5.9
448	P♂	29.7	85.4	28.8	6.8	5.2
449	F1	27.4	85.1	28.8	6.7	5.4
450	P♀	29.2	85.2	29.0	6.7	5.6
451	14QM003	28.1	86.3	28.3	6.7	5.3
452	14QM003H	29.9	84.3	29.4	6.7	5.2
453	P♀	27.9	82.8	29.4	6.7	4.8
454	14QM004H	29.8	86.8	29.3	6.7	5.0
455	14QM004	30.4	88.0	29.4	6.8	4.7
456	14QM005	29.1	85.5	28.9	6.6	5.2
457	14QM005H	29.4	85.7	29.1	6.7	5.3
458	P♀	27.9	82.8	29.4	6.7	4.8
459	14QM006H	29.6	86.3	29.9	6.7	5.4
460	14QM006	29.0	84.9	31.0	6.7	5.2
461	14QM007	29.6	86.5	30.4	6.9	5.4
462	14QM007H	30.0	86.9	29.2	6.8	5.3
463	P♀	27.9	82.8	29.4	6.7	4.8
464	14QM008H	28.6	84.5	29.1	6.7	5.0
465	14QM008	30.9	87.5	32.5	6.9	4.1
466	14QM009	28.1	85.4	28.6	6.7	5.4
467	14QM009H	27.1	85.4	27.3	6.6	5.9
468	P♀	27.9	82.8	29.4	6.7	4.8
469	14QM010H	29.3	86.1	29.5	6.7	4.7

470	14QM010	29.3	87.3	28.2	6.7	5.7
471	14QM011	30.6	87.4	28.5	6.7	5.8
472	14QM011H	29.4	85.8	28.4	6.7	5.4
473	P♀	27.9	82.8	29.4	6.7	4.8
474	14QM012H	30.1	87.4	29.2	6.8	5.8
475	14QM012	30.0	85.2	30.6	6.8	5.3
476	14QM013	28.8	87.2	27.3	6.7	5.4
477	14QM013H	27.0	82.8	26.5	6.6	5.6
478	P♀	27.9	82.8	29.4	6.7	4.8
479	14QM014H	28.8	85.3	29.1	6.7	5.3
480	14QM014	29.6	85.0	28.5	6.8	5.3
481	14QM015	29.5	85.2	27.7	6.7	4.6
482	14QM015H	29.4	85.9	28.4	6.8	5.1
483	P♀	27.9	82.8	29.4	6.7	4.8
484	14QM016H	26.8	84.5	28.8	6.6	4.6
485	14QM016	29.1	85.5	27.8	6.7	5.6
486	14QM017	30.8	86.2	29.1	6.8	4.5
487	14QM017H	29.7	85.7	29.9	6.8	5.3
488	P♀	27.9	82.8	29.4	6.7	4.8
489	14QM018H	27.8	83.2	28.7	6.6	5.1
490	14QM018	29.8	84.0	30.3	6.7	4.5
491	14QM019	28.5	83.2	29.4	6.7	5.7
492	14QM019H	29.0	85.1	29.0	6.7	5.1
493	P♀	27.9	82.8	29.4	6.7	4.8
494	14QM020H	30.6	87.3	30.4	6.8	5.2
495	14QM020	30.8	85.3	30.1	6.7	4.4
496	14QM021	30.7	86.0	30.6	6.8	5.3
497	14QM021H	30.0	86.7	30.2	6.8	5.4
498	P♀	27.9	82.8	29.4	6.7	4.8
499	14QM022H	29.4	87.9	28.7	6.7	5.3
500	14QM022	31.2	86.4	30.8	6.9	5.0
501	14QM023	28.8	86.9	26.9	6.6	4.8
502	14QM023H	30.1	84.6	28.5	6.7	4.7
503	P♀	27.2	84.0	28.4	6.6	5.1
504	14QM024H	31.6	87.1	30.5	7.0	5.2
505	14QM024	30.4	85.2	32.6	6.9	4.6
506	14QM025	30.1	85.8	28.9	6.7	4.9
507	14QM025H	31.2	87.7	30.8	6.8	5.7
508	P♀	27.2	84.0	28.4	6.6	5.1
509	14QM026H	30.4	86.8	28.8	6.8	5.5
510	14QM026	30.1	86.2	28.8	6.7	5.2
511	14QM027					
512	14QM027H	31.1	86.7	29.2	6.8	4.9
513	P♀	27.2	84.0	28.4	6.6	5.1
514	14QM028H	30.0	87.1	31.2	6.8	4.8
515	14QM028	29.1	86.4	28.5	6.8	5.2
516	14QM029	31.6	85.1	29.3	6.8	4.5
517	14QM029H	31.0	85.5	30.0	6.8	5.1
518	P♀	27.2	84.0	28.4	6.6	5.1
519	14QM030H	31.7	87.7	31.2	6.9	4.7
520	14QM030	30.7	85.7	30.3	6.7	4.0
521	14QM031	32.8	87.1	30.3	6.9	4.9
522	14QM031H	30.9	87.5	31.0	6.8	4.8
523	P♀	27.2	84.0	28.4	6.6	5.1
524	14QM032H	30.5	86.6	33.4	6.9	5.4
525	14QM032	29.8	86.9	30.6	6.9	5.7
526	14QM033	27.2	86.6	28.0	6.6	5.5
527	14QM033H	27.8	86.5	29.3	6.7	5.5
528	P♀	27.2	84.0	28.4	6.6	5.1

529	14QM034H	29.5	86.9	29.4	6.7	5.5
530	14QM034	28.0	83.4	29.5	6.7	5.4
531	14QM035	28.2	84.1	27.4	6.6	4.8
532	14QM035H	29.0	84.7	27.8	6.6	5.1
533	P♀	27.2	84.0	28.4	6.6	5.1
534	14QM036H	27.3	83.8	27.1	6.6	5.1
535	14QM036	28.9	85.9	27.9	6.7	5.8
536	14QM037	28.7	85.7	29.4	6.7	4.8
537	14QM037H	28.9	85.4	29.6	6.7	4.8
538	P♀	27.2	84.0	28.4	6.6	5.1
539	14QM038H	28.5	86.2	28.3	6.6	5.2
540	14QM038	28.3	85.3	26.8	6.6	4.8
541	14QM039	27.9	86.3	28.3	6.6	5.2
542	14QM039H	27.9	84.1	28.7	6.7	5.2
543	P♀	27.2	84.0	28.4	6.6	5.1
544	14QM040H	30.1	86.7	30.2	6.8	5.2
545	14QM040	26.6	84.7	27.7	6.6	5.3
546	14QM041	28.8	82.8	30.1	6.7	4.5
547	14QM041H	29.0	83.7	27.7	6.6	4.4
548	P♀	27.2	84.0	28.4	6.6	5.1
549	14QM042H	30.1	87.1	28.5	6.8	5.9
550	14QM042	27.4	85.5	25.9	6.6	5.3
551	14QM043	28.4	86.5	27.8	6.7	5.2
552	14QM043H	28.8	85.4	27.6	6.7	5.7
553	P♀	29.0	86.0	28.8	6.7	5.1
554	14QM044H	28.0	85.2	29.7	6.7	5.5
555	14QM044	28.5	84.3	28.8	6.8	5.6
556	14QM045	29.4	86.5	30.1	6.8	4.8
557	14QM045H	28.6	85.8	31.1	6.7	5.2
558	P♀	29.0	86.0	28.8	6.7	5.1
559	14QM046H	27.4	83.8	28.4	6.6	5.4
560	14QM046	28.8	87.5	29.3	6.7	5.4
561	14QM047	29.3	85.8	31.0	6.7	5.2
562	14QM047H	28.8	86.9	32.7	6.8	5.3
563	P♀	29.0	86.0	28.8	6.7	5.1
564	14QM048H	27.7	84.9	28.8	6.6	5.1
565	14QM048	28.6	83.7	29.3	6.7	4.7
566	14QM049	28.7	85.0	29.6	6.7	4.5
567	14QM049H	27.8	85.1	29.9	6.7	4.8
568	P♀	29.0	86.0	28.8	6.7	5.1
569	14QM050H	29.0	84.8	31.2	6.7	4.7
570	14QM050	28.4	83.6	27.6	6.6	5.1
571	14QM051	28.6	84.0	30.0	6.7	4.7
572	14QM051H	30.1	85.3	29.9	6.7	4.9
573	P♀	29.0	86.0	28.8	6.7	5.1
574	14QM052H	28.9	82.5	30.0	6.7	5.2
575	14QM052	29.0	83.1	29.6	6.7	4.9
576	14QM053	31.7	84.7	32.3	6.8	3.8
577	14QM053H	29.5	85.0	28.3	6.6	5.2
578	P♀	29.0	86.0	28.8	6.7	5.1
579	14QM054H	28.0	85.7	28.1	6.7	5.5
580	14QM054	27.9	85.1	28.2	6.6	4.9
581	14QM055	27.7	86.5	31.4	6.7	5.3
582	14QM055H	29.7	88.9	30.7	6.7	5.4
583	P♀	29.0	86.0	28.8	6.7	5.1
584	14QM056H	30.3	85.9	29.5	6.7	5.1
585	14QM056	30.5	84.5	29.3	6.7	4.7
586	14QM057	28.0	83.1	28.7	6.7	4.7
587	14QM057H	27.8	84.6	26.6	6.6	5.7

588	P♀	29.0	86.0	28.8	6.7	5.1
589	14QM058H	27.6	84.8	28.6	6.7	6.0
590	14QM058	28.0	84.4	27.8	6.6	5.3
591	14QM059	27.2	84.2	26.3	6.6	5.5
592	14QM059H	28.2	84.5	27.0	6.6	5.5
593	P♀	29.0	86.0	28.8	6.7	5.1
594	14QM060H	29.9	85.8	29.0	6.7	5.0
595	14QM060	31.4	86.3	29.3	6.8	5.4
596	14QM061	28.2	83.9	27.5	6.6	5.0
597	14QM061H	28.4	84.8	27.6	6.6	5.6
598	P♀	29.0	86.0	28.8	6.7	5.1
599	14QM062H	29.8	86.0	30.8	6.7	5.4
600	14QM062	31.7	86.3	31.2	6.9	4.7
601	14QM063	28.9	83.7	28.1	6.7	5.1
602	14QM063H	28.7	84.5	30.1	6.7	5.0
603	P♀	30.4	87.0	29.4	6.8	5.6
604	14QM064H	29.5	86.8	29.8	6.7	5.6
605	14QM064	29.2	85.3	29.7	6.7	5.4
606	14QM065	30.2	85.7	29.9	6.7	4.8
607	14QM065H	29.2	86.5	29.7	6.7	5.4
608	P♀	30.4	87.0	29.4	6.8	5.6
609	14QM066H	27.8	83.3	27.5	6.6	5.1
610	14QM066	28.2	86.8	26.5	6.6	5.1
611	14QM067	28.3	86.6	28.0	6.7	5.6
612	14QM067H	28.5	84.3	28.0	6.6	5.4
613	P♀	30.4	87.0	29.4	6.8	5.6
614	14QM068H	28.9	85.0	28.2	6.7	5.6
615	14QM068	29.6	86.8	27.0	6.6	5.6
616	14QM069	27.6	84.6	26.5	6.7	5.9
617	14QM069H	25.1	82.1	24.5	6.5	5.9
618	P♀	30.4	87.0	29.4	6.8	5.6
619	14QM070H	29.1	87.0	28.8	6.7	4.9
620	14QM070	29.6	86.6	29.2	6.7	5.2
621	14QM071	28.6	86.4	26.5	6.6	5.4
622	14QM071H	28.5	85.7	27.2	6.7	5.2
623	P♀	30.4	87.0	29.4	6.8	5.6
624	14QM072H	27.0	85.5	27.4	6.5	5.1
625	14QM072	27.6	83.3	28.1	6.6	4.7
626	14QM073	29.1	85.2	29.1	6.7	5.2
627	14QM073H	28.1	82.8	28.1	6.6	5.0
628	P♀	30.4	87.0	29.4	6.8	5.6
629	14QM074H	28.5	84.0	28.0	6.6	5.9
630	14QM074	29.0	82.2	27.9	6.6	4.8
631	14QM075	28.3	82.4	27.0	6.6	4.3
632	14QM075H	29.4	84.4	27.7	6.7	5.2
633	P♀	30.4	87.0	29.4	6.8	5.6
634	14QM076H					
635	14QM076	27.2	85.4	26.5	6.7	5.7
636	14QM077	27.4	83.8	28.1	6.6	4.7
637	14QM077H	27.4	86.0	28.5	6.6	5.0
638	P♀	30.4	87.0	29.4	6.8	5.6
639	14QM078H	28.4	83.3	28.1	6.6	4.7
640	14QM078	28.2	82.2	27.9	6.7	5.4
641	14QM079	28.5	84.2	29.4	6.6	4.8
642	14QM079H	27.7	82.7	29.4	6.6	4.8
643	P♀	30.4	87.0	29.4	6.8	5.6
644	14QM080H	27.6	84.7	27.1	6.6	4.9
645	14QM080	28.0	84.9	27.6	6.6	4.7
646	14QM081	30.1	86.4	28.6	6.7	4.6

647	14QM081H	30.3	85.9	30.7	6.8	4.4
648	P♀	30.4	87.0	29.4	6.8	5.6
649	14QM082H	29.4	83.3	29.0	6.7	5.0
650	14QM082	30.5	86.4	32.8	6.9	5.0
651	14QM083	29.1	86.0	29.0	6.8	5.4
652	14QM083H	29.8	85.9	28.4	6.7	5.3
653	P♀	28.6	83.4	27.8	6.6	5.1
654	14QM084H	29.4	85.0	29.2	6.7	4.8
655	14QM084	28.6	84.4	30.3	6.7	5.0
656	14QM085	30.8	85.6	30.1	6.8	4.9
657	14QM085H	30.5	85.3	32.1	6.9	5.1
658	P♀	28.6	83.4	27.8	6.6	5.1
659	14QM086H	28.8	84.1	28.5	6.7	5.1
660	14QM086	28.8	85.1	29.4	6.7	5.6
661	14QM087	29.4	85.0	29.4	6.7	5.2
662	14QM087H	30.1	84.6	30.2	6.8	5.7
663	P♀	28.6	83.4	27.8	6.6	5.1
664	14QM088H	30.8	85.6	28.7	6.8	5.6
665	14QM088	30.6	84.3	32.6	6.9	5.0
666	14QM089	29.5	84.9	29.0	6.7	5.8
667	14QM089H	27.9	83.1	28.5	6.7	5.3
668	P♀	28.6	83.4	27.8	6.6	5.1
669	14QM090H	30.8	86.2	31.8	6.8	5.0
670	14QM090	31.6	83.3	31.9	6.7	4.4
671	14QM091	30.4	85.0	30.7	6.8	5.3
672	14QM091H	29.3	84.0	28.9	6.7	4.7
673	P♀	28.6	83.4	27.8	6.6	5.1
674	P♂	30.0	86.2	28.4	6.7	5.1
675	F1	28.0	82.3	29.0	6.7	4.7
676	P♀	29.4	86.4	29.4	6.7	5.3
677	P♀	28.6	83.4	27.8	6.6	5.1
678	14QM092H	28.7	84.8	28.6	6.7	5.4
679	14QM092	31.2	86.1	32.1	6.9	4.8
680	14QM093	27.9	80.4	28.0	6.6	4.3
681	14QM093H	30.9	86.3	30.9	6.9	4.7
682	P♀	28.6	83.4	27.8	6.6	5.1
683	14QM094H	29.8	85.5	30.8	6.7	4.4
684	14QM094	28.9	84.4	28.6	6.7	5.4
685	14QM095	27.9	86.4	28.5	6.6	4.9
686	14QM095H	31.1	87.1	30.3	6.8	5.2
687	P♀	28.6	83.4	27.8	6.6	5.1
688	14QM096H	30.4	86.9	31.1	6.8	4.4
689	14QM096	30.0	84.6	30.9	6.9	4.9
690	14QM097	28.7	84.6	28.0	6.6	4.8
691	14QM097H	29.5	84.5	28.8	6.7	4.8
692	P♀	28.6	83.4	27.8	6.6	5.1
693	14QM098H	30.4	84.6	31.1	6.8	5.2
694	14QM098	28.7	83.7	27.1	6.6	4.8
695	14QM099	27.7	82.0	27.9	6.6	5.2
696	14QM099H	29.6	82.8	29.7	6.8	5.6
697	P♀	28.6	83.4	27.8	6.6	5.1
698	14QM100H	30.3	86.0	29.3	6.7	5.2
699	14QM100	28.9	86.1	29.1	6.8	5.6
700	14QM101	28.0	84.1	27.0	6.6	5.3
701	14QM101H	28.6	84.4	29.3	6.7	5.5
702	P♀	29.8	83.2	29.1	6.7	5.4
703	14QM102H	28.5	86.9	27.0	6.7	5.1
704	14QM102	30.2	86.0	29.0	6.8	4.8
705	14QM103	31.5	88.0	29.5	6.8	5.3

706	14QM103H	30.5	84.8	28.5	6.7	5.2
707	P♀	29.8	83.2	29.1	6.7	5.4
708	14QM104H	29.0	86.6	30.3	6.7	4.7
709	14QM104	30.1	87.1	29.7	6.7	4.5
710	14QM105	29.1	84.3	29.4	6.7	5.4
711	14QM105H	30.5	87.6	30.3	6.8	4.9
712	P♀	29.8	83.2	29.1	6.7	5.4
713	14QM106H	30.3	85.5	30.0	6.7	5.4
714	14QM106	31.0	86.4	28.9	6.8	4.8
715	14QM107	29.4	86.1	31.7	6.7	4.6
716	14QM107H	29.6	84.3	27.6	6.7	5.5
717	P♀	29.8	83.2	29.1	6.7	5.4
718	14QM108H	28.3	83.9	28.2	6.7	5.4
719	14QM108	29.6	85.2	27.3	6.7	5.2
720	14QM109	27.8	85.4	25.9	6.6	5.3
721	14QM109H	29.0	84.7	27.1	6.6	5.0
722	P♀	29.8	83.2	29.1	6.7	5.4
723	14QM110H	30.5	86.5	29.8	6.8	5.8
724	14QM110	29.8	84.8	29.4	6.7	5.7
725	14QM111	30.7	87.5	30.6	6.8	4.6
726	14QM111H	30.2	86.8	28.3	6.7	5.6
727	P♀	29.8	83.2	29.1	6.7	5.4
728	14QM112H	29.9	84.7	27.3	6.7	5.2
729	14QM112	28.8	87.7	27.5	6.7	5.6
730	14QM113	28.8	83.6	28.8	6.7	5.3
731	14QM113H	30.6	84.5	28.6	6.7	5.3
732	P♀	29.8	83.2	29.1	6.7	5.4
733	14QM114H	30.4	85.8	29.6	6.8	5.2
734	14QM114	29.7	84.5	30.4	6.8	4.6
735	14QM115	30.6	87.0	30.1	6.9	5.4
736	14QM115H	31.0	86.3	32.7	7.0	5.4
737	P♀	29.8	83.2	29.1	6.7	5.4
738	14QM116H	28.6	84.6	29.0	6.7	5.6
739	14QM116	29.6	85.2	30.1	6.7	5.1
740	14QM117	28.9	83.3	28.2	6.7	4.5
741	14QM117H	30.2	85.0	29.2	6.8	5.2
742	P♀	29.8	83.2	29.1	6.7	5.4
743	14QM118H	-	-	-	-	-
744	14QM118	27.7	83.1	27.4	6.6	5.1
745	14QM119	31.2	85.0	31.5	6.8	4.5
746	14QM119H	29.6	83.0	30.5	6.8	4.9
747	P♀	29.8	83.2	29.1	6.7	5.4
748	14QM120H	29.2	84.4	28.4	6.7	5.2
749	14QM120	27.4	83.2	26.7	6.5	4.7
750	14QM121	28.9	83.8	30.8	6.7	4.9
751	14QM121H	28.9	85.2	31.2	6.8	4.9
752	P♀	30.1	86.3	30.5	6.8	5.0
753	14QM122H	30.2	85.8	29.0	6.8	4.9
754	14QM122	29.8	85.5	30.5	6.8	5.0
755	14QM123	29.6	87.1	28.7	6.7	5.1
756	14QM123H	30.4	86.0	31.9	6.8	5.5
757	P♀	30.1	86.3	30.5	6.8	5.0
758	14QM124H	29.0	85.0	30.8	6.7	4.8
759	14QM124	30.5	85.7	30.6	6.8	5.4
760	14QM125	28.4	84.7	28.6	6.7	5.1
761	14QM125H	25.9	81.8	27.6	6.6	5.2
762	P♀	30.1	86.3	30.5	6.8	5.0
763	14QM126H	28.1	83.2	29.8	6.7	5.9
764	14QM126	28.5	86.0	30.0	6.8	5.6

765	14QM127	30.8	86.0	30.1	6.8	4.6
766	14QM127H	30.9	86.7	31.7	6.8	4.6
767	P♀	30.1	86.3	30.5	6.8	5.0
768	14QM128H	29.2	84.3	31.2	6.8	4.9
769	14QM128	30.8	80.0	32.5	6.9	4.2
770	14QM129	28.4	84.4	28.5	6.7	5.1
771	14QM129H	31.4	85.5	30.4	6.8	5.7
772	P♀	30.1	86.3	30.5	6.8	5.0
773	14QM130H	30.2	85.7	30.3	6.9	5.1
774	14QM130	30.9	85.5	30.6	6.8	4.6
775	14QM131	29.2	83.7	29.4	6.7	4.7
776	14QM131H	29.3	86.7	30.0	6.8	5.2
777	P♀	30.1	86.3	30.5	6.8	5.0
778	14QM132H	29.1	85.6	29.2	6.7	5.8
779	14QM132	27.9	85.2	27.9	6.7	5.0
780	14QM133	27.9	86.5	29.4	6.7	5.5
781	14QM133H	29.8	84.0	30.9	6.8	5.4
782	P♀	30.1	86.3	30.5	6.8	5.0
783	14QM134H	29.4	85.6	28.6	6.7	5.4
784	14QM134	27.9	83.0	28.0	6.6	5.1
785	14QM135	31.2	86.5	31.8	6.8	5.0
786	14QM135H	31.2	85.0	30.0	6.9	5.6
787	P♀	30.1	86.3	30.5	6.8	5.0
788	14QM136H	28.2	83.8	30.7	6.7	5.2
789	14QM136	31.2	85.2	32.2	6.9	5.1
790	14QM137	30.0	83.5	31.6	6.7	4.6
791	14QM137H	30.5	84.6	31.8	6.8	4.4
792	P♀	30.1	86.3	30.5	6.8	5.0
793	14QM138H	28.3	82.6	29.9	6.7	5.2
794	14QM138	29.5	83.3	29.4	6.7	5.1
795	14QM139	29.9	86.6	29.6	6.8	5.0
796	14QM139H	29.3	84.9	29.4	6.7	5.1
797	P♀	30.1	86.3	30.5	6.8	5.0
798	14QM140H	30.6	86.9	29.7	6.8	5.2
799	14QM140	30.4	86.5	30.7	6.8	5.7
800	14QM141	28.8	83.6	29.6	6.7	4.7
801	14QM141H	30.0	86.1	30.3	6.8	5.1
802	P♀	27.5	84.8	27.7	6.6	5.5
803	14QM142H	29.0	81.7	29.7	6.7	5.2
804	14QM142	29.4	85.7	29.2	6.8	5.3
805	14QM143	29.8	84.0	28.3	6.7	5.0
806	14QM143H	29.7	86.3	28.8	6.7	5.4
807	P♀	27.5	84.8	27.7	6.6	5.5
808	14QM144H	30.5	86.9	29.6	6.8	5.1
809	14QM144	26.6	83.8	26.5	6.5	5.3
810	14QM145	27.8	83.2	27.9	6.6	4.5
811	14QM145H	29.6	87.5	29.6	6.7	5.0
812	P♀	27.5	84.8	27.7	6.6	5.5
813	14QM146H	30.2	86.5	29.4	6.8	5.3
814	14QM146	25.8	83.3	26.1	6.5	4.8
815	14QM147	29.2	87.0	27.9	6.7	4.8
816	14QM147H	30.4	86.0	29.8	6.8	5.2
817	P♀	27.5	84.8	27.7	6.6	5.5
818	14QM148H	31.1	87.2	30.2	6.9	5.2
819	14QM148	29.8	87.3	28.2	6.7	4.9
820	14QM149	28.9	84.6	29.5	6.7	4.4
821	14QM149H	28.9	86.5	28.3	6.6	5.1
822	P♀	27.5	84.8	27.7	6.6	5.5
823	14QM150H	30.7	87.9	29.3	6.8	5.1

824	14QM150	28.4	85.4	27.3	6.7	5.2
825	14QM151	29.3	87.6	27.9	6.7	5.4
826	14QM151H	29.2	87.7	29.0	6.7	5.3
827	P♀	27.5	84.8	27.7	6.6	5.5
828	14QM152H	27.7	83.6	27.2	6.6	5.7
829	14QM152	28.0	85.8	28.6	6.7	5.0
830	14QM153	28.0	88.0	27.8	6.7	5.7
831	14QM153H	28.2	84.7	26.2	6.6	5.9
832	P♀	27.5	84.8	27.7	6.6	5.5
833	14QM154H	28.4	84.0	30.7	6.8	5.1
834	14QM154	30.3	86.2	30.5	6.8	5.0
835	14QM155	28.7	84.1	29.3	6.6	5.2
836	14QM155H	28.3	85.6	29.3	6.7	5.0
837	P♀	27.5	84.8	27.7	6.6	5.5
838	14QM156H	29.4	86.3	29.6	6.8	5.3
839	14QM156	28.6	85.8	28.5	6.6	4.9
840	14QM157	29.4	84.8	30.1	6.8	5.3
841	14QM157H	28.9	87.4	29.4	6.7	5.8
842	P♀	27.5	84.8	27.7	6.6	5.5
843	14QM158H	29.1	85.9	28.2	6.7	5.3
844	14QM158	25.9	83.0	25.1	6.5	5.2
845	14QM159	30.4	85.5	28.4	6.8	5.1
846	14QM159H	29.2	84.8	29.5	6.8	4.8
847	P♀	27.5	84.8	27.7	6.6	5.5
848	14QM160H	28.8	86.3	27.9	6.6	5.6
849	14QM160	29.2	87.2	29.7	6.7	5.6
850	14QM161	27.1	83.8	26.8	6.6	4.9
851	14QM161H	27.4	85.2	25.4	6.5	5.3
852	P♀	29.5	86.1	28.3	6.7	5.6
853	14QM162H	28.7	85.9	27.5	6.7	6.0
854	14QM162	28.0	87.2	27.3	6.6	5.6
855	14QM163	29.8	86.6	28.9	6.8	4.9
856	14QM163H	29.4	87.4	29.6	6.7	4.8
857	P♀	29.5	86.1	28.3	6.7	5.6
858	14QM164H	29.9	86.1	29.8	6.8	5.4
859	14QM164	27.5	83.7	28.7	6.7	5.2
860	14QM165	30.4	85.5	30.8	6.7	4.8
861	14QM165H	28.8	85.8	31.3	6.7	5.4
862	P♀	29.5	86.1	28.3	6.7	5.6
863	14QM166H	31.0	87.1	30.2	6.8	5.5
864	14QM166	28.7	85.2	30.6	6.7	5.3
865	14QM167	30.1	84.3	30.8	6.7	4.6
866	14QM167H	27.7	82.7	28.8	6.7	5.5
867	P♀	29.5	86.1	28.3	6.7	5.6
868	14QM168H	27.9	82.4	28.9	6.7	5.3
869	14QM168	27.1	83.5	27.6	6.6	5.5
870	14QM169	25.8	81.8	25.9	6.5	5.4
871	14QM169H	28.3	84.4	28.3	6.7	5.6
872	P♀	29.5	86.1	28.3	6.7	5.6
873	14QM170H	28.9	83.5	29.1	6.7	5.0
874	14QM170	28.9	85.3	28.9	6.7	5.2
875	14QM171	30.0	86.8	30.0	6.7	4.4
876	14QM171H	29.9	86.7	28.8	6.7	5.1
877	P♀	29.5	86.1	28.3	6.7	5.6
878	14QM172H	28.3	83.1	26.0	6.6	5.3
879	14QM172	28.2	84.2	27.0	6.6	5.1
880	14QM173	29.9	83.9	29.2	6.7	4.8
881	14QM173H	28.9	83.8	27.9	6.6	4.7
882	P♀	29.5	86.1	28.3	6.7	5.6

883	14QM174H	28.7	85.5	29.1	6.7	4.8
884	14QM174	29.4	85.4	29.8	6.7	4.7
885	14QM175	30.1	85.5	30.3	6.9	5.3
886	14QM175H	27.6	83.0	29.5	6.7	5.8
887	P♀	29.5	86.1	28.3	6.7	5.6
888	14QM176H	31.2	86.3	30.2	6.8	5.2
889	14QM176	30.5	85.6	31.3	6.7	4.6
890	14QM177	28.5	83.7	28.5	6.6	4.8
891	14QM177H	29.7	86.5	28.8	6.7	5.1
892	P♀	29.5	86.1	28.3	6.7	5.6
893	14QM178H	30.5	84.7	30.7	6.8	5.0
894	14QM178	29.3	82.1	31.0	6.7	4.4
895	14QM179	29.3	84.5	30.4	6.8	5.3
896	14QM179H	29.7	85.1	29.1	6.8	5.5
897	P♀	29.5	86.1	28.3	6.7	5.6
898	P♂	29.2	87.3	29.0	6.7	5.1
899	F1	30.3	87.1	29.9	6.7	4.9
900	P♀	30.1	84.4	30.3	6.8	5.8

Note: 14QM003- 14QM179 refer to 177 RILs. 14QM003H - 14QM179H refer to 177 F₁₄BC progenies in BC/M population.

Table S8 Genotypes of RIL (A), BC/M (B) and BC/P (C) populations.

A. Genotypes of RIL population.

Number	Marker	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	*BNL1026	A	B	A	A	A	B	A	A	A	B	B	B	B	B	A	A	-	A	A
2	*BNL1053	B	B	B	B	B	A	-	A	A	B	A	A	B	A	A	B	A	A	B
3	*BNL1167	A	B	A	B	A	A	B	B	A	A	B	A	A	A	A	B	B	B	B
4	*BNL1317	A	B	-	B	B	B	B	B	A	A	B	A	A	A	B	B	B	A	B
5	*BNL1495	A	A	B	B	A	A	A	A	B	A	B	A	A	B	A	B	A	A	A
6	*BNL1521	A	A	B	A	B	A	A	A	A	B	B	A	B	A	A	B	A	B	B
7	*BNL1552	A	B	A	A	B	B	A	B	B	A	B	B	B	A	A	B	B	A	B
8	*BNL243	A	A	A	A	A	B	A	A	A	B	B	B	A	A	B	A	A	B	B
9	*BNL2449	A	A	B	B	A	B	B	A	B	A	A	B	A	B	A	B	B	A	A
10	*BNL2485	A	A	A	A	A	B	A	B	A	B	B	B	B	B	-	B	B	B	B
11	*BNL2495	A	B	B	B	A	A	B	B	B	B	B	A	A	B	A	A	A	A	B
12	*BNL2496	A	A	B	B	B	B	B	B	A	A	B	B	B	A	A	B	A	A	A
13	*BNL2827a	A	A	A	A	A	B	A	A	A	B	A	A	B	A	B	B	A	B	A
14	*BNL2827b	A	A	A	A	A	B	A	A	A	B	A	A	B	A	B	B	A	B	A
15	*BNL2877	A	A	B	B	A	B	B	A	A	A	A	A	B	B	B	A	A	A	B
16	*BNL2960	B	B	-	A	B	A	-	B	A	A	A	B	A	B	B	A	B	B	A
17	*BNL3171	B	A	-	A	A	A	A	B	A	B	A	B	A	A	A	B	A	A	B
18	*BNL3261	B	A	-	A	A	A	B	-	A	A	B	A	A	A	-	B	B	B	B
19	*BNL3442a	B	A	B	B	B	A	B	A	A	B	A	A	B	A	B	B	A	B	B
20	*BNL3442b	A	A	B	B	A	A	B	A	B	B	A	B	B	B	B	B	B	A	A
21	*BNL3594	B	B	A	B	A	B	B	B	A	A	B	B	A	B	A	B	B	B	A
22	*BNL3650	A	A	-	A	B	B	-	A	B	A	A	B	B	A	B	B	B	A	B
23	*BNL3661	A	A	A	A	A	A	A	A	A	A	A	A	A	B	A	A	A	A	B
24	*BNL3937	B	B	B	B	B	B	B	B	A	B	A	B	B	A	B	A	A	B	B
25	*BNL4028	B	B	A	A	B	B	A	A	B	A	B	A	A	A	A	A	B	B	-
26	*BNL4030	A	B	A	A	B	A	A	A	B	A	A	A	A	B	A	A	B	A	B
27	*BNL530	A	B	A	B	A	A	B	B	A	A	B	A	B	B	A	A	A	B	B
28	*BNL598	A	A	B	B	B	A	B	A	B	B	A	A	A	A	A	A	A	B	B
29	*C2-0011B	B	A	B	B	A	B	A	A	A	A	A	A	B	A	A	A	A	A	A
30	*C2-0115	B	A	-	A	A	A	-	B	A	B	A	A	A	A	B	B	B	B	B
31	*C2-0135	A	B	B	B	B	A	B	-	B	B	B	A	A	B	A	A	A	A	B
32	*CAU0003	B	B	B	A	A	A	A	A	A	A	A	A	B	B	A	B	A	A	A
33	*CAU0104	B	A	A	B	A	A	A	A	B	A	A	A	B	B	A	A	A	A	B
34	*CAU0161	A	A	A	A	B	A	A	A	B	A	A	A	A	A	A	A	B	A	B
35	*CER0028	A	B	-	A	A	B	A	B	B	B	B	A	A	A	A	B	B	A	A
36	*CER0036	B	A	B	A	A	B	A	A	B	A	A	B	A	A	B	A	B	B	A
37	*CER0042	B	B	B	B	A	B	B	B	A	B	A	B	B	A	B	A	A	B	B

38	*CER0098	A	A	A	A	B	A	A	B	B	A	B	B	B	B	A	A	A	B	A
39	*CER0144	A	A	A	A	B	A	A	B	B	B	B	A	A	B	A	A	A	A	B
40	*CER0165	A	A	B	B	B	A	A	A	B	A	A	A	A	B	A	B	B	A	A
41	*CER0167	B	A	A	A	B	B	A	B	B	A	A	B	B	A	B	B	B	A	B
42	*CER0168	A	A	A	A	A	A	A	A	A	B	B	B	A	A	B	A	A	B	B
43	*CGR5001	B	A	A	A	B	B	A	A	A	B	A	A	B	A	A	A	A	A	A
44	*CGR5009	B	A	B	B	B	A	B	A	A	A	B	A	A	A	B	B	B	B	B
45	*CGR5025	B	B	A	A	A	A	A	A	A	A	B	B	A	A	B	B	B	B	B
46	*CGR5056	A	A	-	B	B	B	B	A	A	A	A	A	A	A	A	A	A	A	A
47	*CGR5108	A	A	-	A	A	B	A	A	A	A	B	A	A	-	A	B	B	B	A
48	*CGR5111	B	A	-	A	A	A	-	B	A	B	B	A	A	A	B	B	B	B	B
49	*CGR5124	B	A	A	A	A	A	A	A	A	A	B	A	A	B	B	B	A	B	
50	*CGR5202	B	A	B	A	B	B	A	A	B	B	B	B	B	A	A	A	B	B	A
51	*CGR5217	B	A	B	A	B	A	A	A	A	B	A	B	B	A	A	B	B	A	A
52	*CGR5331	A	A	B	B	B	A	B	A	B	B	A	B	A	B	B	A	B	A	B
53	*CGR5352	A	A	A	A	A	B	-	A	A	B	B	B	A	A	B	A	A	B	B
54	*CGR5355	-	A	B	A	B	B	A	A	B	A	A	B	B	A	B	B	B	A	B
55	*CGR5372	A	A	A	A	B	B	-	A	B	A	A	B	A	B	B	B	B	A	B
56	*CGR5390	A	A	A	A	A	A	-	A	B	A	B	B	A	B	B	A	B	A	A
57	*CGR5421	A	A	B	B	A	A	B	B	B	-	-	B	A	B	A	A	B	A	A
58	*CGR5423	A	A	B	B	A	B	B	A	A	B	B	A	A	A	B	A	A	A	B
59	*CGR5452	A	A	A	A	B	A	A	B	B	B	B	A	A	B	A	A	A	A	B
60	*CGR5534	A	A	B	B	A	B	B	A	A	A	A	A	B	B	B	A	B	A	A
61	*CGR5539	B	A	A	A	A	A	A	A	A	B	A	A	A	B	A	-	A	-	B
62	*CGR5548	B	B	B	B	A	B	B	B	A	B	A	B	A	B	A	B	A	A	A
63	*CGR5554	A	A	B	B	B	A	B	A	B	B	A	B	A	B	B	A	B	A	-
64	*CGR5576	B	B	B	B	A	B	B	B	B	A	A	A	A	A	A	A	A	A	A
65	*CGR5602	B	B	A	A	B	A	A	A	A	B	A	B	A	A	A	B	A	A	B
66	*CGR5663	A	A	A	A	A	A	A	A	A	B	B	B	A	A	B	A	B	B	A
67	*CGR5675	A	B	B	A	A	B	A	B	A	A	A	A	A	B	A	A	A	B	B
68	*CGR5758	B	B	A	B	B	B	B	B	A	A	B	A	A	A	B	B	B	A	B
69	*CGR5801	B	A	B	A	A	A	B	A	B	A	B	B	B	A	B	B	B	A	B
70	*CGR5806	B	A	B	A	A	A	A	B	A	B	A	B	A	A	A	B	A	A	B
71	*CGR5808	B	A	B	A	A	A	A	B	A	A	A	B	B	A	A	B	B	A	A
72	*CGR5867	A	B	A	B	B	B	B	B	A	A	B	A	A	A	B	B	B	A	B
73	*CGR5871	A	B	A	B	B	A	B	B	A	A	B	B	B	B	A	B	B	B	A
74	*CGR5873	A	B	A	A	A	A	A	B	A	A	A	B	A	B	A	B	B	A	B
75	*CGR5883	B	A	B	A	B	B	A	A	B	A	A	B	B	A	B	B	B	A	B
76	*CGR6017	B	B	A	A	A	B	A	B	B	B	A	A	A	B	B	A	A	B	A
77	*CGR6129	A	B	A	A	A	A	A	A	A	B	B	B	A	B	A	B	A	B	B

78	*CGR6154	B	B	A	B	A	A	-	B	A	A	A	B	B	B	A	B	A	B	B
79	*CGR6254	A	A	B	-	A	A	B	B	B	B	A	B	B	B	B	B	B	B	B
80	*CGR6356	A	A	B	B	B	B	B	A	A	A	A	B	A	A	B	A	A	A	A
81	*CGR6508	A	A	B	B	A	A	B	B	B	B	B	B	A	A	B	A	A	A	A
82	*CGR6525	B	A	B	A	A	A	A	B	B	B	A	A	B	B	A	A	B	A	-
83	*CGR6528	-	A	B	A	A	A	A	B	B	B	B	A	A	B	A	B	A	A	A
84	*CGR6580	B	B	-	A	A	A	A	A	A	A	A	A	B	B	A	B	A	A	A
85	*CGR6586	A	A	A	A	B	B	A	A	B	A	A	B	A	B	B	B	B	A	B
86	*CGR6683	B	A	B	B	B	B	B	A	B	A	A	A	A	A	A	A	B	A	B
87	*CGR6695	B	A	A	A	B	B	A	A	B	A	B	B	A	A	B	B	A	B	A
88	*CGR6732	A	A	B	B	A	B	A	A	B	A	A	B	A	B	A	B	B	A	A
89	*CGR6749	B	B	B	A	A	B	B	A	A	A	A	B	A	A	B	B	B	A	B
90	*CGR6771	B	A	B	B	B	A	B	A	A	A	B	A	A	A	B	B	B	B	B
91	*CGR6784	B	B	B	B	B	B	B	A	B	A	A	A	B	A	A	A	B	A	B
92	*CGR6802	B	-	B	B	B	B	B	A	A	A	B	A	A	B	B	A	B	A	A
93	*CGR6812	A	A	A	A	A	A	A	A	A	B	B	B	A	A	B	A	A	B	B
94	*CGR6857	A	A	B	B	B	B	B	A	A	A	A	A	A	A	A	A	A	A	A
95	*CGR6864	B	B	A	B	A	A	B	B	B	B	B	B	A	B	A	B	B	B	B
96	*CGR6876	B	B	-	B	B	B	B	B	A	A	B	A	A	A	B	B	B	A	B
97	*CGR6880	A	A	A	A	B	A	A	B	B	B	B	A	A	B	A	A	A	A	B
98	*CGR6889	A	B	A	A	B	A	A	A	B	A	B	B	B	A	A	B	A	B	A
99	*CGR6930	A	A	A	A	B	A	A	B	B	B	B	A	A	B	A	A	A	A	B
100	*CIR099	A	A	A	A	A	B	A	A	B	A	A	A	B	A	A	B	A	B	A
101	*CIR139	A	B	A	A	B	B	A	A	A	A	A	A	B	A	A	A	B	B	B
102	*CIR216	B	B	-	B	B	A	-	A	A	A	B	B	B	A	A	B	A	A	B
103	*CIR228	A	A	A	A	A	B	A	B	A	B	B	A	B	B	A	B	B	B	B
104	*CIR307	A	B	A	A	B	A	A	A	B	A	B	B	B	A	A	B	A	B	A
105	*CIR334	A	B	A	A	B	A	A	A	B	A	B	B	B	A	A	B	A	B	A
106	*COT059	A	B	A	A	B	A	A	A	B	A	B	B	B	A	A	B	A	B	A
107	*COT064	A	A	B	B	B	B	-	B	A	A	B	B	B	B	A	B	B	B	A
108	*COT107	A	A	A	B	A	A	B	A	B	B	B	A	A	B	A	A	B	A	B
109	*DC20046	A	A	B	B	B	B	-	A	A	A	A	A	A	A	A	A	A	A	A
110	*DC20094	A	A	-	B	B	A	B	B	A	A	A	B	A	B	A	A	A	A	A
111	*DC20124	B	A	B	B	A	B	B	A	A	A	A	A	B	A	A	A	A	A	A
112	*DC20127	B	A	A	A	A	A	A	B	A	B	A	A	A	A	B	A	B	B	A
113	*DC30107	A	B	B	-	B	-	-	-	B	B	B	A	A	B	A	A	A	A	B
114	*DC40052	A	A	B	B	B	B	-	A	A	A	A	A	A	A	A	A	A	A	A
115	*DC40065	B	A	B	B	A	B	-	A	A	A	A	A	B	A	A	A	A	A	A
116	*DC40122	A	B	A	A	B	B	A	A	A	A	A	A	B	A	A	A	B	B	B
117	*DC40150	A	B	B	B	B	B	B	A	B	B	A	B	B	B	A	B	B	B	A

118	*DC40175	A	B	A	A	A	A	A	A	B	A	B	A	B	B	A	B	A
119	*DC40183	A	B	A	A	A	A	B	A	B	A	B	A	B	B	A	B	A
120	*DC40250	B	B	-	A	A	A	A	A	A	-	A	B	B	A	B	A	A
121	*DC40407	A	B	B	B	A	A	B	B	A	A	A	B	A	B	B	B	A
122	*DC40417	B	A	-	A	B	B	A	A	B	A	A	B	B	A	B	B	A
123	*DPL0003	-	-	-	-	-	-	-	-	-	A	A	B	A	A	B	A	A
124	*DPL0022	B	B	A	A	A	A	B	B	A	A	B	B	A	A	B	B	B
125	*DPL0048	A	B	A	A	A	B	A	-	A	B	B	B	B	B	A	A	A
126	*DPL0050a	B	B	A	A	A	A	A	B	A	B	A	B	A	A	A	B	A
127	*DPL0050b	B	A	B	A	A	A	A	A	A	A	A	B	B	A	B	B	A
128	*DPL0056	B	A	B	B	A	A	B	A	B	A	A	A	B	B	A	A	A
129	*DPL0057	A	A	B	A	A	A	A	B	B	B	A	B	B	B	B	A	B
130	*DPL0070	A	B	B	B	B	A	B	B	B	B	B	A	A	B	A	A	A
131	*DPL0090	A	B	A	A	B	A	-	A	A	B	-	B	A	B	A	B	A
132	*DPL0131	B	A	B	B	B	A	B	A	A	B	A	A	B	A	B	B	B
133	*DPL0152a	A	A	A	A	B	A	A	A	B	B	A	B	A	A	B	A	A
134	*DPL0152b	A	A	B	B	A	B	B	A	A	B	B	A	A	A	B	A	A
135	*DPL0182	A	B	A	A	-	A	A	-	B	A	B	B	B	A	A	B	A
136	*DPL0217	B	A	B	A	B	B	A	A	B	A	B	B	A	A	B	B	A
137	*DPL0244	B	A	B	A	B	B	A	A	-	A	A	-	B	A	B	B	A
138	*DPL0252	B	A	A	A	A	A	B	-	A	B	B	A	A	A	B	A	B
139	*DPL0282	A	A	B	A	B	A	A	B	A	A	A	A	A	B	A	B	B
140	*DPL0303	A	A	A	B	A	A	B	A	B	B	B	A	A	B	A	A	B
141	*DPL0308	A	-	B	B	B	B	B	A	B	A	A	A	A	B	A	B	A
142	*DPL0319	A	A	A	A	B	-	-	A	A	B	A	B	A	A	-	A	B
143	*DPL0491	A	B	A	A	B	A	A	B	B	B	B	A	A	B	A	A	A
144	*DPL0502	A	A	A	A	A	B	A	B	A	B	B	A	B	B	A	B	B
145	*DPL0535	A	A	B	B	B	B	A	A	B	A	A	A	A	B	A	B	B
146	*DPL0562	B	B	A	B	A	A	A	A	A	B	A	A	A	A	A	A	B
147	*DPL0565	A	A	A	B	B	B	B	A	A	A	A	A	A	B	A	A	B
148	*DPL0572	A	A	B	B	A	B	B	A	B	A	A	B	A	B	A	B	B
149	*DPL0590	B	A	A	A	A	A	-	A	A	A	A	B	A	A	B	B	B
150	*DPL0707	A	B	A	B	A	B	B	B	B	A	B	A	A	A	A	B	A
151	*DPL0732	A	A	A	B	A	A	B	A	B	B	B	A	A	B	A	A	B
152	*DPL0752	A	A	B	B	B	B	B	A	A	A	A	A	A	A	A	A	A
153	*DPL0777	B	A	A	A	A	A	A	A	A	B	A	B	B	A	A	B	B
154	*DPL0790	A	B	A	A	A	A	A	B	A	B	B	B	A	B	A	B	B
155	*DPL0847a	A	A	B	B	B	B	B	A	A	A	A	A	A	A	A	A	A
156	*DPL0847b	B	B	-	A	A	B	-	A	A	A	A	B	A	A	B	B	B
157	*DPL0864	A	B	A	A	A	B	A	A	B	B	A	B	B	A	A	A	B

158	*DPL0883	A	A	B	B	B	B	-	B	A	A	B	B	B	B	A	B	B	B	A	
159	*DPL0894	A	A	A	A	A	A	-	A	B	A	B	B	A	B	B	A	B	A	A	
160	*DPL0897	A	B	A	A	A	B	A	A	A	B	B	B	B	B	B	A	A	A	A	
161	*Gh111	A	A	A	B	A	B	B	B	B	B	A	A	B	A	B	B	B	B	B	
162	*Gh120	A	A	A	B	B	B	A	A	A	A	A	A	A	B	A	A	B	A	B	
163	*Gh137	A	B	A	A	A	B	-	A	A	B	B	B	B	B	B	A	A	A	A	
164	*Gh144	A	B	A	B	A	B	-	B	B	A	B	A	A	A	A	A	B	A	A	
165	*Gh145	A	B	B	B	B	B	B	A	B	B	A	B	B	A	B	B	A	B	A	
166	*Gh157	A	A	B	B	A	A	B	A	B	A	B	B	A	B	A	B	A	A	A	
167	*Gh158	A	B	A	B	A	A	B	B	A	A	A	A	B	A	B	B	B	A	B	
168	*Gh197	A	A	-	B	B	A	B	B	A	A	A	A	A	A	B	A	A	A	A	
169	*Gh199	B	B	A	A	B	A	A	B	A	A	A	B	A	B	B	A	B	B	A	
170	*Gh220	B	B	B	B	A	-	B	B	A	B	A	B	B	A	B	A	A	B	B	
171	*Gh247	A	B	-	B	B	B	B	B	A	A	B	A	A	A	B	B	B	A	B	
172	*Gh256	A	A	A	A	B	A	A	B	B	A	B	B	B	B	A	A	A	B	A	
173	*Gh260	A	A	B	B	B	B	B	B	A	A	B	B	A	A	B	A	B	B	B	
174	*Gh268	B	A	-	A	A	A	A	A	B	B	A	A	B	A	A	B	B	A	A	
175	*Gh27	A	A	A	B	A	B	B	B	B	B	A	A	B	A	B	B	B	B	B	
176	*Gh273	A	A	B	A	B	A	-	A	B	B	B	A	A	A	B	B	A	A	B	
177	*Gh298	B	A	A	A	B	B	A	A	B	B	B	B	B	A	A	A	B	B	A	
178	*Gh308	A	B	A	B	B	B	B	A	B	B	A	B	B	A	B	B	A	B	A	
179	*Gh316	A	A	-	A	A	A	-	A	A	A	B	B	A	B	B	B	B	B	A	
180	*Gh320	A	B	A	-	A	B	-	B	B	A	B	A	A	A	A	A	B	-	A	
181	*Gh327	A	B	A	A	B	A	A	B	B	B	B	A	A	A	A	A	B	B	A	
182	*Gh388	B	B	A	A	A	A	-	A	A	A	B	B	B	A	B	A	B	A	A	
183	*Gh398	A	B	A	A	A	A	A	A	A	B	B	B	A	B	A	B	A	B	B	
184	*Gh451	A	B	B	A	B	B	A	B	B	A	B	B	B	A	A	B	B	A	B	
185	*Gh454	B	A	A	A	A	A	A	A	B	B	B	A	B	A	A	B	B	A	A	
186	*Gh474	A	B	-	B	B	B	B	A	B	B	-	B	B	A	B	B	A	B	A	
187	*Gh499	A	A	-	B	A	B	B	B	B	B	A	A	B	A	B	B	B	B	B	
188	*Gh501	A	-	A	A	A	B	A	A	B	B	A	B	B	A	B	A	A	B	B	
189	*Gh529	A	A	B	A	A	B	A	B	A	A	B	A	A	A	B	B	B	B	B	
190	*Gh56	B	A	B	B	A	B	B	A	B	A	B	A	B	A	A	A	A	A	A	
191	*Gh60	A	B	A	A	A	B	A	A	B	B	A	B	B	A	B	A	A	B	B	
192	*Gh616	A	B	A	A	B	B	A	A	A	A	A	A	A	B	A	A	A	B	B	B
193	*Gh631	B	A	-	B	A	A	B	A	B	B	B	A	A	B	A	A	B	A	B	
194	*Gh64	B	A	B	B	A	A	A	A	B	A	B	A	B	B	A	A	B	A	B	
195	*Gh663	A	B	-	A	A	A	A	B	B	B	B	A	A	B	A	B	B	A	A	
196	*Gh72	A	B	A	A	B	B	A	A	A	A	A	A	B	A	A	A	B	B	B	
197	*HAU0250	A	A	A	A	A	B	-	A	A	B	B	B	A	A	B	A	A	B	B	

198	*HAU0423	B	A	B	A	A	A	A	B	A	B	A	A	A	B	A	A	B		
199	*HAU0483	B	A	-	A	B	B	A	A	B	A	A	B	B	A	B	B	A	B	
200	*HAU0635	A	B	A	B	B	B	-	B	A	A	B	B	A	B	A	A	B	A	B
201	*HAU0639	A	A	B	A	A	A	B	A	A	A	B	B	A	B	B	B	B	B	A
202	*HAU0878	A	B	A	A	B	B	A	A	A	A	A	A	B	A	A	A	B	B	B
203	*HAU0921	B	A	A	A	B	B	A	A	B	A	A	B	B	A	B	B	B	A	B
204	*HAU1001	A	B	A	A	A	A	A	A	A	A	A	B	A	B	A	A	B	A	B
205	*HAU1057	B	A	A	B	B	B	B	A	B	A	A	A	A	A	A	A	B	A	B
206	*HAU1129	B	A	A	A	B	B	A	A	A	B	B	B	A	A	B	A	B	A	A
207	*HAU1316	A	B	B	B	A	A	B	A	A	A	A	B	B	A	A	A	B	A	A
208	*HAU1321	A	B	B	B	A	A	B	A	A	A	A	B	B	A	A	A	B	A	A
209	*HAU1332	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
210	*HAU1371	B	B	A	A	A	B	A	A	A	A	A	B	A	A	B	B	B	A	B
211	*HAU1378	A	A	A	A	A	B	A	A	A	A	A	B	A	A	B	A	B	B	A
212	*HAU1382	B	B	B	B	B	B	B	A	A	A	B	A	A	B	B	B	A	A	A
213	*HAU1413	B	B	A	A	A	B	A	B	B	B	A	B	A	B	B	A	A	B	A
214	*HAU1417	A	A	A	A	A	A	A	A	A	B	A	B	A	A	B	A	A	B	A
215	*HAU1455	A	B	B	B	B	B	B	A	A	A	A	A	A	B	A	A	A	A	B
216	*HAU1460	A	-	A	A	A	A	A	A	A	A	A	B	A	A	B	B	B	A	B
217	*HAU1470a	A	B	B	B	A	A	B	B	B	A	A	B	A	B	B	A	A	A	A
218	*HAU1470b	A	B	A	B	A	A	A	A	A	A	A	B	A	B	B	A	A	A	A
219	*HAU1483a	A	B	B	B	B	B	B	A	B	B	A	B	B	A	B	B	A	B	A
220	*HAU1483b	A	B	B	B	B	B	B	A	B	B	A	B	B	A	B	B	A	B	A
221	*HAU1571	A	A	B	B	B	A	B	A	B	B	A	A	A	A	A	A	A	B	B
222	*HAU1603	B	B	B	A	A	A	B	A	A	A	B	B	B	A	B	A	B	A	A
223	*HAU1618	B	A	A	A	B	A	A	B	A	A	B	A	B	A	B	B	B	B	B
224	*HAU190	B	A	A	A	B	A	A	B	A	B	B	A	B	A	B	B	A	B	B
225	*HAU2004	B	B	A	A	B	A	A	-	A	B	A	B	A	A	A	B	A	A	B
226	*HAU2424	A	B	B	A	-	-	-	-	B	B	B	A	B	B	A	B	B	A	A
227	*HAU2504	A	-	A	A	B	A	A	A	B	B	B	B	B	A	A	B	A	A	B
228	*HAU2558	A	A	B	B	A	B	-	A	B	A	A	B	A	B	A	A	A	A	A
229	*HAU2625	B	A	B	A	B	B	A	A	B	A	A	B	B	A	B	B	B	A	B
230	*HAU2768	B	A	B	A	B	B	B	-	B	A	A	B	B	A	B	B	B	A	B
231	*HAU2786a	B	A	B	B	B	B	A	B	B	B	A	B	A	A	A	B	A	B	B
232	*HAU2786b	B	B	A	A	A	B	A	B	B	B	A	B	A	B	B	A	A	B	A
233	*HAU2857	A	A	B	B	B	B	B	A	B	A	A	B	A	A	A	A	B	A	B
234	*HAU3069	B	A	B	B	A	A	B	A	A	A	A	A	A	A	A	A	B	A	B
235	*HAU3071	A	A	B	B	A	B	B	A	A	A	A	A	B	B	B	A	B	A	B
236	*HAU3177	-	A	B	B	A	A	B	B	A	B	A	B	A	A	B	A	A	A	A
237	*JESPR154	B	B	A	A	B	A	A	B	A	B	A	B	A	A	A	B	A	A	B

238	*JESPR295	A	B	B	B	A	B	B	B	A	B	A	A	A	B	A	A	B	B	B	
239	*JESPR297	A	B	A	A	A	B	-	-	A	B	B	B	B	B	B	A	A	A	A	
240	*JESPR304	B	A	B	B	A	A	B	A	A	A	B	A	A	A	B	B	A	A	A	
241	*MGHES18	B	A	-	A	B	B	A	A	-	A	A	B	-	A	B	B	B	A	B	
242	*MGHES24	A	A	B	B	B	B	B	B	A	A	B	B	B	B	A	B	B	B	A	
243	*MGHES31	A	A	B	B	B	A	A	A	B	B	A	A	A	A	A	A	A	B	B	
244	*MGHES58	B	A	A	A	B	B	A	A	A	B	A	A	B	A	A	A	A	A	A	
245	*MUSS059	A	B	A	A	B	A	-	A	A	B	B	A	A	B	B	A	B	A	B	
246	*MUSS193	B	B	A	A	A	A	A	A	A	A	B	B	A	A	B	B	B	A	B	
247	*MUSS422	A	B	A	A	A	A	A	A	B	A	B	A	B	A	B	B	A	B	A	
248	*NAU1014	A	A	A	A	A	A	A	A	A	A	B	B	A	B	B	B	B	B	A	
249	*NAU1042	A	B	A	A	B	B	A	A	A	A	A	A	B	A	A	A	B	B	B	
250	*NAU1043	B	A	A	A	B	B	A	A	A	B	A	A	B	A	A	A	A	A	A	
251	*NAU1093	B	A	A	A	B	B	A	A	B	A	A	B	B	A	B	B	B	-	B	
252	*NAU1218	B	A	B	A	B	B	A	A	B	A	A	B	B	A	B	B	B	A	B	
253	*NAU1269	A	B	A	A	B	B	A	A	A	A	A	A	B	A	A	A	B	B	B	
254	*NAU1282	B	A	B	B	B	A	B	B	A	A	B	A	B	A	B	B	B	B	B	
255	*NAU1357	B	B	B	A	A	B	A	B	B	A	B	A	B	B	B	A	B	B	B	
256	*NAU2026	A	B	A	A	B	A	A	A	B	A	A	A	A	-	A	A	B	A	B	
257	*NAU2139	A	A	B	B	B	B	B	B	A	A	A	B	A	B	A	B	A	B	A	
258	*NAU2140	A	B	B	B	B	A	B	A	A	A	A	A	B	A	B	A	B	B	B	
259	*NAU2152	A	B	-	A	B	B	A	A	A	A	B	B	A	B	A	B	A	B	A	
260	*NAU2218	B	A	A	A	A	B	A	A	A	B	A	A	A	A	A	B	B	B	B	
261	*NAU2265	A	B	A	A	B	A	A	A	A	B	B	A	A	B	B	A	B	A	B	
262	*NAU2277	A	B	A	A	B	A	-	A	A	B	B	A	A	B	B	A	B	A	B	
263	*NAU2343	A	A	A	A	A	A	-	A	A	B	B	-	A	A	B	A	A	B	A	
264	*NAU2460	A	B	A	A	B	B	A	A	A	A	B	B	A	B	A	B	A	B	A	
265	*NAU2701	A	B	B	B	B	B	B	B	A	A	B	A	A	A	A	A	B	B	A	
266	*NAU2715	A	B	B	B	B	A	B	B	B	B	B	A	A	B	A	A	A	A	B	
267	*NAU2742	B	A	B	B	B	B	B	B	B	B	A	B	A	-	A	B	A	B	B	
268	*NAU2873	B	A	B	B	B	A	B	A	A	A	B	A	B	-	B	B	B	B	B	
269	*NAU2893	A	A	B	B	A	B	A	A	B	A	A	B	A	A	A	A	A	A	A	
270	*NAU2894	B	A	B	B	A	A	-	A	A	A	A	A	A	A	A	A	A	B	A	B
271	*NAU2957	A	B	B	B	B	A	B	A	A	A	A	A	B	A	B	A	B	B	B	
272	*NAU2960	A	A	A	A	A	B	A	A	A	B	B	A	B	A	A	B	B	B	B	
273	*NAU2984	B	A	A	A	B	A	B	B	A	B	B	B	A	A	B	A	B	A	A	
274	*NAU3052	B	B	-	B	B	B	B	B	A	A	B	A	A	A	B	B	B	A	B	
275	*NAU3100	A	B	A	A	B	A	A	B	B	B	B	A	A	A	A	A	B	B	A	
276	*NAU3112	B	B	A	B	B	B	B	B	A	B	A	B	B	A	B	A	A	B	B	
277	*NAU3177	A	B	A	A	A	A	A	B	A	B	B	B	A	B	A	B	A	B	B	

278	*NAU3181	B	A	B	A	A	B	B	B	A	B	A	A	B	A	B	A	A	A	A	
279	*NAU3217	B	A	A	A	A	B	A	A	B	B	A	A	A	B	A	A	A	A	B	
280	*NAU3254	A	A	A	A	A	A	A	A	B	B	B	A	A	B	A	A	B	A	A	
281	*NAU3308	B	B	B	B	B	B	B	A	B	A	A	A	A	A	A	A	B	A	B	
282	*NAU3384	A	B	-	B	B	B	B	A	B	A	B	A	B	A	B	B	A	B	A	
283	*NAU3385	A	B	A	A	A	A	-	A	B	A	B	A	B	A	B	B	A	B	A	
284	*NAU3390	A	B	B	B	B	B	A	A	A	A	B	B	A	B	A	B	A	B	A	
285	*NAU3404	B	B	A	A	A	A	A	B	A	A	A	B	A	B	A	B	B	A	A	
286	*NAU3437	B	B	A	A	B	B	-	B	A	A	A	B	B	A	A	A	B	B	A	
287	*NAU3468	A	A	B	B	B	B	B	A	B	A	A	A	A	A	A	A	A	B	A	B
288	*NAU3519	B	B	B	B	A	A	B	B	A	A	A	B	B	A	A	A	A	A	A	
289	*NAU3695	A	A	B	A	A	A	A	A	B	A	A	A	B	B	A	A	B	A	A	
290	*NAU3736	A	B	A	A	B	A	A	A	B	A	B	B	B	A	A	B	A	B	A	
291	*NAU3765	B	B	B	A	B	A	-	B	A	-	A	B	A	A	A	B	A	A	B	
292	*NAU3820	A	A	B	A	A	B	A	-	A	A	B	A	A	A	B	B	B	B	B	
293	*NAU3839	B	A	B	B	B	B	A	B	B	B	A	B	A	A	A	B	A	B	B	
294	*NAU3868	B	B	-	B	B	A	B	A	A	B	B	B	A	B	B	A	B	A	A	
295	*NAU3901	-	-	B	B	-	B	-	-	-	-	A	-	-	B	-	A	-	-	A	-
296	*NAU3934	A	A	B	B	A	B	B	A	A	B	B	A	A	A	B	A	A	A	B	
297	*NAU3966	A	B	A	B	A	A	B	B	A	A	A	A	B	A	B	B	B	A	B	
298	*NAU3995a	A	B	A	A	A	B	A	B	B	B	A	B	A	B	B	A	A	B	A	
299	*NAU3995b	A	A	B	B	B	B	B	B	B	B	A	B	A	A	A	B	A	B	B	
300	*NAU4034	B	B	A	A	A	A	A	A	A	A	B	B	B	A	B	A	B	A	A	
301	*NAU4045	A	B	-	A	A	A	A	B	A	B	B	B	A	B	A	B	A	B	B	
302	*NAU4064	B	A	B	B	A	A	B	B	A	B	A	B	A	A	B	A	A	A	A	
303	*NAU5072	A	B	B	B	-	A	B	B	B	B	B	A	A	B	A	A	A	A	B	
304	*NAU5120	B	B	-	B	B	B	B	A	A	A	B	A	B	A	B	A	A	A	A	
305	*NAU5260	A	A	B	B	B	B	B	B	A	-	B	B	B	A	A	B	A	A	A	
306	*NAU5330	B	B	A	B	B	A	A	B	B	B	B	B	B	B	B	B	B	B	B	
307	*NAU5428	A	B	B	A	B	A	A	A	A	A	B	B	A	B	A	B	A	B	A	
308	*NAU5434	B	A	A	A	B	B	A	A	B	A	A	B	B	A	B	B	B	A	B	
309	*NAU5474	B	B	-	B	B	B	B	A	A	B	A	A	A	B	B	B	A	B		
310	*NAU6240	A	A	B	B	A	B	B	A	A	A	B	B	A	A	B	A	A	B	A	
311	*NAU6309	A	B	A	A	B	A	A	A	B	A	B	B	B	A	A	B	A	B	A	
312	*NAU6367	A	B	A	A	A	A	A	A	B	A	B	A	B	A	B	B	A	B	A	
313	*NAU748	A	B	B	B	A	B	A	-	B	A	A	B	B	A	A	A	A	B	B	
314	*NAU797	A	B	A	A	B	B	A	A	A	A	A	A	B	A	A	A	B	B	B	
315	*NAU828	A	B	A	A	B	B	A	A	A	A	A	A	B	A	A	A	B	B	B	
316	*NAU833a	A	B	A	A	B	B	A	A	A	A	A	A	B	A	A	A	B	B	B	
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318	*NAU845	A	A	A	A	B	B	-	A	B	A	A	B	A	B	B	B	B	A	B
319	*NAU862	B	A	A	B	B	B	B	A	A	A	B	A	A	A	B	A	A	A	A
320	*NAU874	B	A	-	B	-	B	B	A	B	A	A	A	B	A	A	A	B	A	B
321	*NAU895	A	B	A	A	B	A	A	A	A	B	B	A	A	B	B	A	B	A	B
322	*NAU896	B	B	-	B	A	A	B	B	A	B	B	A	A	B	A	A	A	B	B
323	*NAU935	A	A	B	B	B	B	-	B	A	A	B	B	B	B	A	B	B	B	A
324	*NAU943	A	A	B	B	A	A	B	A	B	B	B	A	A	B	A	A	B	A	B
325	*NBRI0014	B	B	B	B	B	B	B	B	A	A	B	B	B	B	A	B	B	B	A
326	*NBRI0694	B	B	A	A	A	A	A	A	A	B	B	A	A	B	B	B	B	B	B
327	*PGML0014	A	A	-	B	B	A	B	A	B	A	A	A	A	B	A	B	B	A	A
328	*PGML0120	A	A	B	B	B	B	B	B	A	A	B	B	A	A	B	A	B	B	B
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639	*ICR10344	A	A	A	A	A	A	A	A	A	B	B	A	B	B	B	A	A	A	
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653	*ICR12228	A	A	A	A	A	B	A	B	A	B	B	B	B	B	A	-	B	B	B

Note:'-' referred to the missing data.

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44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67
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