Scientific
Research
Publishing

Constructing Genetic Linkage Maps Using the Whole Genome Sequence of Pacific Bluefin Tuna (*Thunnus orientalis*) and a Comparison of Chromosome Structure among Teleost Species

Tsubasa Uchino[1], Yoji Nakamura[2], Masashi Sekino[2], Wataru Kai[2], Atushi Fujiwara[2], Motoshige Yasuike[2], Takuma Sugaya[3], Himeko Fukuda[1], Motohiko Sano[1], Takashi Sakamoto[1*]

[1]Faculty of Marine Science, Tokyo University of Marine Science and Technology, Tokyo, Japan
[2]Research Center for Aquatic Genomics, National Research Institute of Fisheries Science, Fisheries Research Agency, Yokohama, Japan
[3]Research Center for Marine Invertebrate Animals, National Research Institute of Fisheries and Environment of Inland Sea, Fisheries Research Agency, Hiroshima, Japan
Email: *takashis@kaiyodai.ac.jp

Abstract

Pacific bluefin tuna (*Thunnus orientalis*) is one of the most economically important species in the Percomorpha group of teleost fishes. Their migrations are extensive and depend upon continuous swimming at a high rate of speed throughout their life. The draft genome sequence of this species has been reported but remains highly fragmented. We constructed a Pacific bluefin tuna genetic linkage map using microsatellite markers developed on each of the scaffolds from the draft genome sequence to link these genome fragments and understand the genomic structure of species in Percomorpha. Of the 606 polymerase chain reaction microsatellite primer pairs tested, 473 were polymorphic in the mapping populations for the linkage analysis. We constructed sex-specific maps for 24 linkage groups consisting of 470 markers, which allowed us to place scaffolds that cumulatively represented 20.8% (153.8 Mb) of the sequenced genome onto the linkage groups. The distribution of orthologous genes on the chromosomes of tuna and four other teleost fish species suggested that the constitution of tuna chromosomes is closest to that of medaka. Both species have the 24 chromosomes of the ancestral teleost, including several chromosomal inver-

---

*Corresponding author.

sions. The integrated map developed in this study will be useful to construct a complete physical map to conduct comparative teleost genomics and genetic studies on economically useful traits in Pacific bluefin tuna.

Keywords

Pacific Bluefin Tuna, Microsatellite Marker, Genetic Linkage Map

1. Introduction

Pacific bluefin tuna (*Thunnus orientalis*) is one of the most economically important species of fish, and their migrations are unique, as they swim quickly and continuously throughout their life. This continuous swimming ability enables Pacific bluefin tuna to migrate long distances in the Pacific Ocean. Continual swimming is required, so that water containing oxygen flows continuously over the gills; this is a special feature of *Thunnus* and closely related species. Tuna have superior swimming ability due to a large quantity of red muscle, a rapid metabolic rate, large body size, and their unique shape and swimming form, although details remain unknown. Moreover, the tuna growth rate is very high, as they can grow 50 cm in total length in 1 year. Maximum length and weight are about 2.5 m and 300 kg, respectively. These unique ecological features of Pacific bluefin tuna originate from their genome.

Tuna farmers generally use natural seed for broodstock. However, tuna catch is restricted by international fishing regulations created as a result of recent decreases in wild population numbers [1]. Thus, a breeding system that depends on the recruitment of naturally occurring siblings is difficult to maintain. The complete life-cycle has been established recently for Pacific bluefin tuna aquaculture [2] and artificial seed is now being used for production. Therefore, there is much interest in creating broodstock with commercially valuable genetic traits.

Several whole genome sequences have been reported recently in teleosts because of the development of high-throughput sequencing methods. Whole genome sequences have been registered in public databases for model fish, such as zebrafish (*Danio rerio*) [3] and medaka (*Oryzias latipes*) [4] as well as for other fish, such as fugu (*Takifugu rubripes*) [5], *Tetraodon* (*Tetraodon nigroviridis*) [6], stickleback (*Gasterosteus aculeatus*) [7], and Pacific bluefin tuna [8].

The draft Pacific bluefin tuna genome sequence was generated using the Roche 454 FLX Titanium and Illumina GaIIx next-generation sequencing platforms [8]. Whole genome shotgun sequencing and assembly provided 192,169 contigs (>500 bp) and 16,802 scaffolds (>2 kb). The N50 values, which are used to evaluate connectivity of the assembly, are 7588 bp (contigs) and 136,950 bp (scaffolds), respectively.

Cytological studies [9] [10] have reported that *Thunnus* species have 24 pairs of chromosomes. Draft genome sequence when merged should, therefore, only have 24 huge fragments corresponding to each chromosome. The draft genome sequence of this species is highly fragmented, and constructing a genetic linkage map is an effective way to link the sequence fragments. Genetic linkage maps have been used as an anchor for fish [11] [12], plants [13]-[16], and domestic animals [17]. A genetic linkage map is constructed by developing genetic markers on scaffolds and examining the linkage relationships between the markers. However, no genetic linkage map has been constructed for Pacific bluefin tuna. Several different classes of polymorphic markers could be used to construct genetic linkage maps. Repetitive sequence regions called microsatellites (MS) (or short tandem repeats) are abundant in eukaryotic genomes and have the potential to exhibit high polymorphism in a mapping population. MS markers also have the benefit of being multi-allelic within species, and therefore, unlike single nucleotide polymorphism markers (SNPs), MS markers can be used to track the unique segregation phases of both male- and female-specific parental alleles in their progeny. When parents are doubly heterozygous for SNP markers, the linkage phase of heterozygous progeny cannot be assessed. Only a few MS markers have been developed for Pacific bluefin tuna [18], and therefore, there is a need to develop additional markers for this species.

Recently, four novel candidates for vertebrate SD genes were reported, all of them in fishes. These include *amhy* in the Patagonian pejerrey [19], *Gsdf* in *Oryzias luzonensis* [20], *Amhr*2 in fugu [21] and *sdY* in rainbow

trout [22]. There are multiple sex-determining regions in teleost fishes that do not possess homology to one another due to the turnover of sex chromosomes [23]. In bluefin tuna the sex-determining region has been identified to by XY based, and male-specific marker (*male delta* 6 or *Md*6) has been characterized [24]. There is no syntenic information about *Md*6 and those sex-determining regions in teleost fishes. One of the objectives of this study was to localize the sex-determining locus within the genomic scaffolds corresponding to the genetic linkage map placements by mapping *Md*6 using an adjacent MS marker.

Comparative genome studies have revealed the evolution of chromosomes among several fish species. These studies suggest that the medaka genome has the conserved genomic structure of the MTZ ancestor (the last common ancestor of three fishes, medaka, *Tetraodon*, and zebrafish) and no major chromosomal rearrangements have occurred for more than 300 million years (My) [4] [25], whereas the zebrafish genome has experienced many interchromosomal rearrangements during evolution due to extensive translocations. A comparative genome study of fugu supported their hypothesis and discussed inter-chromosomal rearrangements in the fugu and *Tetraodon* lineages [12]. Tongue sole also experienced three major chromosomal fusion events after divergence from the common ancestor with medaka, *Tetraodon*, and fugu [26]. A high density genetic map with tiled genomic platyfish contigs revealed that the platyfish and medaka karyotypes are remarkably similar with few interchromosomal translocations but with numerous intrachromosomal rearrangements (transpositions and inversions) since their lineages diverged about 120 Mya [27]. That study also suggested that stickleback and *Tetraodon* arose by fusion of pairs of ancestral chromosomes. These results suggest that the chromosomal constitution and synteny of fish in Percomorpha are highly conserved, with few inter-chromosomal rearrangements despite substantial phylogenetic distances among the taxa compared [28] [29]. Percomorpha is a large group in Acanthopterygii that includes medaka, platyfish, fugu, *Tetraodon*, stickleback, tongue sole, European seabass, and Pacific bluefin tuna. Accordingly, constructing a genetic map for other non-model fish species in Percomorpha using gene information on scaffolds from whole genome sequences will provide new aspects for comparative studies in this group.

The aim of the present study was to construct a genetic linkage map for Pacific bluefin tuna based on draft genome sequence information to understand the genome structure of this species in Percomorpha. We extracted an F1 full-sib population of young Pacific bluefin tuna as a mapping population. We constructed a linkage map using MS markers developed on each of the scaffolds and examined preservation of chromosome structure in four other fully sequenced fish species.

2. Materials and Methods

2.1. Mapping Population

Many full-sib progeny and their parents were prepared to construct a linkage map for the mapping population. Unlike other fish that spawn easily, one-to-one mating is very difficult in Pacific bluefin tuna. Thus, we tried to extract full-sib progeny from young fish spawned naturally from several parents. We collected 500 progeny (18 days old) derived from a small number of parents based on our visual observations at Amami Station, Seikai National Fisheries Research Institute, FRA. The parents of these young fish were derived from wild fish captured offshore of Shimane in the Japan Sea and reared 3 years at Amami Station, Seikai National Fisheries Research Institute, FRA. The whole bodies of the small fish were preserved in 100% ethanol until extraction of genomic DNA. DNA extraction was conducted using the Quickgene system (Fujifilm, Tokyo, Japan), following the manufacturer's protocol. Candidate adult parents of these progeny were treated using the same method, except a fin clip was collected as the sample. Genomic DNA was amplified using the Illustra GenomiPhi Amplification Kit (GE Healthcare, Milwaukee, WI, USA) following the manufacturer's protocol. A parental analysis of 500 young individuals was performed using 11 MS loci to select the full-sib progeny. Parent-offspring hypotheses were examined based on genotypic incompatibilities between putative parents and offspring using the exclusion method. The parentage assignment test in PARFEX software [30] was used with the exclusion method. We allowed for a few genotype mismatches (<2) between offspring and parents per MS marker due to missing data or the influence of a null allele.

2.2. Development of Microsatellite Markers

The 16,802 scaffolds that comprise the Pacific bluefin tuna genome assembly are distributed from 1.02 Mbp to

1.98 Kbp [8]. The positional information of longer scaffolds was revealed using linkage analysis during construction of the tuna physical map. Therefore, we selected the longest 1000 scaffolds as mapping candidates. Primer 3 [31] was used to design the appropriate polymerase chain reaction (PCR) primers for the near-detected MS regions that had repeat units ranging from two to five nucleotides. The size of the amplified PCR product was set to 100 - 400 bp in the reference sequence. We selected one PCR primer pairs from each scaffold, and 606 PCR primer pairs for MS were tested for polymorphism in the mapping population (**Supplementary Table S1**).

2.3. Genotyping and Linkage Analysis

Multiplex PCR was used to simultaneously amplify four targeted loci. The universal primer-multiplex PCR method [32] was adapted to amplify the four primer pairs. This method uses multiple universal primers each labeled with a unique fluorescent tag (FAM, VIC, NED, and PET) to co-amplify multiple loci, including size overlapping markers [32]. The sequence information for the universal primers is shown in **Supplementary Table S1**. We used the Type-it Microsatellite PCR kit (Qiagen, Hilden, Germany) for multiplex PCR, following the manufacturer's recommendations. PCR amplifications were performed in a 10 µl reaction volume consisting of 5 µl Qiagen multiplex master mix, 1 µl Qiagen Q solution, 0.02 µM forward primer, 0.2 µM reverse primer, and 0.2 µM fluorescently tagged universal primers corresponding to each tailed primer. The following PCR conditions were used: initial denaturation at 94˚C for 5 min, 28 cycles of 94˚C for 30 sec, 58˚C for 90 sec and 72˚C for 30 sec, eight cycles of 94˚C for 30 sec, 53˚C for 90 sec, and 72˚C for 30 sec, followed by final extension at 59˚C for 3 min. The PCR products were heat denatured and a fragment analysis was performed on an Applied Biosystems 3130×l Genetic Analyzer (Applied Biosystems, Foster City, CA, USA) using a LIZ-600 size standard (Life Technologies, Carlsbad, CA, USA). Allele sizes were subsequently assessed and scored using GENE MAPPER ver. 4.0 (Life Technologies). After obtaining the genotyped data for each marker, the alleles were identified as paternal or maternal, which enabled construction of male-specific and female-specific linkage maps. We used MapDisto software [33] to identify each linkage group and determine the order of the MS markers in each linkage group using a log of odds threshold of 4.0. Finally, map distances were calculated using the Kosambi function. Segregation of each marker was analyzed using the chi-square test for goodness of fit to the expected Mendelian ratio in a backcross model (1:1). We focused on markers that showed significant distortion at the 5% level, after a Bonferroni correction for multiple testing. The estimated genome coverage of the map was calculated using the method 4 of Chakravarti *et al.* [34], $c = 1 - e^{-2dn/L}$, where d is the average interval of markers, n is the number of markers, and L is the length of the linkage map. Differences in the recombination rates between the male and female linkage maps were evaluated by calculating the interval of common contiguous markers in the female and male linkage maps.

2.4. Mapping Sex-Linked Sequences

The DNA sequence of the male characteristic fragment *Md*6 has been identified in cultured Pacific bluefin tuna and a BLAST search against the Pacific bluefin tuna genome assembly showed highest identity (Expect value: 8^{e-139}) with contig *BADN*01109032 on scaffold Ba00007445 [24]. We designed four appropriate PCR primer sets for four MS regions on the scaffold to locate *Md*6 on the genetic linkage map (**Supplementary Table S1**). Then, we performed a linkage analysis using the same method as used for the other MS markers.

2.5. Genome Sequence and Amino Acid Sequence Comparisons

The amino acid sequence data of four teleosts (fugu, medaka, stickleback, and *Tetraodon*) were downloaded from the Ensembl database to construct the Oxford grid [35]. A protein BLAST search was performed for the five teleost sequences (Ensembl fishes and tuna) with an E-value $< 10^{-5}$. Orthologous gene pairs were defined as one reciprocal best hit. Core genes conserved among the five teleosts were defined as the real orthologous gene set. Oxford grids were constructed to study the synteny and examine the distribution of the orthologous genes.

3. Results

3.1. Selection of the Mapping Population

Estimated parent-offspring pairs were mainly comprised of eight groups (groups 1 - 8) (**Supplementary Figure**

S1 and **Supplementary Table S2**) derived from eight male and four female parents. Many individuals are needed to construct a linkage map, so we extracted 193 full-sib progeny (group 5).

3.2. Development of Microsatellite Markers

The total length of the 1000 selected scaffolds was 302 Mbp, accounting for 40.7% of all scaffolds. Of the 606 PCR primer pairs tested for MS, 473 were polymorphic in the mapping population.

3.3. Constructing the Genetic Linkage Map

Ninety-three group 5 progeny and their parents were used as the mapping population. We used 473 PCR primers to perform the linkage analysis. We constructed sex-specific maps for 24 linkage groups consisting of 470 markers (**Table 1** and **Figure 1**). Among the informative markers used in the linkage analysis, 99.4% of the markers showed detectable linkage relationships with each other. Three markers were not linked to any other marker.

Table 1. Summary of genetic and physical map of Pacific bluefin tuna.

	Genetic map						Total no. of markers	Physical map	
	Male			Female				No. of anchored scaffolds	Size (bp)
LGs	Genetic distance (cM)	No. of markers	Marker interval (cM)	Genetic distance (cM)	No. of markers	Marker interval (cM)			
LG1	5.4	19	0.3	69.5	25	2.9	26	26	7,311,548
LG2	41.3	14	3.2	45.5	14	3.5	19	19	4,013,609
LG3	55.7	16	3.7	66.5	16	4.4	20	20	7,566,954
LG4	60.9	20	3.2	56.3	16	3.8	26	26	7,445,291
LG5	36.7	18	2.2	76.9	20	4.0	22	22	8,683,432
LG6	53.0	12	4.8	54.0	12	4.9	14	14	5,824,343
LG7	19.4	11	1.9	62.3	16	4.2	17	17	3,758,735
LG8	34.5	18	2.0	34.9	11	3.5	19	19	5,886,385
LG9	30.4	12	2.8	50.5	13	4.2	17	17	4,872,438
LG10	43.3	16	2.9	66.2	15	4.7	22	22	7,525,825
LG11	34.7	12	3.2	73.9	15	5.3	19	19	6,890,034
LG12	41.6	20	2.2	64.1	15	4.6	23	23	7,880,459
LG13	84.2	14	6.5	92.3	17	5.8	20	20	6,805,915
LG14	35.7	18	2.1	53.3	14	4.1	20	20	8,512,497
LG15	54.1	17	3.4	41.1	13	3.4	18	18	8,527,022
LG16	45.7	16	3.0	49.8	16	3.3	21	21	7,004,297
LG17	35.8	13	3.0	27.1	15	1.9	19	19	6,185,918
LG18	25.9	18	1.5	47.5	19	2.6	21	21	5,107,399
LG19	37.0	13	3.1	33.8	9	4.2	14	14	4,691,049
LG20	40.4	14	3.1	55.4	12	5.0	18	18	6,731,092
LG21	52.1	20	2.7	67.2	20	3.5	25	25	8,650,511
LG22	64.5	16	4.3	41.3	14	3.2	16	16	4,817,797
LG23	26.0	12	2.4	29.2	13	2.4	16	16	3,887,699
LG24	34.9	15	2.5	73.9	16	4.9	18	18	5,216,393
Total	992.9	374	2.7	1332.3	366	3.7	470	470	153,796,642
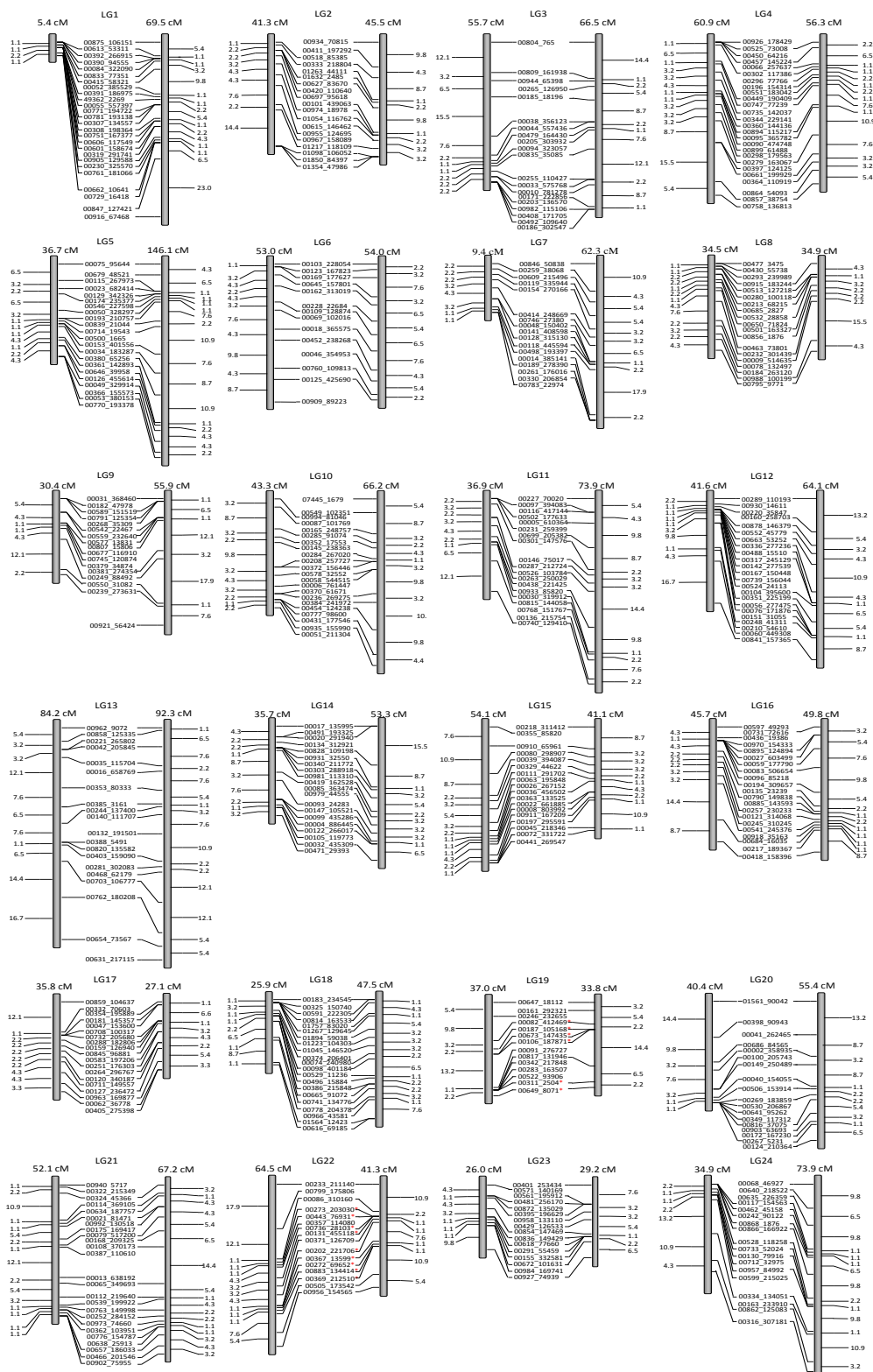
Figure 1. Male and female genetic linkage maps of *T. orientalis*. Vertical squares represents Male (left) and Female linkage group, respectively. Genetic distances between adjacent markers are shown above in Kosambi mapping function (cM). Common marker between two sexes is bridged by connected lines. Markers with red asterisks (*) showed a significant segregation distortion from the expected Mendelian 1:1 segregation in female map.

The male map consisted of 24 linkage groups with 374 MS markers. The total length of the linkage groups was 992.9 cM, and the mean distance between two markers was 2.7 cM. The sizes of individual linkage groups ranged from 5.4 to 84.2 cM (mean, 41.4 cM). The number of markers per linkage group varied from 11 to 20, with a mean of 15.6 markers per linkage group. The estimated genome coverage of the map was 86.5%.

The female map included 366 markers in 24 linkage groups. This map spanned 1332.3 cM, and mean spacing between two markers was 3.7 cM. The sizes of the female linkage groups ranged from 27.1 to 92.3 cM (mean, 55.5 cM). The number of markers per linkage group varied from 9 to 25, with a mean of 15.3 markers per group. The estimated genome coverage of the map was 86.5%.

The ratio of male map length to female map length was 1.0:1.4. The distribution of the intervals between contiguous common markers in both linkage maps was almost the same (**Figure 2**), although several linkage groups clearly showed different recombination rates in specific regions or linkage groups (**Supplementary Figure S2**). In particular, the genetic distance between the common markers in LG1, LG5, LG7, LG11, LG14, LG18, and LG24 on the female map was higher than the male genetic distance. In contrast, LG15 and LG22 showed higher genetic distances on the male map.

3.4. Mapping the Sex-Linked Sequence

The MS marker (07445_1679), which was developed in scaffold Ba00007445, was only polymorphic in females and mapped to the LG10 terminal region on the female map (**Figure 1**). Orthologues of several sex-determining genes in teleosts [23] but were not found on the LG10 scaffold of the integrated genetic linkage map.

3.5. Integration of the Genetic Linkage Maps with the Physical Map

Developing MS markers to specific regions of each scaffold allowed us to integrate the genetic and physical maps into a consolidated genome map. We anchored 470 scaffolds to be consistent with the order of markers determined on the genetic linkage maps. Thus, we placed scaffolds that cumulatively represented 20.8% (153.8 Mb) of the sequenced genome onto the linkage groups (**Table 1**). In total, 4243 genes estimated in the tuna draft genome assembly have been included in these scaffolds [8].

3.6. Comparison of Genome Structure in Other Teleosts

Constructing the integrated Pacific bluefin tuna map made it possible to compare conserved sequence regions with those of other teleosts. We identified 6445 pairs of orthologous genes among tuna and four other teleosts (fugu, medaka, stickleback, and *Tetraodon*). Then, we extracted 1381 gene pairs from these orthologous genes
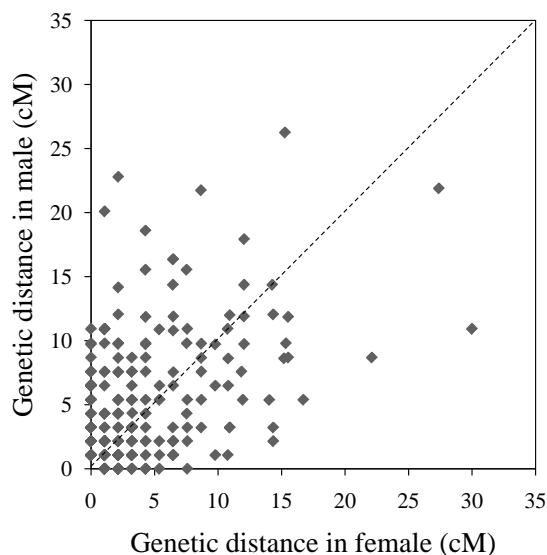
Figure 2. Recombination ratio between male map and female map. The common intervals flanked by adjacent markers from the 24 linkage groups are compared.

and mapped them on the integrated map. We constructed an Oxford grid [35] for Pacific bluefin tuna against the four teleosts based on the number of orthologous genes on each linkage group/chromosome. These results indicated that 24 pairs of chromosomes in tuna and medaka showed a clear one-to-one relationship (**Figure 3**). Comparisons with the other three fish species also indicated highly conserved one-to-one relationships, although there were several one-to-two and one-to-three relationships between homologous chromosomes. For example, fugu chromosome 1 corresponded to LG3, LG19, and LG21 in Pacific bluefin tuna (**Figure 3(b)**). Stickleback chromosome 1 corresponded to LG2 and LG13 in Pacific bluefin tuna. A similar result was observed in stickleback chromosome 4 with LG10 and LG23 in Pacific bluefin tuna (**Figure 3(c)**). Three one-to-two relationships were detected between *Tetraodon* (chromosomes 1 - 3) and Pacific bluefin tuna (LG4 and LG10, LG19 and LG21, and LG2 and LG8) (**Figure 3(d)**).

We constructed an integrated map to compare the Pacific bluefin tuna and medaka chromosome structures. Homologous sequence regions across several chromosome pairs between tuna and medaka revealed reciprocal homology relationships as well as reverse orientation orderings. Thus, several inversions may have occurred in either genome (**Figure 4** and **Supplementary Figure S3**).
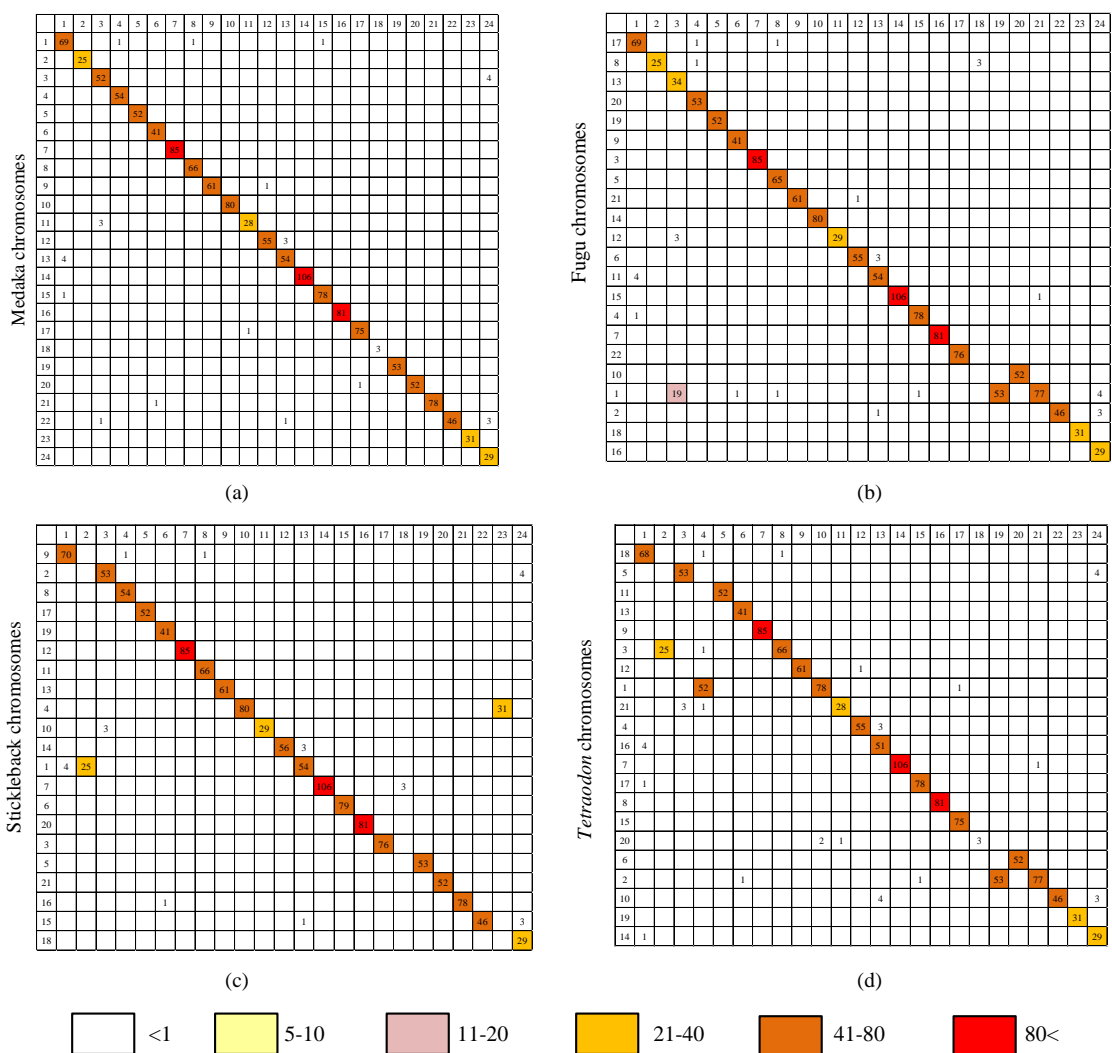
Figure 3. Oxford grid comparing genomes of *T. orientalis* and four model fishes. Commonly conserved 1378 orthologous genes among five fishes were plotted into Oxford grids. Each number in a cell indicates the number of orthologs in each genome. Each grids were drawn by specific color according to the number of orthologous, The number of each linkage group of *T. orientalis* was determined in this study. (a) *T. orientalis*-Medaka comparison; (b) *T. orientalis*-Fugu comparison; (c) *T. orientalis*-Stickleback comparison; (d) *T. orientalis*-Tetraodon comparison.
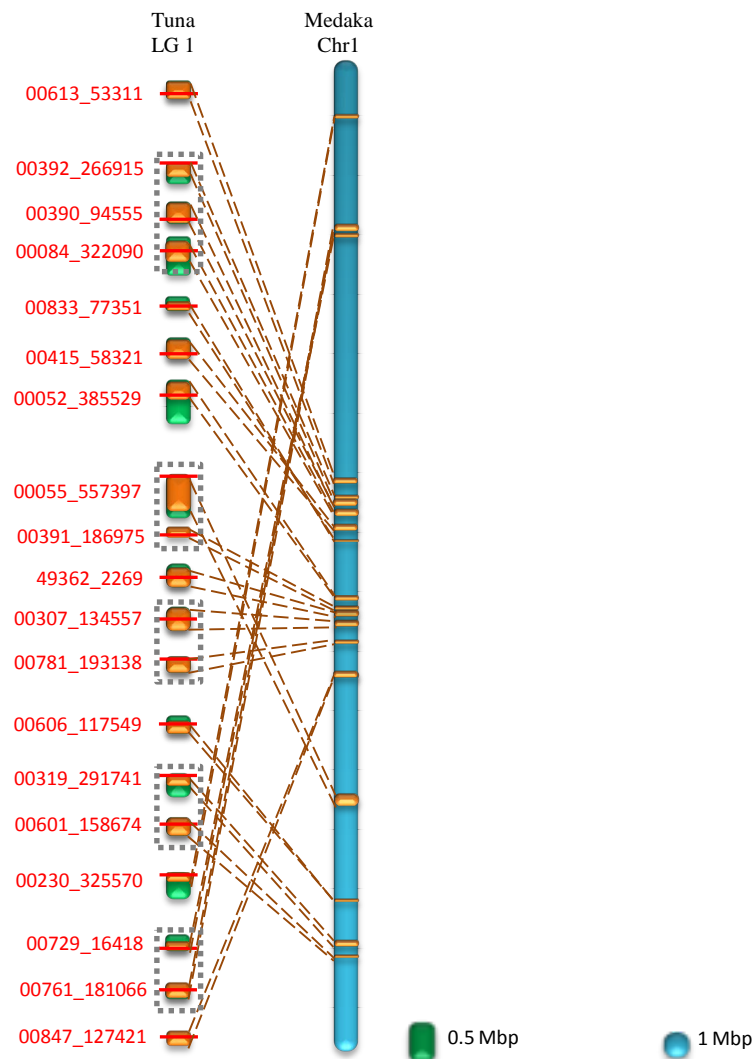
Figure 4. Comparison of chromosome structure between Pacific bluefin tuna LG 1 and medaka Chr 1. Red number indicates MS marker name, orange square indicates homologous region between tuna and medaka. Boxes with dotted lines indicate areas in which marker order is uncertain.

4. Discussion

In this study, we constructed an integrated map composed of 24 linkage groups with 470 MS markers. The integrated map will be a useful resource to develop a complete physical map, conduct comparative genomic studies in teleosts, and perform genetic studies of economically useful traits in Pacific bluefin tuna.

The karyotype composition of Pacific bluefin tuna was two pairs of metacentric, three pairs of submetacentric, two pairs of subtelocentric, and 17 pairs of acrocentric chromosomes. The numbers of linkage groups on the sex-specific maps agreed with the number of chromosome pairs suggested from microscopic observations [9]. Scaffolds integrated with linkage groups will have to be detected on chromosome samples using fluorescence *in situ* hybridization to reveal the relationships between linkage groups and chromosomes, as in other fish [12] [36]. It is also desirable to locate scaffolds or contigs that include unique repeats in telomeric or centromeric regions.

Coverage of the male and female genomes by the maps was 86.5% respectively; thus, the chromosomes were covered comprehensively by this linkage map. However, mean lengths of the linkage groups were somewhat shorter (male: 41.4 cM, female: 55.5 cM) compared with linkage maps of other closely related teleosts [11] [37]-[40], suggesting the absence of a marker at the end of a chromosome and that the mapped scaffolds lack telomeric and centromeric repeats. Restriction site-associated DNA (RAD) tag sequencing [41] using a next-

generation sequencer is useful to develop several thousand single nucleotide polymorphism markers close to restriction endonuclease sites. This method has been applied to construct linkage maps for several teleosts [27] [42]-[45]. The integrated map in this study provides a framework for constructing high density-linkage map using RAD tag sequencing.

Total map length between males and females was almost the same compared with that of several other teleosts [12] [38] [46] [47], although the female map was somewhat longer than that of the male map (ratio F:M, 1.4:1). The distributions of the common marker intervals between the male and female maps were not different.

The *MD*6 sex-linked sequence was mapped to the LG10 terminal region on the female linkage map. Because the mapping population in this study was 18 days old, we could not distinguish phenotypic sex. Therefore, we could not perform a linkage analysis between genotypic and phenotypic sex. A mapping population that distinguishes phenotypic sex will be needed to map the sex-determining region in the future. Sex-determining genes reported in other teleosts [23] were not found on LG10 of the integrated map. Therefore, it will be necessary to map these genes on our genetic linkage map to determine the relationships between these sex-determining genes and sex in Pacific bluefin tuna.

The comparison of chromosome structure among the five fish species suggested that Pacific bluefin tuna chromosomes were very similar to those of medaka, but traces of several inter-chromosomal rearrangements were detected in the other fish. A comprehensive amino acid sequence comparison of orthologous genes among the five teleosts (including Pacific bluefin tuna) supported that Pacific bluefin tuna is phylogenetically closer to stickleback than to medaka [8]. Taken together, Pacific bluefin tuna are more phylogenetically related to stickleback than to medaka but not in chromosome structure. The medaka genome has the conserved genomic structure of the MTZ ancestor and has not experienced any major rearrangements for more than 300 My. Our results suggest that the chromosome structure of the Pacific bluefin tuna could also be the conserved structure of the MTZ-ancestor because of the high similarity between the chromosome structures of the two species. Yellowtail (Perciformes) chromosome structure is highly similar with that of the MTZ ancestor [48]. Our results support these yellowtail results at the whole genome level.

Stickleback [27], fugu, and *Tetraodon* [12] have experienced chromosome fusion events two or three times since diverging from the MTZ ancestor, which presumably had 24 chromosome pairs. Stickleback chromosome 1 corresponded to LG2 and LG13 in Pacific bluefin tuna. A similar trace was observed in stickleback chromosome 4 with LG10 and LG23 in Pacific bluefin tuna. These one-to-two relationships are potential traces of inter-chromosomal rearrangements in a lineage phylogenetically diverged from the two species. In this case, fusion of two chromosomes or chromosome fission in the stickleback lineage could have occurred after divergence from the common ancestor. Our comparative study did not consider intra-chromosomal rearrangements that diverged from the MTZ ancestor. An investigation of macro or micro-synteny among fish species in which whole genome sequences are available is needed to understand the detailed characteristics of Pacific bluefin tuna chromosome structure and to estimate rearrangement events in the Perciformes lineage.

It was a surprising and new finding that medaka and Pacific bluefin tuna have similar chromosome constitutions, even though these two species are evolutionary distant in Percomorpha and differ morphologically and physiologically. This result suggests that other fish in Percomorpha may have a similar chromosome constitution and traces of inter-chromosomal changes. It is also possible that chromosome constitution does not always reflect phylogenetic distance based on other genetic factors, such as nucleotide or amino acid sequences. Several chromosome pairs and homologous sequence regions between tuna and medaka were in reverse orientation between these two species. Chromosome inversion may have occurred from ectopic recombination between homologous sequences or breakage of chromosomes and erroneous repair of free ends by non-homologous end-joining [49]. Genes at recombination breakpoints occasionally experience a fission or fusion event with other genes during chromosomal inversion, fusion, or translocation. Such a phenomenon has been explained as the mechanism of novel gene birth [49]. Thus, different genes are detected in these boundary regions of Pacific bluefin tuna and medaka.

Pacific bluefin tuna has high market value, but wild populations have decreased in recent years [1]. The complete lifecycle of this species has been closed for aquaculture, and artificial seed is being used for production [2]. Therefore, there is interest in creating brood stocks with commercially valuable traits, such as rapid growth. A genetic linkage map with many DNA markers is needed to efficiently find markers associated with quantitative trait loci (QTL) that can be used in marker-assisted selection breeding programs to genetically improve traits, such as disease resistance, high growth rate, and sex determination in Pacific bluefin tuna seed and seedlings.

QTL analyses [50] for specific traits have been performed in many fish including groups phylogenetically close to Pacific bluefin tuna in Percomorpha, such as two yellowtail species (*Seriola quinqueradiata* and *Seriola lalandi*) in Carangidae [37] [51] and Japanese flounder (*Paralichthys olivaceus*) and Atlantic halibut (*Hippoglossus hippoglossus*) in Pleuronectiformes [45] [52] [53]. In this study, we developed sex-specific linkage maps using a tuna draft genome sequence. The mean distances between two markers in the male and female maps were 2.7 cM and 3.7 cM, respectively. This marker density is sufficient to perform a rough QTL analysis [54]. The linkage map will be a useful resource for QTL analyses of economically useful traits in this species. Moreover, it could be used to elucidate the genetic basis of the ecologically unique traits of Pacific bluefin tuna. Integrated sequence information from the linkage maps will help identify responsible genes in candidate regions detectable by QTL analysis.

Acknowledgements

References

[1] Masuma, S., Takebe, T. and Sakakura, Y. (2011) A Review of the Broodstock Management and Larviculture of the Pacific Northern Bluefin Tuna in Japan. *Aquaculture*, **315**, 2-8. http://dx.doi.org/10.1016/j.aquaculture.2010.05.030

[2] Sawada, Y., Okada, T., Miyashita, S., Murata, O. and Kumai, H. (2005) Completion of the Pacific Bluefin Tuna *Thunnus orientalis* (Temminck et Schlegel) Life Cycle. *Aquaculture Research*, **36**, 413-421. http://dx.doi.org/10.1111/j.1365-2109.2005.01222.x

[3] Howe, K., Clark, M.D., Torroja, C.F., Torrance, J., Berthelot, C., Muffato, M., Collins, J.E.J., Humphray, S., McLaren, K., Matthews, L., McLaren, S., Sealy, I., Caccamo, M., Churcher, C., Scott, C., Barrett, J.C., Koch, R., Rauch, G.-J., White, S., Chow, W., Kilian, B., Quintais, L.T., Guerra-Assunção, J.A., Zhou, Y., Gu, Y., Yen, J., Vogel, J.-H., Eyre, T., Redmond, S., Banerjee, R., Chi, J., Fu, B., Langley, E., Maguire, S.F., Laird, G.K., Lloyd, D., Kenyon, E., Donaldson, S., Sehra, H., Almeida-King, J., Loveland, J., Trevanion, S., Jones, M., Quail, M., Willey, D., Hunt, A., Burton, J., Sims, S., McLay, K., Plumb, B., Davis, J., Clee, C., Oliver, K., Clark, R., Riddle, C., Elliot, D., Eliott, D., Threadgold, G., Harden, G., Ware, D., Mortimore, B., Mortimer, B., Kerry, G., Heath, P., Phillimore, B., Tracey, A., Corby, N., Dunn, M., Johnson, C., Wood, J., Clark, S., Pelan, S., Griffiths, G., Smith, M., Glithero, R., Howden, P., Barker, N., Stevens, C., Harley, J., Holt, K., Panagiotidis, G., Lovell, J., Beasley, H., Henderson, C., Gordon, D., Auger, K., Wright, D., Raisen, C., Dyer, L., Leung, K., Robertson, L., Ambridge, K., Leongamornlert, D., McGuire, S., Gilderthorp, R., Griffiths, C., Manthravadi, D., Nichol, S., Barker, G., Whitehead, S., Kay, M., Brown, J., Murnane, C., Gray, E., Humphries, M., Sycamore, N., Barker, D., Saunders, D., Wallis, J., Babbage, A., Hammond, S., Mashreghi-Mohammadi, M., Barr, L., Martin, S., Wray, P., Ellington, A., Matthews, N., Ellwood, M., Woodmansey, R., Clark, G., Cooper, J.D., Tromans, A., Grafham, D., Skuce, C., Pandian, R., Andrews, R., Harrison, E., Kimberley, A., Garnett, J., Fosker, N., Hall, R., Garner, P., Kelly, D., Bird, C., Palmer, S., Gehring, I., Berger, A., Dooley, C.M., Ersan-Ürün, Z., Eser, C., Geiger, H., Geisler, M., Karotki, L., Kirn, A., Konantz, J., Konantz, M., Oberländer, M., Rudolph-Geiger, S., Teucke, M., Osoegawa, K., Zhu, B., Rapp, A., Widaa, S., Langford, C., Yang, F., Carter, N.P., Harrow, J., Ning, Z., Herrero, J., Searle, S.M.J., Enright, A., Geisler, R., Plasterk, R.H.A., Lee, C., Westerfield, M., de Jong, P.J., Zon, L.I., Postlethwait, J.H., Nüsslein-Volhard, C., Hubbard, T.J.P., Roest Crollius, H., Rogers, J., Stemple, D.L., Begum, S., Lloyd, C., Lanz, C., Raddatz, G. and Schuster, S.C. (2013) The Zebrafish Reference Genome Sequence and Its Relationship to the Human Genome. *Nature*, **496**, 498-503.

[4] Kasahara, M., Naruse, K., Sasaki, S., Nakatani, Y., Qu, W., Ahsan, B., Yamada, T., Nagayasu, Y., Doi, K., Kasai, Y., Jindo, T., Kobayashi, D., Shimada, A., Toyoda, A., Kuroki, Y., Fujiyama, A., Sasaki, T., Shimizu, A., Asakawa, S., Shimizu, N., Hashimoto, S.-I., Yang, J., Lee, Y., Matsushima, K., Sugano, S., Sakaizumi, M., Narita, T., Ohishi, K., Haga, S., Ohta, F., Nomoto, H., Nogata, K., Morishita, T., Endo, T., Shin-I, T., Takeda, H., Morishita, S. and Kohara, Y. (2007) The Medaka Draft Genome and Insights into Vertebrate Genome Evolution. *Nature*, **447**, 714-719. http://dx.doi.org/10.1038/nature05846

[5] Aparicio, S., Chapman, J., Stupka, E., Putnam, N., Chia, J.-M., Dehal, P., Christoffels, A., Rash, S., Hoon, S., Smit, A., Gelpke, M.D.S., Roach, J., Oh, T., Ho, I.Y., Wong, M., Detter, C., Verhoef, F., Predki, P., Tay, A., Lucas, S., Richardson, P., Smith, S.F., Clark, M.S., Edwards, Y.J.K., Doggett, N., Zharkikh, A., Tavtigian, S.V., Pruss, D., Barnstead, M., Evans, C., Baden, H., Powell, J., Glusman, G., Rowen, L., Hood, L., Tan, Y.H., Elgar, G., Hawkins, T., Venkatesh, B., Rokhsar, D. and Brenner, S. (2002) Whole-Genome Shotgun Assembly and Analysis of the Genome of *Fugu rubripes*. *Science* (New York, N.Y.), **297**, 1301-1310.

[6] Jaillon, O., Aury, J.-M., Brunet, F., Petit, J.-L., Stange-Thomann, N., Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A., Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C., Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N., Castellano, S., Anthouard, V., Jubin, C., Castelli, V., Katinka, M., Vacherie, B., Biémont, C., Skalli, Z., Cattolico, L., Poulain, J., De Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Coutanceau, J.-P., Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., McEwan, P., Bosak, S., Kellis, M., Volff, J.-N., Guigó, R., Zody, M. C., Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D., Robinson-Rechavi, M., Laudet, V., Schachter, V., Quétier, F., Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissenbach, J. and Roest Crollius, H. (2004) Genome Duplication in the Teleost Fish *Tetraodon nigroviridis* Reveals the Early Vertebrate Proto-Karyotype. *Nature*, **431**, 946-957. http://dx.doi.org/10.1038/nature03025

[7] Jones, F.C., Grabherr, M.G., Chan, Y.F., Russell, P., Mauceli, E., Johnson, J., Swofford, R., Pirun, M., Zody, M.C., White, S., Birney, E., Searle, S., Schmutz, J., Grimwood, J., Dickson, M.C., Myers, R.M., Miller, C.T., Summers, B.R., Knecht, A.K., Brady, S.D., Zhang, H., Pollen, A.A., Howes, T., Amemiya, C., Baldwin, J., Bloom, T., Jaffe, D.B., Nicol, R., Wilkinson, J., Lander, E.S., Di Palma, F., Lindblad-Toh, K. and Kingsley, D.M. (2012) The Genomic Basis of Adaptive Evolution in Three Spine Sticklebacks. *Nature*, **484**, 55-61. http://dx.doi.org/10.1038/nature10944

[8] Nakamura, Y., Mori, K., Saitoh, K., Oshima, K., Mekuchi, M., Sugaya, T., Shigenobu, Y., Ojima, N., Muta, S., Fujiwara, A., Yasuike, M., Oohara, I., Hirakawa, H., Chowdhury, V.S., Kobayashi, T., Nakajima, K., Sano, M., Wada, T., Tashiro, K., Ikeo, K., Hattori, M., Kuhara, S., Gojobori, T. and Inouye, K. (2013) Evolutionary Changes of Multiple Visual Pigment Genes in the Complete Genome of Pacific Bluefin Tuna. *Proceedings of the National Academy of Sciences of the United States of America*, **110**, 11061-11066. http://dx.doi.org/10.1073/pnas.1302051110

[9] Ida, H., Oka, N. and Hayashigaki, K. (1991) Karyotypes and Cellular DNA Contents of Three Species of the Subfamily Clupeinae. *Japanese Journal of Ichthyology*, **38**, 289-294.

[10] Soares, R.X., Bertollo, L.A.C., Costa, G.W.W.F. and Molina, W.F. (2013) Karyotype Stasis in Four Atlantic Scombridae Fishes: Mapping of Classic and Dual-Color FISH Markers on Chromosomes. *Fisheries Science*, **79**, 177-183. http://dx.doi.org/10.1007/s12562-013-0602-0

[11] Kai, W., Kikuchi, K., Fujita, M., Suetake, H., Fujiwara, A., Yoshiura, Y., Ototake, M., Venkatesh, B., Miyaki, K. and Suzuki, Y. (2005) A Genetic Linkage Map for the Tiger Puffer Fish, *Takifugu rubripes*. *Genetics*, **171**, 227-238. http://dx.doi.org/10.1534/genetics.105.042051

[12] Kai, W., Kikuchi, K., Tohari, S., Chew, A.K., Tay, A., Fujiwara, A., Hosoya, S., Suetake, H., Naruse, K., Brenner, S., Suzuki, Y. and Venkatesh, B. (2011) Integration of the Genetic Map and Genome Assembly of fugu Facilitates Insights into Distinct Features of Genome Evolution in Teleosts and Mammals. *Genome Biology and Evolution*, **3**, 424-442. http://dx.doi.org/10.1093/gbe/evr041

[13] Sato, S., Nakamura, Y., Kaneko, T., Asamizu, E., Kato, T., Nakao, M., Sasamoto, S., Watanabe, A., Ono, A., Kawashima, K., Fujishiro, T., Katoh, M., Kohara, M., Kishida, Y., Minami, C., Nakayama, S., Nakazaki, N., Shimizu, Y., Shinpo, S., Takahashi, C., Wada, T., Yamada, M., Ohmido, N., Hayashi, M., Fukui, K., Baba, T., Nakamichi, T., Mori, H. and Tabata, S. (2008) Genome Structure of the Legume, *Lotus japonicas*. *DNA Research*, **15**, 227-239. http://dx.doi.org/10.1093/dnares/dsn008

[14] Ren, Y., Zhao, H., Kou, Q., Jiang, J., Guo, S., Zhang, H., Hou, W., Zou, X., Sun, H., Gong, G., Levi, A. and Xu, Y. (2012) A High Resolution Genetic Map Anchoring Scaffolds of the Sequenced Watermelon Genome. *PloS One*, **7**, e29453. http://dx.doi.org/10.1371/journal.pone.0029453

[15] Yang, H., Tao, Y., Zheng, Z., Zhang, Q., Zhou, G., Sweetingham, M.W., Howieson, J.G. and Li, C. (2013) Draft Genome Sequence, and a Sequence-Defined Genetic Linkage Map of the Legume Crop Species *Lupinus angustifolius* L. *PloS One*, **8**, e64799.

[16] Ma, X.-F., Jensen, E., Alexandrov, N., Troukhan, M., Zhang, L., Thomas-Jones, S., Farrar, K., Clifton-Brown, J., Donnison, I., Swaller, T. and Flavell, R. (2012) High Resolution Genetic Mapping by Genome Sequencing Reveals Genome Duplication and Tetraploid Genetic Structure of the Diploid *Miscanthus sinensis*. *PloS One*, **7**, e33821. http://dx.doi.org/10.1371/journal.pone.0033821

[17] Wong, A.K., Ruhe, A.L., Dumont, B.L., Robertson, K.R., Guerrero, G., Shull, S.M., Ziegle, J.S., Millon, L.V., Broman, K.W., Payseur, B.A. and Neff, M.W. (2010) A Comprehensive Linkage Map of the Dog Genome. *Genetics*, **184**, 595-605. http://dx.doi.org/10.1534/genetics.109.106831

[18] Morishima, K., Yamamoto, H., Sawada, Y., Miyashita, S. and Kato, K. (2009) Developing 23 New Polymorphic Microsatellite Markers and Simulating Parentage Assignment in the Pacific Bluefin Tuna, *Thunnus orientalis*. *Molecular Ecology Resources*, **9**, 790-792. http://dx.doi.org/10.1111/j.1755-0998.2008.02144.x

[19] Hattori, R.S., Murai, Y., Oura, M., Masuda, S., Majhi, S.K., Sakamoto, T., Fernandino, J.I., Somoza, G.M., Yokota, M. and Strussmann, C.A. (2012) A Y-Linked Anti-Mullerian Hormone Duplication Takes over a Critical Role in Sex Determination. *Proceedings of the National Academy of Sciences*, **109**, 2955-2959. http://dx.doi.org/10.1073/pnas.1018392109

[20] Myosho, T., Otake, H., Masuyama, H., Matsuda, M., Kuroki, Y., Fujiyama, A., Naruse, K., Hamaguchi, S. and Sakai-

zumi, M. (2012) Tracing the Emergence of a Novel Sex-Determining Gene in Medaka, *Oryzias luzonensis*. *Genetics*, **191**, 163-170. http://dx.doi.org/10.1534/genetics.111.137497

[21] Kamiya, T., Kai, W., Tasumi, S., Oka, A., Matsunaga, T., Mizuno, N., Fujita, M., Suetake, H., Suzuki, S., Hosoya, S., Tohari, S., Brenner, S., Miyadai, T., Venkatesh, B., Suzuki, Y. and Kikuchi, K. (2012) A Trans-Species Missense SNP in Amhr2 Is Associated with Sex Determination in the Tiger Pufferfish, *Takifugu rubripes* (Fugu). *PLoS Genetics*, **8**, e1002798. http://dx.doi.org/10.1371/journal.pgen.1002798

[22] Yano, A., Nicol, B., Jouanno, E., Quillet, E., Fostier, A., Guyomard, R. and Guiguen, Y. (2013) The Sexually Dimorphic on the Y-Chromosome Gene (sdY) Is a Conserved Male-Specific Y-Chromosome Sequence in Many Salmonids. *Evolutionary Applications*, **6**, 486-496. http://dx.doi.org/10.1111/eva.12032

[23] Kikuchi, K. and Hamaguchi, S. (2013) Novel Sex-Determining Genes in Fish and Sex Chromosome Evolution. *Developmental Dynamics*, **242**, 339-353. http://dx.doi.org/10.1002/dvdy.23927

[24] Agawa, Y., Iwaki, M., Komiya, T., Honryo, T., Tamura, K., Okada, T., Yagishita, N., Kobayashi, T. and Sawada, Y. (2014) Identification of Male Sex-Linked DNA Sequence of the Cultured Pacific Bluefin Tuna *Thunnus orientalis*. *Fisheries Science*, **81**, 113-121. http://dx.doi.org/10.1007/s12562-014-0833-8

[25] Naruse, K., Tanaka, M., Mita, K., Shima, A., Postlethwait, J. and Mitani, H. (2004) A Medaka Gene Map: The Trace of Ancestral Vertebrate Proto-Chromosomes Revealed by Comparative Gene Mapping. *Genome Research*, **14**, 820-828. http://dx.doi.org/10.1101/gr.2004004

[26] Chen, S., Zhang, G., Shao, C., Huang, Q., Liu, G., Zhang, P., Song, W., An, N., Chalopin, D., Volff, J.-N., Hong, Y., Li, Q., Sha, Z., Zhou, H., Xie, M., Yu, Q., Liu, Y., Xiang, H., Wang, N., Wu, K., Yang, C., Zhou, Q., Liao, X., Yang, L., Hu, Q., Zhang, J., Meng, L., Jin, L., Tian, Y., Lian, J., Yang, J., Miao, G., Liu, S., Liang, Z., Yan, F., Li, Y., Sun, B., Zhang, H., Zhang, J., Zhu, Y., Du, M., Zhao, Y., Schartl, M., Tang, Q. and Wang, J. (2014) Whole-Genome Sequence of A Flatfish Provides Insights into ZW Sex Chromosome Evolution and Adaptation to a Benthic Lifestyle. *Nature Genetics*, **46**, 253-260. http://dx.doi.org/10.1038/ng.2890

[27] Amores, A., Catchen, J., Nanda, I., Warren, W., Walter, R., Schartl, M. and Postlethwait, J.H. (2014) A RAD-Tag Genetic Map for the Platyfish (*Xiphophorus maculatus*) Reveals Mechanisms of Karyotype Evolution among Teleost Fish. *Genetics*, **197**, 625-641. http://dx.doi.org/10.1534/genetics.114.164293

[28] Kawahara, R., Miya, M., Mabuchi, K., Lavoué, S., Inoue, J.G., Satoh, T.P., Kawaguchi, A. and Nishida, M. (2008) Interrelationships of the 11 Gasterosteiform Families (Sticklebacks, Pipefishes, and Their Relatives): A New Perspective Based on Whole Mitogenome Sequences from 75 Higher Teleosts. *Molecular Phylogenetics and Evolution*, **46**, 224-236. http://dx.doi.org/10.1016/j.ympev.2007.07.009

[29] Setiamarga, D.H.E., Miya, M., Yamanoue, Y., Mabuchi, K., Satoh, T.P., Inoue, J.G. and Nishida, M. (2008) In Terrelationships of Atherinomorpha (Medakas, Flyingfishes, Killifishes, Silversides, and Their Relatives): The First Evidence Based on Whole Mitogenome Sequences. *Molecular Phylogenetics and Evolution*, **49**, 598-605. http://dx.doi.org/10.1016/j.ympev.2008.08.008

[30] Sekino, M. and Kakehi, S. (2011) PARFEX v1.0: An EXCEL^{TM}-Based Software Package for Parentage Allocation. *Conservation Genetics Resources*, **4**, 275-278. http://dx.doi.org/10.1007/s12686-011-9523-3

[31] Untergasser, A., Cutcutache, I., Koressaar, T., Ye, J., Faircloth, B.C., Remm, M. and Rozen, S.G. (2012) Primer3—New Capabilities and Interfaces. *Nucleic Acids Research*, **40**, e115. http://dx.doi.org/10.1093/nar/gks596

[32] Blacket, M.J., Robin, C., Good, R.T., Lee, S.F. and Miller, A.D. (2012) Universal Primers for Fluorescent Label Ling of PCR Fragments—An Efficient and Cost-Effective Approach to Genotyping by Fluorescence. *Molecular Ecology Resources*, **12**, 456-463. http://dx.doi.org/10.1111/j.1755-0998.2011.03104.x

[33] Lorieux, M. (2012) MapDisto: Fast and Efficient Computation of Genetic Linkage Maps. *Molecular Breeding*, **30**, 1231-1235. http://dx.doi.org/10.1007/s11032-012-9706-y

[34] Chakravarti, A., Lasher, L.K. and Reefer, J.E. (1991) A Maximum Likelihood Method for Estimating Genome Length Using Genetic Linkage Data. *Genetics*, **128**, 175-182.

[35] Edwards, J.H. (1991) The Oxford Grid. *Annals of Human Genetics*, **55**, 17-31. http://dx.doi.org/10.1111/j.1469-1809.1991.tb00394.x

[36] Fujiwara, A., Fujiwara, M., Nishida-Umehara, C., Abe, S. and Masaoka, T. (2007) Characterization of Japanese Flounder Karyotype by Chromosome Bandings and Fluorescence *in Situ* Hybridization with DNA Markers. *Genetica*, **131**, 267-274. http://dx.doi.org/10.1007/s10709-006-9136-z

[37] Ohara, E., Nishimura, T., Nagakura, Y., Sakamoto, T., Mushiake, K. and Okamoto, N. (2005) Genetic Linkage Maps of Two Yellowtails (*Seriola quinqueradiata* and *Seriola lalandi*). *Aquaculture*, **244**, 41-48. http://dx.doi.org/10.1016/j.aquaculture.2004.10.022

[38] Reid, D.P., Smith, C.-A., Rommens, M., Blanchard, B., Martin-Robichaud, D. and Reith, M. (2007) A Genetic Linkage Map of Atlantic Halibut (*Hippoglossus hippoglossus* L.). *Genetics*, **177**, 1193-1205.

http://dx.doi.org/10.1016/j.aquaculture.2004.10.022

[39] Castaño-Sánchez, C., Fuji, K., Ozaki, A., Hasegawa, O., Sakamoto, T., Morishima, K., Nakayama, I., Fujiwara, A., Masaoka, T., Okamoto, H., Hayashida, K., Tagami, M., Kawai, J., Hayashizaki, Y. and Okamoto, N. (2010) A Second Generation Genetic Linkage Map of Japanese Flounder (*Paralichthys olivaceus*). *BMC Genomics*, **11**, 554. http://dx.doi.org/10.1186/1471-2164-11-554

[40] Fuji, K., Koyama, T., Kai, W., Kubota, S., Yoshida, K., Ozaki, A., Aoki, J., Kawabata, Y., Araki, K., Tsuzaki, T., Okamoto, N. and Sakamoto, T. (2014) Construction of a High-Coverage Bacterial Artificial Chromosome Library and Comprehensive Genetic Linkage Map of Yellowtail *Seriola quinqueradiata*. *BMC Research Notes*, **7**, 200. http://dx.doi.org/10.1186/1756-0500-7-200

[41] Baird, N.A., Etter, P.D., Atwood, T.S., Currey, M.C., Shiver, A.L., Lewis, Z.A., Selker, E.U., Cresko, W.A. and Johnson, E.A. (2008) Rapid SNP Discovery and Genetic Mapping Using Sequenced RAD Markers. *PloS One*, **3**, e3376. http://dx.doi.org/10.1371/journal.pone.0003376

[42] Amores, A., Catchen, J., Ferrara, A., Fontenot, Q. and Postlethwait, J.H. (2011) Genome Evolution and Meiotic Maps by Massively Parallel DNA Sequencing: Spotted Gar, an Outgroup for the Teleost Genome Duplication. *Genetics*, **188**, 799-808. http://dx.doi.org/10.1534/genetics.111.127324

[43] Everett, M.V., Miller, M.R. and Seeb, J.E. (2012) Meiotic Maps of Sockeye Salmon Derived from Massively Parallel DNA Sequencing. *BMC Genomics*, **13**, 521. http://dx.doi.org/10.1186/1471-2164-13-521

[44] Kakioka, R., Kokita, T., Kumada, H., Watanabe, K. and Okuda, N. (2013) A RAD-Based Linkage Map and Comparative Genomics in the Gudgeons (Genus Gnathopogon, Cyprinidae). *BMC Genomics*, **14**, 32. http://dx.doi.org/10.1186/1471-2164-14-32

[45] Palaiokostas, C., Bekaert, M., Davie, A., Cowan, M.E., Oral, M., Taggart, J.B., Gharbi, K., McAndrew, B.J., Penman, D.J. and Migaud, H. (2013) Mapping the Sex Determination Locus in the Atlantic Halibut (*Hippoglossus hippoglossus*) Using RAD Sequencing. *BMC Genomics*, **14**, 566. http://dx.doi.org/10.1186/1471-2164-14-566

[46] Sakamoto, T., Danzmann, R.G., Gharbi, K., Howard, P., Ozaki, A., Khoo, S.K., Woram, R.A., Okamoto, N., Ferguson, M.M., Holm, L.E., Guyomard, R. and Hoyheim, B. (2000) A Microsatellite Linkage Map of Rainbow Trout (*Oncorhynchus mykiss*) Characterized by Large Sex-Specific Differences in Recombination Rates. *Genetics*, **155**, 1331-1345.

[47] Singer, A., Perlman, H., Yan, Y., Walker, C., Corley-Smith, G., Brandhorst, B. and Postlethwait, J. (2002) Sex-Specific Recombination Rates in Zebrafish (*Danio rerio*). *Genetics*, **160**, 649-657.

[48] Aoki, J.-Y., Kai, W., Kawabata, Y., Ozaki, A., Yoshida, K., Koyama, T., Sakamoto, T. and Araki, K. (2015) Second Generation Physical and Linkage Maps of Yellowtail (*Seriola quinqueradiata*) and Comparison of Synteny with Four Model Fish. *BMC Genomics*, **16**, 406. http://dx.doi.org/10.1186/s12864-015-1600-7

[49] Guillén, Y. and Ruiz, A. (2012) Gene Alterations at Drosophila Inversion Breakpoints Provide Prima Facie Evidence for Natural Selection as an Explanation for Rapid Chromosomal Evolution. *BMC Genomics*, **13**, 53. http://dx.doi.org/10.1186/1471-2164-13-53

[50] Yue, G.H. (2013) Recent Advances of Genome Mapping and Marker-Assisted Selection in Aquaculture. *Fish and Fisheries*, **15**, 376-396. http://dx.doi.org/10.1111/faf.12020

[51] Ozaki, A., Yoshida, K., Fuji, K., Kubota, S., Kai, W., Aoki, J., Kawabata, Y., Suzuki, J., Akita, K., Koyama, T., Nakagawa, M., Hotta, T., Tsuzaki, T., Okamoto, N., Araki, K. and Sakamoto, T. (2013) Quantitative Trait Loci (QTL) Associated with Resistance to a Monogenean Parasite (*Benedenia seriolae*) in Yellowtail (*Seriola quinqueradiata*) through Genome Wide Analysis. *PloS One*, **8**, e64987. http://dx.doi.org/10.1371/journal.pone.0064987

[52] Fuji, K., Kobayashi, K., Hasegawa, O., Coimbra, M.R.M., Sakamoto, T. and Okamoto, N. (2006) Identification of a Single Major Genetic Locus Controlling the Resistance to Lymphocystis Disease in Japanese Flounder (*Paralichthys olivaceus*). *Aquaculture*, **254**, 203-210. http://dx.doi.org/10.1016/j.aquaculture.2005.11.024

[53] Song, W., Pang, R., Niu, Y., Gao, F., Zhao, Y., Zhang, J., Sun, J., Shao, C., Liao, X., Wang, L., Tian, Y. and Chen, S. (2012) Construction of High-Density Genetic Linkage Maps and Mapping of Growth-Related Quantitative Trail Loci in the Japanese Flounder (*Paralichthys olivaceus*). *PloS One*, **7**, e50404. http://dx.doi.org/10.1371/journal.pone.0050404

[54] Broman, K.W. (1999) Review of Statistical Methods for QTL Mapping in Experimental Crosses. *Lab Animal*, **30**, 44-52.

Supplementary Figures and Tables

Table S1. The information of PCR primers used in this study. These primers are categorized as follows. A: used in parentage test. B: used in linkage mapping.

Category	Scaffold ID	Forward Primer ID	Forward Primer Sequences (5'-3')	Forward Primer Tm (°C)	Reverse Primer ID	Reverse Primer Sequences (5'-3')	Reverse Primer Tm (°C)	Expected Allele Size (bp)	MS Unit Size	Perfect or Imperfect	Simple Notation
B	Ba00002	00002_358935_F	tttgtcagtgggaaacaatctg	60.0	00002_358935_R	gtggtgtgtgtgtttgtacgtg	59.9	140	2	perfect	(CA)14
B	Ba00003	00003_495686_F	gtgtggaagcaacaagcaaata	60.2	00003_495686_R	tggatttgggtacaggtaaagg	60.1	321	2	perfect	(AC)36
B	Ba00004	00004_886445_F	agcatctgtgtctgcataatgg	60.2	00004_886445_R	cgacaatgtgacatgtttgttg	59.9	148	2	perfect	(CA)12
B	Ba00005	00005_610364_F	caaaggggattttagtctgctg	60.1	00005_610364_R	cttgccaaaaacctcgacttac	60.2	141	2	imperfect with gaps	(GT)16
B	Ba00006	00006_761447_F	gcaagcatatggcacatttaga	60.1	00006_761447_R	atcttgctcctcctcttcctct	60.0	130	2	imperfect with no gaps	(TG)42
B	Ba00007	00007_770851_F	gccccatatgtacatggagttt	60.0	00007_770851_R	gggcgttattctagtgatgtttg	59.9	185	2	perfect	(AC)21
B	Ba00008	00008_803992_F	catttggttttctttggtccat	60.1	00008_803992_R	tccaaaaccagaaaggacactt	60.0	128	2	imperfect with no gaps	(AC)15
B	Ba00009	00009_514635_F	tgtgcttcgtaaacacaacctc	60.2	00009_514635_R	gaggctgcaggatatgaatagg	60.1	111	2	imperfect with no gaps	(AC)21
B	Ba00010	00010_781278_F	ggtgaattcaattgccagtttag	59.9	00010_781278_R	ccattacttacttctcgcccag	60.1	106	2	perfect	(CA)14
B	Ba00011	00011_657238_F	atcacgtttatttagccccgaga	60.0	00011_657238_R	atgagaccgttaacattttgcc	60.2	141	2	perfect	(AC)16
B	Ba00013	00013_638192_F	tgacctcttcccaatggactat	59.8	00013_638192_R	gctcagtctctggtttcctgtc	60.4	142	2	imperfect with no gaps	(AC)19
B	Ba00014	00014_385141_F	gattccacatggtcagcttgta	60.0	00014_385141_R	ctccaaaaggaaagtcaaccac	60.0	139	2	perfect	(CA)22
B	Ba00015	00015_721830_F	aagcgctactttcaggtgagtc	60.1	00015_721830_R	ctcactactcccacctggagat	59.6	138	2	perfect	(CA)13
B	Ba00016	00016_658769_F	tttaatttgtcacccgtctgtg	59.9	00016_658769_R	catgtctccatattttccgtga	59.8	121	2	perfect	(AC)13
B	Ba00017	00017_135995_F	cactgttgctctgggtaaaggt	60.6	00017_135995_R	ccgggtttgatatattgtgctt	60.1	150	2	perfect	(TG)16
B	Ba00018	00018_365575_F	ttcagttatgggtctgggctat	59.9	00018_365575_R	ctgaaacatgtatggttgtggg	60.2	143	2	perfect	(AC)15
B	Ba00019	00019_259174_F	gagtgatggcctggatagactc	60.1	00019_259174_R	gtctgcctgtctgtctgttcac	60.0	123	2	imperfect with no gaps	(CA)25
B	Ba00020	00020_291940_F	tagcatatttgtattcgggcac	59.0	00020_291940_R	ccctgaagtcagtcaaggtaca	59.3	116	2	perfect	(AC)17
B	Ba00021	00021_81471_F	cttgtggatggcacagagatag	59.8	00021_81471_R	caagtcacgcataaaaaccaga	60.2	140	2	imperfect with no gaps	(TG)24
A	Ba00022	03538_117_F	tgatgttttcacagagaaccaga	59.8	03538_117_R	cggttcaggtatgtcagagtga	60.2	177	2	perfect	(TG)13
B	Ba00022	00022_661885_F	agataccgcagggattatctga	60.0	00022_661885_R	aaaataaaaatcagcccacacg	60.2	146	2	imperfect with gaps	(TG)25
B	Ba00023	00023_682414_F	tgtccaatatagcaagcagtgg	60.2	00023_682414_R	gctgtggtatttacatttgcga	60.0	135	2	imperfect with gaps	(TC)22
B	Ba00026	00026_267152_F	acagcccctattcacaatgagt	59.9	00026_267152_R	gtgagccttcacaaacaacaag	59.8	107	2	imperfect with gaps	(TG)32
B	Ba00027	00027_603499_F	tctgacaccaccatatagcacc	59.9	00027_603499_R	tggagacgacgatcctaatgta	59.6	400	2	perfect	(CA)21
B	Ba00028	00028_464941_F	aaactgtgggacatgttctttt	57.6	00028_464941_R	cagaaacacaaccctaaccctc	59.9	201	2	perfect	(CA)21
B	Ba00029	00029_643815_F	tgtgtgtgtgtgaatgtgtgtg	60.0	00029_643815_R	taatccctcgagacgtgaattt	60.0	102	2	perfect	(TG)15
B	Ba00030	00030_319912_F	ttgtccctggagaaaagtgttt	60.0	00030_319912_R	acatgggaacacataggacaca	60.2	128	2	perfect	(TG)21
B	Ba00031	00031_368460_F	ttcctctgtgtgaactgaagcaga	60.2	00031_368460_R	gagatgaggcagaacatctgtg	59.9	101	2	imperfect with no gaps	(AC)21
B	Ba00032	00032_435309_F	gccagaggaaaagacagagaaa	60.0	00032_435309_R	tcaggtaggacagctcacaaaa	59.9	103	2	perfect	(GT)14

Continued

B	Ba00033	00033_575768_F	gcgaggaaccttcagttcatac	60.1	00033_575768_R	tgcagtgtctcaattttgctct	60.1	129	2	perfect	(AC)20
B	Ba00034	00034_183287_F	aattgccagttgaagtgtgtgt	59.6	00034_183287_R	gacatgtacctttgttctggca	60.0	131	2	perfect	(TG)22
B	Ba00035	00035_115704_F	gcagagtttcatacatggtgga	60.0	00035_115704_R	gtcatgggaaaatgaagcaaat	60.2	125	2	perfect	(GT)19
B	Ba00036	00036_456502_F	tggaaagttgttgttatgcacc	59.9	00036_456502_R	aaaacaaccaaaccaaccaaac	60.0	110	2	perfect	(GT)20
B	Ba00038	00038_356123_F	caaatagccagacagacagcac	59.9	00038_356123_R	actgacagacagaccagacagg	59.4	147	2	imperfect with no gaps	(TG)24
B	Ba00039	00039_394087_F	ggaggatgaggtgttgctctac	60.1	00039_394087_R	tagttgaaggcgtcatgacatt	59.6	109	2	perfect	(AC)18
B	Ba00040	00040_154055_F	gcatctacctcctcttttggaa	59.7	00040_154055_R	ccctcaaagcaaattttgaac	60.0	101	2	perfect	(TG)13
B	Ba00041	00041_262465_F	aactttgacttgatgatggcg	60.1	00041_262465_R	ttgacagctatgggatgtgttc	60.0	146	2	imperfect with no gaps	(AT)19
B	Ba00042	00042_205845_F	aagtgatggaaacacgactgtg	60.1	00042_205845_R	tgtatgctgactccccatagtg	60.0	137	2	imperfect with no gaps	(GT)16
B	Ba00044	00044_557436_F	tgctggatgggataagaagttt	60.0	00044_557436_R	tattccagaggcatcttcagtg	59.3	145	2	perfect	(GT)19
B	Ba00045	00045_218346_F	agcatttagcaagtgaagcaaa	59.2	00045_218346_R	caaattctctctctcctcagcc	59.6	397	2	perfect	(TG)45
B	Ba00046	00046_354953_F	actgtctgctcctgtcgtaaca	60.0	00046_354953_R	cccctctttgctcttaatctga	59.9	366	2	perfect	(CA)17
B	Ba00047	00047_153600_F	ctctctcctcctccttgtgtgt	59.9	00047_153600_R	attttccctctgtgttggtttg	60.3	234	2	perfect	(GA)22
B	Ba00048	00048_150402_F	cagtctctggctctgtcaaa	59.8	00048_150402_R	caggagacaaatctgaccttcc	60.1	145	2	imperfect with no gaps	(AC)18
B	Ba00049	00049_329914_F	cttgcagacatctctctccctt	60.0	00049_329914_R	gaatgccaatgcaaaagtgtaa	60.0	130	2	imperfect with gaps	(TG)30
B	Ba00050	00050_328297_F	tctgctcctgttcatgtctgat	59.9	00050_328297_R	gcctgtaatgcttcatttaggg	60.0	148	2	imperfect with no gaps	(TG)29
B	Ba00051	00051_211304_F	gcatgtccaatattcagctcag	59.7	00051_211304_R	attgatttgtgtggaaaaggct	59.9	294	2	perfect	(TG)18
B	Ba00052	00052_385529_F	gccgttagcatggctaaaatac	60.0	00052_385529_R	tcatcactgagccagacagagt	60.1	137	2	imperfect with no gaps	(AC)24
B	Ba00053	00053_380153_F	gtctttctgtctgggtttgtcc	60.0	00053_380153_R	aagcacatgtttttctccctgt	60.0	126	2	imperfect with no gaps	(CA)20
B	Ba00054	00054_476399_F	ggggacttcagtcattctgttc	60.0	00054_476399_R	gttattagaaagcatgcagggc	60.1	285	2	perfect	(AC)14
B	Ba00055	00055_557397_F	cacctggtaagtgttaaagggg	59.8	00055_557397_R	gaacagcttgctgtgcataatc	59.9	122	2	perfect	(GT)14
B	Ba00056	00056_277475_F	cagatgccaaaccaactctgta	60.2	00056_277475_R	tgcaacagctagcattcttcat	60.1	146	2	perfect	(TG)17
B	Ba00057	00057_560819_F	cacgtcacaggctatttgtcat	60.1	00057_560819_R	taaagaaggaccaaaaggacca	60.0	138	2	imperfect with no gaps	(TG)19
B	Ba00058	00058_544515_F	gcaagagcaggtagtgtttcaa	59.6	00058_544515_R	gcatatgctcagaagagagtgc	59.3	121	2	imperfect with no gaps	(CA)29
B	Ba00059	00059_177790_F	ggtacaccctgcagttttgaat	60.3	00059_177790_R	tggctgttaaatagctccctgt	60.2	330	2	perfect	(AC)30
B	Ba00060	00060_449308_F	cacatggtcaaacgttttctgt	59.9	00060_449308_R	taaacgtctcaacaggatgtgg	60.0	117	2	perfect	(TG)13
B	Ba00061	00061_227060_F	ggaagcagtgtgactgtgaaag	60.0	00061_227060_R	ggttctaaggcctaatgctgaa	59.8	118	2	imperfect with no gaps	(TG)18
B	Ba00062	00062_36778_F	ttcaagggcaataaagtgtgtg	60.0	00062_36778_R	ttctcgttctcttctctcccctg	60.0	243	2	imperfect with no gaps	(TG)29
B	Ba00063	00063_195848_F	cttgcacagtggaaatccataa	60.0	00063_195848_R	tttactgtgtttaatgcacccg	59.9	128	2	imperfect with gaps	(GT)24
B	Ba00065	00065_349693_F	cttgcagcaacagagatacacc	59.9	00065_349693_R	cactgctgattttatgcttcg	59.9	150	2	imperfect with no gaps	(CA)19
B	Ba00066	00066_257637_F	atctgggtccagcaaatatcac	60.2	00066_257637_R	ctcttggcttatcgtgacctct	59.9	106	2	imperfect with no gaps	(TG)18

Continued

B	Ba00067	00067_289897_F	catccagcttattggtgcatta	60.0	00067_289897_R	agagcaggaatcaaaattggaa	60.1	196	2	perfect	(AC)22
B	Ba00068	00068_46927_F	ctttcatttcccaagaaacgtc	60.0	00068_46927_R	agtcagtgataggtgttggcct	60.1	309	2	imperfect with no gaps	(CA)25
B	Ba00069	00069_102016_F	ttttcctggtaaattcaccctc	59.4	00069_102016_R	ttcacactgttggtttctgtcc	60.1	127	2	imperfect with no gaps	(CA)15
B	Ba00070	00070_316720_F	ctgtggtgtttgtacgtcaggt	60.0	00070_316720_R	aaacggacacagctgagaaaat	60.2	307	2	perfect	(TA)19
B	Ba00072	00072_331722_F	ggaggaaccataattgtccgta	60.1	00072_331722_R	cacagtgataacaaccctttgc	59.5	117	2	Imperfect with gaps	(AC)15
B	Ba00074	00074_240980_F	ggaaagtcagctcaggagaaaa	60.0	00074_240980_R	aaatacagacacccaaacagca	59.5	146	2	imperfect with no gaps	(GT)20
B	Ba00075	00075_95644_F	ctgttgatgactggagaaggct	60.8	00075_95644_R	cactcactcactcgcacacata	60.0	129	2	imperfect with no gaps	(TG)19
B	Ba00076	00076_171876_F	agaatatttctgtccctgccaa	60.0	00076_171876_R	gttgggtataaatgcctggtgt	60.0	140	2	perfect	(AC)13
B	Ba00077	00077_231443_F	cctcagttcagcctctgtctct	60.2	00077_231443_R	tcatatacctgcttacaaccgc	59.2	112	2	perfect	(GT)13
B	Ba00078	00078_132497_F	aatgattgtctaggccacatcc	60.2	00078_132497_R	caggggtctaaacctcacactc	60.0	122	2	imperfect with no gaps	(TG)20
B	Ba00079	00079_517200_F	ggtttgcatttggctattcttc	60.0	00079_517200_R	ttgcaacatgtgattgaaacaa	60.0	128	2	imperfect with no gaps	(TG)16
B	Ba00080	00080_298907_F	tgcacgtgatattttgatgatg	59.5	00080_298907_R	ctgatgttgagaacagaggctg	60.1	144	2	perfect	(GT)16
B	Ba00082	00082_412469_F	ccacactgactgactggatgat	60.0	00082_412469_R	atttcctttacctgcaatcctg	59.5	148	2	perfect	(CA)16
B	Ba00083	00083_506654_F	tttctggtgtactgaaacggtg	60.1	00083_506654_R	tgtcactttagccctgccttat	60.2	316	2	perfect	(CA)23
B	Ba00084	00084_322090_F	aggattgtgtgcaccataactg	59.9	00084_322090_R	tgatctcactcacagatacagca	58.5	121	2	perfect	(TG)18
B	Ba00085	00085_363474_F	atctcctctaggagctgtgtgc	60.1	00085_363474_R	gcggaaaatacagagtggaatc	60.0	135	4	perfect	(AGAC)7
B	Ba00086	00086_310160_F	caggacttacaatccctcttgc	60.1	00086_310160_R	caacaatgcatttctctctcca	60.3	147	2	imperfect with no gaps	(CA)33
B	Ba00087	00087_101769_F	tccgacaacttaaaattggctt	60.0	00087_101769_R	catgcaggtcagcatagttgat	60.2	163	2	perfect	(TG)21
B	Ba00089	00089_38868_F	ctgtttcaatattgccctgaca	60.0	00089_38868_R	agtccagtctcccaaaatgtgt	59.9	138	2	perfect	(CA)19
B	Ba00090	00090_474748_F	ctgtctttgagggaagcaaaat	59.8	00090_474748_R	ctgcagacaagacacacaaaca	60.0	126	2	imperfect with no gaps	(TG)15
B	Ba00091	00091_276727_F	cccagtgagaaggctaaggtaa	59.8	00091_276727_R	atcattcacagacgatgtttgc	60.0	116	2	perfect	(GT)14
B	Ba00093	00093_24283_F	agtatccagattgccaaattgc	60.3	00093_24283_R	attttattaggcttcctggggga	60.2	148	2	imperfect with gaps	(TG)21
B	Ba00094	00094_323057_F	cacattgcaacttatgcacaga	59.8	00094_323057_R	aatcagttgctcaatgctgaga	60.0	141	2	perfect	(AC)15
B	Ba00095	00095_365782_F	gtacccattaggctgtagtggc	59.9	00095_365782_R	aaaacaattgacaccaaccaca	60.2	117	4	imperfect with no gaps	(TTTG)9
B	Ba00096	00096_85218_F	ttctgtctctgctcttgtttgc	59.8	00096_85218_R	gctgagttgccatcacattaaa	60.1	121	2	perfect	(TG)12
B	Ba00097	00097_394083_F	tcaaggacaagagtgtgtgcat	60.8	00097_394083_R	tccaaggtcctactgtccatct	60.0	121	2	imperfect with no gaps	(TG)18
B	Ba00098	00098_401184_F	ggcaaggactctctgtctgtct	60.1	00098_401184_R	aacaatacggtcaccaagtgtg	59.8	142	4	imperfect with no gaps	(TATG)9
B	Ba00099	00099_435286_F	gtgtcaaaccctcaaggaaaac	59.9	00099_435286_R	cacatggctcttttcctctct	59.9	141	2	imperfect with no gaps	(GT)21
B	Ba00100	00100_205743_F	cccaggcagtgtattgtgagt	60.0	00100_205743_R	ataagcagcatgagtgaaggtg	59.4	132	2	imperfect with gaps	(TG)28
B	Ba00101	00101_439063_F	gcaagtatgttggagctctgtg	59.9	00101_439063_R	agcagtaaaagtggaaatgcc	59.7	140	2	imperfect with no gaps	(TG)17
B	Ba00103	00103_228054_F	atgcagtatgacaaggtcatgg	59.9	00103_228054_R	ttaagtcaggtgtgtgtccctg	60.1	167	2	perfect	(TG)18

Continued

B	Ba00104	00104_395600_F	aaatttgggccctatttgaatc	60.4	00104_395600_R	gctaatgttgtcatgctgcact	60.3	120	2	imperfect with gaps	(TG)15
B	Ba00105	00105_119773_F	tcacccagttatttgtcccttt	59.7	00105_119773_R	ggacaagatttgcagtgtgtgt	60.1	146	2	imperfect with no gaps	(AC)17
B	Ba00106	00106_187871_F	cgacaagaagctaaacccactt	59.8	00106_187871_R	aggcctagagatatcgcatctg	59.9	119	2	perfect	(GT)12
B	Ba00108	00108_370173_F	cttctgcttttcatgcttgtg	60.1	00108_370173_R	aagttgggggtgaaaaagtgta	59.8	119	2	imperfect with no gaps	(GT)20
B	Ba00109	00109_128874_F	tgctgttggctgctacactact	60.1	00109_128874_R	ctttgtcacagcttgtcctgtc	60.0	150	2	perfect	(CA)26
B	Ba00110	00110_99146_F	ccgtcgtgtagtgttgtccata	60.9	00110_99146_R	aggatactactaccaccgctgc	59.7	104	2	perfect	(TG)22
B	Ba00111	00111_291702_F	tttaaggggaaagacaaatcctc	59.8	00111_291702_R	gtttgctgaaagaaggaaaacg	60.3	114	2	perfect	(AC)20
B	Ba00112	00112_219640_F	tcagatgagagatgcagagagc	59.9	00112_219640_R	aatgatggggttaaatttgtgc	60.0	128	2	perfect	(AC)14
B	Ba00113	00113_423636_F	ttcttgcgctttatttctcaca	60.0	00113_423636_R	gtccccaaaggtgacctaagtt	60.6	104	2	perfect	(CA)17
B	Ba00114	00114_369105_F	tctgtagactgagctggtggaa	60.1	00114_369105_R	tgctcaactgcagacttgtttt	60.1	123	2	perfect	(CA)16
B	Ba00115	00115_267973_F	atctcgacaaatgatgatgctg	60.1	00115_267973_R	ggtccaagtgtgtctgtgtgtt	60.0	119	2	perfect	(AC)16
B	Ba00116	00116_417144_F	ttacattgctgctgtgtgtgaa	60.4	00116_417144_R	cacacatcacatcttgcatctg	60.2	138	2	imperfect with no gaps	(GT)22
B	Ba00117	00117_154563_F	gaggaagcactcctcactccta	60.0	00117_154563_R	aagctgtgtgggaaagtagctc	60.0	146	3	perfect	(AGC)10
B	Ba00118	00118_445594_F	gtgcgagtttacccactttacc	59.9	00118_445594_R	ttaagtggctctctcttcctgg	60.0	150	2	perfect	(AC)24
B	Ba00119	00119_335944_F	ggttaggatttgcatgtgtgtg	60.3	00119_335944_R	caagggattgagaggctaattg	60.1	145	2	imperfect with no gaps	(TC)18
B	Ba00120	00120_340187_F	aaactgtctccatccaactggt	59.9	00120_340187_R	agaaaacacatggcactgacac	60.1	128	2	imperfect with no gaps	(AC)20
B	Ba00121	00121_314068_F	cacagccatcaagaagattcaa	60.3	00121_314068_R	gttggtttgaccattacaagca	59.9	136	2	perfect	(GT)20
B	Ba00122	00122_266017_F	tttgtaccagaaacgcaatgac	60.0	00122_266017_R	attggatggcatgggagtatag	60.1	143	2	imperfect with no gaps	(AC)22
B	Ba00123	00123_167823_F	ccttctttgttggtctgctttc	60.3	00123_167823_R	ccactggtcccttaagtagctg	60.2	137	2	imperfect with no gaps	(TG)19
A	Ba00124	03220_1809_F	tgaatgcctatttgtgtccaag	60.0	03220_1809_R	actttctatcccacatcgtgct	60.0	300	3	imperfect with no gaps	(ATT)16
B	Ba00124	00124_210364_F	cattccaaagcgttgtgtttta	60.0	00124_210364_R	agatttccccaattctttccat	60.0	169	2	perfect	(TG)19
B	Ba00125	00125_425690_F	ggtcctgtccttctcatattgc	60.0	00125_425690_R	gtggtgagctgatttacgtctg	59.8	262	2	perfect	(GT)16
B	Ba00126	00126_455614_F	gcatcgcatcataggcatacta	60.1	00126_455614_R	tatctctcacacacttgcccac	60.2	143	2	imperfect with no gaps	(TG)21
B	Ba00127	00127_236472_F	gtatgacatccgttcacaatgg	60.1	00127_236472_R	ttagcatgttttgaggttccct	60.0	105	2	imperfect with no gaps	(AC)19
B	Ba00128	00128_315130_F	caacatctggaccataagcaga	60.1	00128_315130_R	ttcgttctggtatgcatttttg	60.0	124	2	imperfect with no gaps	(GT)21
B	Ba00129	00129_342326_F	catgatgtgtcaaccaccacta	59.3	00129_342326_R	tttgagtttgtggtgaggaatg	60.0	130	2	perfect	(AC)12
B	Ba00130	00130_79916_F	cctgagttctgttacagctccat	59.8	00130_79916_R	acttcaatgtaaaaacaccccg	60.1	124	2	imperfect with gaps	(GT)19
B	Ba00131	00131_455118_F	ccagaacaactgctacatctgg	59.8	00131_455118_R	gcagacaccatgtttacaagc	59.7	148	2	perfect	(AC)19
B	Ba00132	00132_191501_F	atttccctgactttgagtgcat	60.0	00132_191501_R	cctctcctgcttcatcactgta	59.5	125	2	imperfect with no gaps	(TG)38
B	Ba00133	00133_441269_F	ttggcaaccatgcaatatagtc	59.9	00133_441269_R	gagtctattgacaacaaggccc	60.0	136	3	perfect	(GAT)10
B	Ba00134	00134_312921_F	tgacaagtctttctactgaggca	59.2	00134_312921_R	tcttttgaatggcttcactctca	60.0	121	2	perfect	(CA)13
B	Ba00135	00135_23239_F	agaagatcaccacattggcttt	60.0	00135_23239_R	aaggcgtgtcaatatctgtgtg	60.1	142	2	perfect	(CA)21

Continued

B	Ba00136	00136_215754_F	ctgtggacatatgagggtttca	59.9	00136_215754_R	ggacactgagtactgaacgctg	60.0	134	2	imperfect with no gaps	(GT)21
B	Ba00139	00139_63813_F	tgagtggacagcttttcttcaa	60.0	00139_63813_R	gtctgcatgcaaagaaacacat	60.2	150	2	perfect	(TG)19
B	Ba00140	00140_111707_F	gacatgtgacagaaagcaaagc	59.9	00140_111707_R	cagctgactcaccaaacaacat	60.2	131	2	imperfect with no gaps	(GT)21
B	Ba00141	00141_408598_F	ccatactgtcctcaggcttacc	60.0	00141_408598_R	tgtgtaagagagagagagaga-gagc	57.9	150	2	imperfect with no gaps	(AC)32
B	Ba00142	00142_277539_F	tgttttttggtgtgtacagaggc	60.1	00142_277539_R	gcttttgttaagctgaaatggg	60.1	141	2	perfect	(AC)13
B	Ba00143	00143_408087_F	attcaagctgtatgattggcct	60.0	00143_408087_R	ttcagatttttaacaagccggt	60.0	133	2	perfect	(GT)19
B	Ba00145	00145_238363_F	agcctcccttgtatgtttaccc	60.6	00145_238363_R	atgtggtgattaattgcactgg	59.8	129	2	imperfect with no gaps	(AC)24
B	Ba00146	00146_75017_F	aataaaccaaaactgacacgca	59.6	00146_75017_R	ggctgttgctcactgttatgtc	59.8	130	2	imperfect with no gaps	(AC)17
B	Ba00147	00147_105521_F	cagagcataagcattccaaaca	60.3	00147_105521_R	tatgggtgttaagagcaaggct	60.2	360	2	perfect	(CA)25
B	Ba00149	00149_250489_F	ttttcccatagagttagcgcag	60.7	00149_250489_R	ccatcattattgccctcttagc	60.0	136	2	perfect	(CT)16
B	Ba00150	00150_9590_F	tcggctcactctgctgtattta	60.0	00150_9590_R	agcatatcagtctctgggcatt	60.1	246	2	perfect	(TG)18
B	Ba00151	00151_31055_F	gtcctgaggagttgactgttcc	60.2	00151_31055_R	aattagcctgctgtgctggtgta	60.0	120	2	perfect	(GT)24
B	Ba00152	00152_78998_F	tcaaacactaacagagcaggga	59.9	00152_78998_R	gttaaacagcttgttggcattg	59.7	143	2	perfect	(GT)17
B	Ba00153	00153_401556_F	gtctaggactgccaaaaactgg	60.2	00153_401556_R	atgttcattttgggctgaatct	59.8	147	2	imperfect with no gaps	(CA)26
B	Ba00154	00154_270166_F	tcctgctctgtgctcacatact	60.1	00154_270166_R	gactggtgtgtaagcagtttcg	59.8	110	2	perfect	(CA)18
B	Ba00155	00155_332581_F	ncctcttgttgcgtaagctg	59.8	00155_332581_R	taacttgagtttggaaggggaa	60.0	144	2	imperfect with no gaps	(AC)35
B	Ba00156	00156_123482_F	ggaagaagggatcacaacagac	60.0	00156_123482_R	tgctgggagaaatctaagatcc	59.7	115	2	imperfect with no gaps	(AG)18
B	Ba00159	00159_126940_F	ttgagccggaaaagatagagag	60.0	00159_126940_R	acacgttacaaaatgtgcaagc	60.1	144	2	perfect	(TG)17
B	Ba00160	00160_258703_F	gtcagagtgttgagacaggcac	60.0	00160_258703_R	ttttgctggtgattgaaaactg	60.1	169	2	perfect	(CA)16
B	Ba00161	00161_292321_F	attacacccagtttacatcggc	60.1	00161_292321_R	aatgggtgtgttcagacagatg	59.9	149	2	perfect	(CT)12
B	Ba00162	00162_313019_F	tttctctctctcccccctctctt	60.0	00162_313019_R	cacaagagccatgtgttttagc	59.8	144	2	imperfect with no gaps	(TC)19
B	Ba00163	00163_233910_F	agtagaggtgtgggatgctgtt	60.1	00163_233910_R	tcctgtcatgctcacaataacc	60.0	124	2	perfect	(TG)15
B	Ba00165	00165_248757_F	gatttaaccaatcctccatcca	60.0	00165_248757_R	aaatcatttctcttttggtgcc	59.5	268	2	perfect	(AC)17
B	Ba00166	00166_89208_F	attgccaaaccatatccacttc	60.1	00166_89208_R	tggtcctctactccatccaagt	60.0	122	2	imperfect with no gaps	(CA)20
B	Ba00167	00167_150448_F	acactgattctcagctgctctg	59.8	00167_150448_R	gaggtgagcgcacatatatcct	60.5	149	3	imperfect with no gaps	(CAG)11
B	Ba00168	00168_209325_F	tgaccaattaaatgagccagtg	60.0	00168_209325_R	ttcctacttgtgtgtctgcctc	59.4	169	2	perfect	(AC)18
B	Ba00169	00169_177627_F	ttacctggtcagaaactcagca	59.9	00169_177627_R	catgcctgtgacctacagaaag	59.8	131	2	perfect	(CA)16
B	Ba00171	00171_222856_F	cagacgagcagacagacagttc	60.2	00171_222856_R	cctcttgttcactgctaatccc	60.1	131	2	imperfect with gaps	(CA)30
B	Ba00172	00172_167230_F	tgtttctaggcggtttggtatt	59.9	00172_167230_R	ggtgcaccagtaaacacaaatg	60.3	174	2	perfect	(TG)16
B	Ba00174	00174_235377_F	aagtccatatcagcctgaggaa	60.1	00174_235377_R	tcaacacagtctgcttgatcct	59.9	122	2	perfect	(AG)18
B	Ba00175	00175_169417_F	gctggggagttaaattccttct	60.0	00175_169417_R	tatcacagacaaagccactggt	59.7	130	2	imperfect with no gaps	(GT)23
B	Ba00178	00178_369300_F	acagtaacaaggggtctcgatg	60.4	00178_369300_R	cacatatgacacagtctggcaa	59.6	106	2	imperfect with no gaps	(GT)18

Continued

B	Ba00179	00179_24241_F	cttttaggctggaaccagtcac	60.2	00179_24241_R	tgtgtgtatttgtgcttgtggga	60.1	186	2	imperfect with no gaps	(AG)18
B	Ba00180	00180_52086_F	aacggcgaaaagaagtaggag	59.9	00180_52086_R	ttcatgtcctcacaatcacaca	60.0	153	2	perfect	(GT)18
B	Ba00181	00181_145357_F	ttttctgctttttcctcttccag	60.0	00181_145357_R	gtttccacagaggagatcaacc	60.0	139	2	imperfect with no gaps	(GT)18
B	Ba00182	00182_47978_F	ctgtgctccctgtgtattttg	59.7	00182_47978_R	catgaaagcatgaatgtgtgtg	60.0	123	2	perfect	(AC)18
B	Ba00183	00183_234545_F	ccatgatccacagtttgtatgc	60.3	00183_234545_R	cactcaggacggatattcacaa	60.0	116	2	perfect	(TG)13
B	Ba00184	00184_263120_F	ttgacaatggtgtgtctctct	59.9	00184_263120_R	tgactcacacacacatacgctc	59.8	140	2	imperfect with gaps	(TC)31
B	Ba00185	00185_18196_F	cacactctgacacgactcacaa	60.0	00185_18196_R	ttcatggactttggatgacaag	60.0	137	2	perfect	(CA)18
B	Ba00186	00186_302547_F	aatgaccttcttcttcccccttc	60.0	00186_302547_R	gacatgcagcttcattcatctc	59.9	240	2	imperfect with no gaps	(AC)32
B	Ba00187	00187_105168_F	gtgaatgaaaagtgcggtacaa	60.0	00187_105168_R	gatttaaactcccaacattgtgt	57.1	129	3	perfect	(ATA)8
B	Ba00189	00189_278390_F	agccaattgagactgtgagtga	59.9	00189_278390_F	aaggagagaagtaaaatatggcga	59.7	149	2	perfect	(CA)15
B	Ba00191	00191_224363_F	gcaatagttgtagtgggcacag	59.7	00191_224363_R	gtgtgtatgtatgtgtgcgtgc	60.0	225	2	perfect	(GT)18
B	Ba00193	00193_210757_F	atggtggtgaaaaacaatttcc	60.0	00193_210757_R	cattgtgtgcacacaggaccataa	60.9	138	2	imperfect with no gaps	(AT)18
B	Ba00194	00194_309657_F	acagcccatctctgtctctctc	60.0	00194_309657_R	atagaacagtgggagtggttgg	60.3	127	2	perfect	(AC)17
B	Ba00196	00196_154314_F	tggcctgcagtatttacacagt	59.7	00196_154314_R	ctctggatctatggcgtctctc	60.4	105	2	perfect	(TG)21
B	Ba00197	00197_295591_F	ttggaccttgctaaaaatcctc	59.6	00197_295591_R	cacaaaatcaaagcgtcattgt	60.0	119	2	perfect	(AC)22
B	Ba00198	00198_258441_F	ttttctggcatgattttgtgttc	60.0	00198_258441_R	tataagctcatacagtccgccc	60.5	145	2	perfect	(AC)13
B	Ba00199	00199_174137_F	gggggactaaagggatacagtc	60.1	00199_174137_R	tcctgcatcttacaggacagaa	59.9	123	2	perfect	(GT)18
B	Ba00202	00202_221706_F	caggcctctgctagacaacata	59.5	00202_221706_R	taatcgctgttccatgagattg	60.1	148	2	perfect	(GT)16
B	Ba00203	00203_136570_F	ttcatatatcttgccgaaccct	59.8	00203_136570_R	aaacgactgtcaatctatgtttgc	59.6	144	2	perfect	(AC)22
B	Ba00205	00205_303932_F	cgcagtgcaagcatcttaatag	60.1	00205_303932_R	tctcaaaattcccgtcttctgt	60.1	140	2	imperfect with no gaps	(GT)28
B	Ba00208	00208_257727_F	gccaaagtttcactgggtctac	60.0	00208_257727_R	ccctgtctttctctctggctaa	60.0	114	2	perfect	(AC)13
B	Ba00210	00210_54610_F	gaagggagacaccatctacgac	60.0	00210_54610_R	gcaactccatatgtcaccagaa	60.0	150	3	imperfect with no gaps	(AGT)16
B	Ba00212	00212_127426_F	ggtccgtccctaccacatctat	61.3	00212_127426_R	gctatatcaggcagatgcacag	59.9	146	2	perfect	(CA)19
B	Ba00213	00213_68215_F	tacacaaaagccagcgtaagaa	60.0	00213_68215_R	tgtcagtgctcatgtttgtgtc	59.8	125	2	perfect	(AC)16
B	Ba00214	00214_171320_F	ttgtcactgtctgcctctgttt	60.0	00214_171320_R	ccgaaaccaattactagactgaca	59.6	246	2	perfect	(AC)19
B	Ba00215	00215_56434_F	ctcaaacttctccccagtcatc	60.1	00215_56434_R	cagtgaccgtgtcattcatctc	60.6	121	2	perfect	(AC)14
B	Ba00217	00217_189367_F	tcctctgaagtgatggaaacac	59.2	00217_189367_R	accccgggggaaataagtaagta	60.0	297	2	perfect	(GT)31
B	Ba00218	00218_311412_F	gggtttggatcgaaatgtatgt	60.0	00218_311412_R	gcacacaaggctgctactactg	60.1	141	2	perfect	(GT)16
B	Ba00220	00220_358437_F	accacaagtctttctcaagggga	60.2	00220_358437_R	gatgcaataccatcaaggaggt	60.2	151	2	imperfect with no gaps	(AC)22
B	Ba00221	00221_265802_F	cttgtccttcctgtcagagctt	60.1	00221_265802_R	cattctcctgtcctgtttcctt	59.6	118	2	imperfect with no gaps	(TG)16
B	Ba00222	00222_65123_F	gctctcagttgcttgtcacatc	60.1	00222_65123_R	gttattgtgccccaatttgttt	60.0	145	2	perfect	(CA)15
B	Ba00227	00227_70020_F	gagaacactgacagaatgcagg	59.9	00227_70020_R	caccaaaacctacacaacgaaa	59.9	317	2	perfect	(CA)18
B	Ba00228	00228_22684_F	ctagtatgtgaccacccagcaa	60.1	00228_22684_R	caatattgccaaagcatcaaga	60.1	290	2	perfect	(CA)19

Continued

B	Ba00229	00229_230871_F	gagagaagagagaaagggtagggtg	59.8	00229_230871_R	aacctgacaaatcctgatccat	59.7	104	2	perfect	(GT)17
B	Ba00230	00230_325570_F	attttcctagtaacagggctca	57.1	00230_325570_R	ctctctgccttggaaagacatt	59.9	120	2	perfect	(GT)16
B	Ba00231	00231_259399_F	aatgccaacgttttattctgct	60.0	00231_259399_R	atctgtttccaagcaacaaggt	60.0	223	2	perfect	(GA)27
B	Ba00232	00232_301439_F	taccagctgaacacagcaatct	59.9	00232_301439_R	aatactgaaggaaatgagcgga	60.1	147	2	perfect	(CA)18
B	Ba00233	00233_211140_F	cctgtagatgggggtgtgtatt	60.0	00233_211140_R	ttccagcagcttataacttccc	59.8	129	2	perfect	(TG)12
B	Ba00236	00236_269275_F	tgtctgagcactttcatgtgtg	60.0	00236_269275_R	tctgctgaccagtatgagtgct	60.1	131	2	imperfect with no gaps	(GT)17
B	Ba00239	00239_273631_F	tgaatggttaatcggactgttg	59.9	00239_273631_R	caaatagtttgggggtttgtgt	60.0	136	2	imperfect with no gaps	(GT)21
B	Ba00242	00242_90122_F	aagtggaagtggactgtgtgtg	60.1	00242_90122_R	acagcatgtacacagggaaatg	59.9	248	2	perfect	(CA)27
B	Ba00244	00244_137400_F	cccgacaatgactaatgtctca	60.0	00244_137400_R	cagtgctgatgagtgcttttc	60.1	341	2	perfect	(AC)20
B	Ba00245	00245_310245_F	acactgctgcaagactgtagga	60.1	00245_310245_R	tgaagaagggtgcatgtgtaag	60.2	139	2	imperfect with no gaps	(CA)23
B	Ba00246	00246_232655_F	tgttttctgtccttccgatttt	60.0	00246_232655_R	gtgaagactgtgacagctgagg	60.1	276	2	imperfect with no gaps	(AC)24
B	Ba00248	00248_41311_F	tctctgagatggtgtgtgtgtg	59.8	00248_41311_R	actggctgattaaagcaggatt	59.3	136	2	imperfect with no gaps	(GT)22
B	Ba00249	00249_88492_F	tatctgggtgtcacttgtcctg	60.0	00249_88492_R	gagattgttcgtaactccccag	60.0	122	2	perfect	(TG)19
B	Ba00250	00250_172203_F	aaatcatctgccctactcctga	60.1	00250_172203_R	caggaacacacatacacccact	59.8	150	2	perfect	(GT)15
B	Ba00251	00251_176303_F	caagtgaggtaatgaatcagcg	59.8	00251_176303_R	cacatgttggcaagattcagat	60.0	131	2	imperfect with no gaps	(TG)20
B	Ba00252	00252_284152_F	gcttgttgtctgggagttatcc	60.0	00252_284152_R	actagagccagccactaggatg	59.9	101	2	perfect	(CA)17
B	Ba00254	00254_115440_F	tggctgtaacaagtacaacatgc	60.1	00254_115440_R	cgtgaattatggagtctgtcca	60.0	125	2	imperfect with no gaps	(AC)18
B	Ba00255	00255_110427_F	atgaccctccagactcctgtaa	60.0	00255_110427_R	attgtggtatgacgaggtaggg	60.1	143	2	perfect	(GT)21
B	Ba00257	00257_230233_F	cccaacaccaatacacattcac	60.0	00257_230233_R	ttagggcagctgttaccatttt	60.0	144	2	imperfect with no gaps	(CA)18
B	Ba00259	00259_38068_F	tccctctctctctctcatccag	60.1	00259_38068_R	aaatccgtctgttgaccctcta	60.0	233	2	perfect	(TG)22
B	Ba00260	00260_213233_F	gagaggggactagggtcaaact	60.0	00260_213233_R	ggtgagtctttgttgctgtctg	60.0	204	2	perfect	(AC)17
B	Ba00261	00261_176016_F	gtgctcgctctcttttttctctc	59.9	00261_176016_R	ctggtttgtcaaggctctctct	60.1	327	2	perfect	(CA)22
B	Ba00262	00262_114168_F	gccgtttgtagaacaaggattc	60.0	00262_114168_R	cagagtgagacaaataaggaacga	59.8	237	2	perfect	(TG)21
B	Ba00263	00263_250029_F	actagcatcatgcacactccag	60.3	00263_250029_R	tagactgagagcaatgatcgga	60.0	120	2	imperfect with no gaps	(CA)17
B	Ba00264	00264_296767_F	gagtcagatcttgggctcactt	59.9	00264_296767_R	tccctataaatggatgattggc	60.0	137	2	perfect	(AC)13
B	Ba00265	00265_126950_F	gacatgtagtgtgttggatgggg	60.2	00265_126950_R	cattaaggggacttgctttttg	60.0	147	2	imperfect with no gaps	(GT)17
B	Ba00267	00267_52317_F	gatgaagctgaggaagaggaaa	60.0	00267_52317_R	aaagaagcactccagatgaagc	60.0	226	2	perfect	(CA)18
B	Ba00268	00268_35309_F	tttgtatgagtcatccgctgtt	59.6	00268_35309_R	ggctcctctgttagtggctaga	60.0	152	2	perfect	(TG)13
B	Ba00269	00269_183859_F	gtatctggtatctccacccacc	59.6	00269_183859_R	aagtctccaaaccagctctcag	60.1	145	2	imperfect with no gaps	(CA)20
B	Ba00271	00271_88447_F	aaatgcagagatccacacaatg	60.0	00271_88447_R	taccacaaatgttctggctcac	60.0	112	2	imperfect with gaps	(TG)17
B	Ba00272	00272_69652_F	atttctagccaaggctcatttg	59.8	00272_69652_R	catttagcaggtcacaaaccaa	60.0	268	2	perfect	(GT)15
B	Ba00273	00273_203030_F	acccagaaaagcaagttacagc	59.8	00273_203030_R	ggacaatgaaaagacatacgca	60.0	137	2	perfect	(GT)18
B	Ba00274	00274_94421_F	gttcaactcgtaacaaggtccc	59.9	00274_94421_R	gcatttgcaatacatttgcagt	60.0	376	2	perfect	(AC)26

Continued

B	Ba00275	00275_165989_F	catgtcacctcactgtcctcat	60.0	00275_165989_R	tggcactgaaagaaagtttgtg	60.3	126	2	imperfect with no gaps	(CA)20
B	Ba00279	00279_163067_F	caacaacagcaatatccagcat	60.0	00279_163067_R	cctgctcctcatacacacacat	60.1	124	2	imperfect with no gaps	(GT)21
B	Ba00280	00280_100118_F	aaacgaaacaggatgaggagaa	60.1	00280_100118_R	ggtttgtgttgcaatctaagca	60.2	146	2	perfect	(AC)15
B	Ba00281	00281_302083_F	acatgaacctttacaccaccc	60.0	00281_302083_R	tacttcacacgatggctcattc	60.1	206	2	perfect	(GT)16
B	Ba00283	00283_163507_F	tgacctcttgttcattcttcca	59.7	00283_163507_R	caagcaaatacaaaacaacacaga	59.3	113	2	perfect	(TG)15
B	Ba00284	00284_267020_F	gatttacataaaaagcccgcag	60.0	00284_267020_R	gcctctgtttaccaaccaagtc	60.0	273	2	imperfect with no gaps	(TG)21
B	Ba00285	00285_91074_F	acaaccatctggtgtgtatgga	60.2	00285_91074_R	cagctgcctcactctatcaatg	60.0	126	2	imperfect with gaps	(CA)25
B	Ba00287	00287_212724_F	gactggtgagtttgcacagatg	60.8	00287_212724_R	gcaaaacaatacactgccttca	60.2	122	2	perfect	(TG)15
B	Ba00288	00288_182806_F	ttccattcagaaaacaatgcac	60.0	00288_182806_R	atacacaggttgcctttgatcc	60.3	102	3	perfect	(ATG)9
B	Ba00289	00289_110193_F	aacgaaaccgctgtaaaacaat	59.9	00289_110193_R	cccattcatttgagtaggggta	60.1	345	2	perfect	(CT)27
B	Ba00291	00291_55459_F	ggaatgggatgatagtggactg	60.6	00291_55459_R	tctgtctctgtctcttgcttgc	59.9	147	2	imperfect with no gaps	(TG)31
B	Ba00293	00293_239989_F	gtgggagtgcattgtctgtaaa	60.0	00293_239989_R	aaggactcctacactctctgcg	60.1	164	2	perfect	(CA)15
B	Ba00294	00294_168402_F	gctttattcctgtctctcccct	60.1	00294_168402_R	tttcaagggcagttgaattttt	60.0	285	2	perfect	(CA)18
B	Ba00296	00296_77766_F	tccaagcattatgtgcgaatac	60.0	00296_77766_R	gaggggagtgagcttcagttac	59.4	147	2	imperfect with no gaps	(CA)17
B	Ba00298	00298_179563_F	gggaaaagaagggagagaatgt	60.0	00298_179563_R	actgcagcttaccctgaaactc	60.0	136	2	imperfect with no gaps	(CA)28
B	Ba00299	00299_219226_F	ttgaattgtctgatgtcaaggg	60.0	00299_219226_R	tgtgggctaattacatgtcagc	60.0	200	2	perfect	(AC)25
B	Ba00301	00301_147576_F	ccctcccattctctctctctct	60.3	00301_147576_R	tgggtatgccattaaagcaaat	60.6	131	2	imperfect with gaps	(CT)27
B	Ba00302	00302_117386_F	ccaagcaaccaggtttatgaat	60.2	00302_117386_R	tgtttctgtatgcacagctacg	59.1	127	2	imperfect with no gaps	(AC)22
B	Ba00303	00303_288918_F	tgtaacttcctgtgtctggtgg	60.1	00303_288918_R	agaatgaccactgaatacgcct	60.0	149	2	perfect	(CA)15
B	Ba00307	00307_134557_F	tgctaaatcggtggagttcttt	60.1	00307_134557_R	aggcaatgtttgagatgacctt	60.0	129	2	perfect	(AC)17
B	Ba00308	00308_198364_F	gtgcagttatggttgcatgttt	59.9	00308_198364_R	aaacaaagcactgaaagaagcc	59.9	179	2	perfect	(TG)17
B	Ba00311	00311_2504_F	tgtattttgcctaatttgctgg	59.2	00311_2504_R	catgtctctgacttccatcctg	59.7	142	2	Imperfect with no gaps	(TG)25
B	Ba00315	00315_214426_F	gtattcctctgtgccgtagacc	60.0	00315_214426_R	cgtggtctgttgacatgaaagt	60.1	237	2	perfect	(AC)16
B	Ba00316	00316_307181_F	tgaccagtaaagcacagattgg	60.2	00316_307181_R	agtaagaactggtggctggtgt	60.1	191	2	perfect	(TG)17
B	Ba00317	00317_245129_F	actgaatcagccctcgctataa	60.2	00317_245129_R	ggccacagccttctgtattatc	60.0	155	2	perfect	(TG)19
B	Ba00319	00319_291741_F	cagtgtgtctcaagggagtctg	59.9	00319_291741_R	cgcacataacttctctcattgc	59.9	114	2	imperfect with no gaps	(GT)20
B	Ba00320	00320_152143_F	tcacacaagtctaacctgcacc	60.2	00320_152143_R	aggatggcaaacagtctgatct	60.1	265	2	perfect	(GT)21
B	Ba00321	49362_2269_F	tttggactgtgattggaaactg	60.0	49362_2269_R	tcaggaaattccattatgaccc	60.0	287	2	perfect	(TG)17
B	Ba00322	00322_215349_F	aagagctatgacagaattgtcgg	59.8	00322_215349_R	attctcatttccatggttgctg	61.2	110	2	perfect	(CA)15
B	Ba00323	00323_106563_F	ttactcaccacacacatgcaaa	60.1	00323_106563_R	ggatcggacaagaagtggttag	60.0	146	2	perfect	(AC)12
B	Ba00324	00324_45366_F	gagttgcatgtgaagtgtccat	60.0	00324_45366_R	gttttcttttctcctcctggct	60.2	266	2	perfect	(TG)20
B	Ba00325	00325_150740_F	acagctgtggtgctgagataga	60.1	00325_150740_R	ttttcacagagtcattgttggc	60.2	103	2	perfect	(AG)15
B	Ba00327	00327_126646_F	acgggagatgaatcatgacag	59.9	00327_126646_R	tatgtcagactacactgcgcct	60.0	113	2	perfect	(TG)15

Continued

B	Ba00329	00329_44622_F	taaagggaaacgccatagtgac	60.4	00329_44622_R	cggacaggaaaatacactcaca	60.0	122	2	perfect	(TG)17
B	Ba00330	00330_206854_F	gccagagcaaccaaattaaatc	60.0	00330_206854_R	atgtggtagcaaaatggtgttg	59.8	230	2	perfect	(TG)23
B	Ba00332	00332_70603_F	acacgacacacacaaacagtga	60.2	00332_70603_R	caacttctgcacctcgtctatg	59.9	151	2	perfect	(AC)17
B	Ba00333	00333_218804_F	tttgcatcatcattgtcactca	60.1	00333_218804_R	agcatggaagagcagttacaca	59.9	150	2	perfect	(TG)13
B	Ba00334	00334_134051_F	ttgtttttctcaggcttttggt	60.1	00334_134051_R	acgcacacacacatatggtaca	59.8	150	2	imperfect with no gaps	(TG)15
B	Ba00336	00336_277236_F	cacttaagtctcccctctgtg	60.2	00336_277236_R	ncagttcaggacaagtaaaacatc	58.0	255	2	imperfect with no gaps	(TG)23
B	Ba00337	00337_63516_F	cacatcctcactcagagactgc	60.1	00337_63516_R	atgattgcattttcttcctcgt	60.0	325	2	perfect	(AC)16
B	Ba00338	00338_132157_F	ttacctggagcaaacaaaggat	60.0	00338_132157_R	tggtgcattgctaataaacctg	60.0	282	2	perfect	(AC)19
B	Ba00340	00340_211772_F	tatatgtggcgtcttgtgctct	59.8	00340_211772_R	tatattcccatgcatagtcgca	60.3	133	2	imperfect with no gaps	(GT)17
B	Ba00342	00342_217848_F	taatcacgctatctccgaacaa	59.7	00342_217848_R	accattctcacgttcacacttg	60.1	350	2	perfect	(GT)27
B	Ba00344	00344_229141_F	agatgtagcctccctctgtgag	59.9	00344_229141_R	cttcttgtgtttgtgtgcgttt	60.3	144	2	imperfect with no gaps	(AC)15
B	Ba00348	00348_249836_F	tagcaggtcttgatgtagcagc	59.7	00348_249836_R	ctggcaagtacaccctctctct	59.9	324	2	imperfect with no gaps	(GA)17
B	Ba00349	00349_117312_F	ttcaacgtgtgctgagctaaat	60.0	00349_117312_R	atgtttgcagaatgtttcacg	60.0	197	2	perfect	(GT)21
B	Ba00351	00351_225199_F	actctgccaattgtgtgtatgc	60.1	00351_225199_R	tgtcatgggatagtttggtcag	59.9	128	2	imperfect with no gaps	(AC)23
B	Ba00352	00352_17553_F	ccctaacctcagtcctgttgtc	60.0	00352_17553_R	gtcacaatctcccttctgttc	60.0	122	2	perfect	(TG)18
B	Ba00353	00353_80333_F	atcacttttctcctcacacgcc	59.8	00353_80333_R	tatcgttcagacaccgtactgc	60.2	256	2	perfect	(CA)40
B	Ba00354	00354_195889_F	cacttactactgctgcactggg	60.0	00354_195889_R	acatcagtgacatgctccaatc	60.0	283	2	perfect	(GA)16
B	Ba00355	00355_85820_F	gcaagtgcaacattaggtgtgt	60.1	00355_85820_R	ctgcatgaaaatcagaccacat	60.0	126	2	perfect	(TG)20
B	Ba00357	00357_114080_F	atttccatagacccacatccac	60.0	00357_114080_R	catctgtttagctgatggcaag	59.9	130	2	perfect	(CA)14
B	Ba00360	00360_144136_F	cattgtagtcctcagtgggtga	60.0	00360_144136_R	taatccttttcaaggctctgc	59.9	108	2	perfect	(TG)20
B	Ba00361	00361_142893_F	gatcgtgtatgacactggagga	60.0	00361_142893_R	tgttaagcactttgagctgcat	60.1	137	3	perfect	(TGA)11
B	Ba00362	00362_103951_F	tggtgattacaggtcaaagctg	60.2	00362_103951_R	tggttggaagcttttattggt	59.9	101	2	perfect	(TG)24
B	Ba00363	00363_133525_F	tacatttccattacgagcaacg	60.0	00363_133525_R	gccatggcttctttaaaaactg	60.1	271	2	perfect	(AT)16
B	Ba00364	00364_110919_F	tctgttaaatcagccagcagaa	60.0	00364_110919_R	cggaaaaccactgttaccctta	60.3	265	2	perfect	(AC)23
B	Ba00366	00366_155573_F	gtcgctgagattctgtgcatac	59.9	00366_155573_R	cgttccaatgaggctagactgt	60.7	143	2	perfect	(AC)21
B	Ba00367	00367_13599_F	taacacttgcattgggtttgtt	59.4	00367_13599_R	tgaaagacaatgtttcggaatg	60.0	135	2	imperfect with no gaps	(AC)21
B	Ba00368	00368_199352_F	acatacagtgcgtgtggacatt	60.4	00368_199352_R	cttgttcttggaaaccctgaag	60.1	114	2	perfect	(GT)16
B	Ba00369	00369_212510_F	agctggagagtgtaggcacatt	60.3	00369_212510_R	gaagaaagatgggcgacattag	60.1	141	2	perfect	(AC)15
B	Ba00370	00370_61671_F	ggttgcacattttgtttgagaa	60.0	00370_61671_R	ttttatttttggcctgctgagt	60.1	112	3	perfect	(AGT)12
B	Ba00371	00371_126709_F	gaatcacgcatccaaaactgta	60.0	00371_126709_R	gttgacgcatgtcattcaagtt	60.0	145	2	perfect	(AC)19
B	Ba00372	00372_156446_F	acccatacatgtgctgtgtctt	59.4	00372_156446_R	ccgtgtttctttatctctgggg	60.0	145	2	perfect	(TG)16
B	Ba00373	00373_285303_F	acaggccacaaactatctccat	59.9	00373_285303_R	gacagagagagggaggggtg	61.2	122	2	perfect	(CA)16
B	Ba00374	00374_206401_F	atgcgaaaaagaaaacgtcatt	60.0	00374_206401_R	acacctgcaacacatgaaaaag	60.1	135	2	perfect	(TG)19
B	Ba00379	00379_34874_F	tgcatagcctgaaacaagacac	60.3	00379_34874_R	cagctatcaaacctgcctctct	60.0	133	2	Imperfect with no gaps	(TG)19

Continued

B	Ba00380	00380_65256_F	actatcagcatcatcatcacgg	60.0	00380_65256_R	tcatgctccatatttcccttct	59.9	271	2	perfect	(AC)18
B	Ba00382	00382_106409_F	aatcaccctcatcgatatcacc	60.1	00382_106409_R	nctctctctctctctctctcactca	59.0	226	2	perfect	(TG)15
B	Ba00384	00384_241972_F	agatcatgcctgtgtttgaatg	60.0	00384_241972_R	atgcgcaaatcctaaaatccta	60.0	186	2	perfect	(TG)17
B	Ba00385	00385_3161_F	aggagctgcttctgtctaaacg	60.2	00385_3161_R	agcctcacgatacctaaaacca	60.0	142	2	perfect	(GT)15
B	Ba00386	00386_215848_F	tgtatctagctcctgagacccc	59.7	00386_215848_R	ttattccttcacccctactga	59.8	149	2	imperfect with no gaps	(TG)24
B	Ba00387	00387_110610_F	gaaatggggagtttgagagaca	60.5	00387_110610_R	acacacactgagctaaaggcaa	60.0	137	2	perfect	(CA)16
B	Ba00388	00388_5491_F	atagcagttaagcagcagaggg	60.1	00388_5491_R	ttggtccaaccagggtataaaa	60.4	293	2	perfect	(CA)25
B	Ba00389	00389_86907_F	ttttcactgctgactgctgaat	60.1	00389_86907_R	aataatgtgtcaggtaggggttg	59.2	183	2	perfect	(AC)15
B	Ba00390	00390_94555_F	gcatgaaagtccagcaattgta	60.1	00390_94555_R	gtgttgttttttgacagccacat	59.9	143	2	imperfect with no gaps	(TG)27
B	Ba00391	00391_186975_F	taaaagagcggcattgtgtcta	59.9	00391_186975_R	gtaatgagaaaagcagccaacc	60.1	134	2	perfect	(TG)23
B	Ba00392	00392_266915_F	tgtctgtctctctctctgcctctg	59.9	00392_266915_R	gatcccatcattaaaaggctca	60.3	133	2	Imperfect with no gaps	(CA)31
B	Ba00395	00395_196629_F	agtcatccaaaaatgactggct	60.0	00395_196629_R	cacacctgcactaaaactggtc	59.7	117	2	imperfect with no gaps	(GT)26
B	Ba00396	00396_49430_F	tttgacctgcctttcttgctat	60.3	00396_49430_R	cagtgaggtcagaattgctctg	60.1	110	3	perfect	(TTA)12
B	Ba00397	00397_124125_F	aggattggaatgtgaaatggag	60.2	00397_124125_R	gttctatcccaagaagcacacc	60.0	139	2	imperfect with no gaps	(GT)20
B	Ba00398	00398_90943_F	taatccgatagtcgtttcctgg	60.3	00398_90943_R	cgtctatgggacactgactctg	59.8	132	2	imperfect with gaps	(TG)16
B	Ba00401	00401_253434_F	cgtttatgtctcaggggaaaag	60.0	00401_253434_R	ccggtaaaactctaacaccagc	60.1	208	2	perfect	(TG)26
B	Ba00403	00403_159090_F	ccagtagtcgctctgcttacct	60.1	00403_159090_R	tagatctcagatgggagtgggt	60.0	164	2	perfect	(TG)17
B	Ba00405	00405_275398_F	gactgatctgtggaggacactg	59.8	00405_275398_R	ttaacaatagtgcaaaacccc	60.1	135	4	imperfect with gaps	(TTGT)8
B	Ba00408	00408_171705_F	tcccagtttgatgtgaagacac	60.0	00408_171705_R	cttttgatgggagaaccgttac	59.9	232	2	perfect	(TG)17
B	Ba00409	00409_36083_F	tatatgacgtccgaaagctgaa	59.7	00409_36083_R	accactatggcacagaacacag	60.1	110	2	imperfect with no gaps	(CA)26
B	Ba00411	00411_197292_F	gaaagcttattaacccgcctct	60.1	00411_197292_R	tgatcccaatgtctctttacca	59.4	324	2	imperfect with gaps	(AC)19
B	Ba00414	00414_248669_F	gagcattcactaatgcataccg	59.6	00414_248669_R	tgatgcaccatgtgttcttgta	60.0	145	2	imperfect with no gaps	(AC)28
B	Ba00415	00415_58321_F	cagcctcattagagagagggaa	60.0	00415_58321_R	tgtaagtatgcgccagagaaaa	59.9	149	2	perfect	(AC)14
B	Ba00418	00418_158396_F	ttgtgtgaattgcatgttgtgt	59.9	00418_158396_R	tgtttcacacacagctcagaca	60.6	112	2	perfect	(TG)14
B	Ba00419	00419_162528_F	agtcgtactgtggggaaaaaga	60.0	00419_162528_R	attgcccatcagtcctcttcta	60.1	130	2	imperfect with no gaps	(TG)20
B	Ba00420	00420_110640_F	tctctctcctcctctctctctc	59.1	00420_110640_R	agggattagggaggttcaaaaa	60.2	111	2	perfect	(CA)14
B	Ba00425	00425_185935_F	ccaaatgtttgtcagatgcaat	59.9	00425_185935_R	ttggtgtgtttttccaagttctg	60.1	139	2	imperfect with no gaps	(CA)21
B	Ba00426	00426_225612_F	tttagcccattgaccttttgtt	59.9	00426_225612_R	gaagtccagaccagctgagagt	60.1	140	2	imperfect with no gaps	(CA)24
B	Ba00429	00429_126533_F	gttctgaacctttgtggtctcc	60.0	00429_126533_R	gtgtgtgtgggggtggtaac	61.0	128	2	perfect	(AC)17
B	Ba00430	00430_55738_F	cccgactatgtgtgactagcg	60.7	00430_55738_R	cagccagtgatgtgtgtgtatg	60.1	278	2	perfect	(AC)19
B	Ba00431	00431_177546_F	ctgtctgtgtctgtgtggggaata	60.0	00431_177546_R	ttagactggaggtaggctggag	59.9	135	2	perfect	(AC)15
B	Ba00436	00436_19386_F	ctcattcatcccttcctctgac	60.1	00436_19386_R	gagtcatgaacagaaacctccc	60.0	140	2	perfect	(TG)17

Continued

B	Ba00437	00437_117112_F	tccttagtacgcctcattgtga	59.8	00437_117112_R	tgtgtgtgtgttgtgtgtgt	59.5	119	2	imperfect with gaps	(CT)24
B	Ba00438	00438_221425_F	gacacagccgaagagaagaact	60.1	00438_221425_R	aaaaatgcccttgatgctgtat	59.9	149	2	perfect	(AC)15
B	Ba00439	00439_256922_F	ccaacctccataccttcagaat	59.4	00439_256922_R	nctgcaaagttgtagcagattta	57.6	135	2	imperfect with no gaps	(AC)22
B	Ba00441	00441_269547_F	acagcactctgactccaatgaa	59.9	00441_269547_R	ttagactgagacctgagccaca	60.1	286	2	perfect	(TG)19
B	Ba00443	00443_76931_F	ttgcccatctggagtaaagact	60.1	00443_76931_R	ctgcaatagaggaaagaggagc	59.6	142	2	imperfect with no gaps	(TG)17
B	Ba00444	00444_36874_F	tcaaactgcccttttgaagat	60.1	00444_36874_R	cagaaagctgtttcttttgcct	60.1	234	2	perfect	(AT)12
B	Ba00445	00445_150042_F	ggatgtgttggatgggactatt	60.0	00445_150042_R	agcttgtttgttcatgggaaat	59.9	188	2	perfect	(CA)15
B	Ba00448	00448_48208_F	caaaacatgtgtgaggaggaaa	60.0	00448_48208_R	gtgtcctgtctggaaacacaag	59.7	146	2	perfect	(GT)17
B	Ba00449	00449_190409_F	taacagccaaaacaaatatgcg	60.0	00449_190409_R	atgcatctgaaccactgaaatg	60.0	121	2	imperfect with no gaps	(AC)21
B	Ba00450	00450_64216_F	ttttttcccttggcagttgtat	59.9	00450_64216_R	aatttgtccccgaaagtaacct	60.1	244	2	perfect	(GT)14
B	Ba00452	00452_238268_F	tgggacactaggaagaggaaaa	60.1	00452_238268_R	tcattatggctcctggaatagc	60.4	141	2	perfect	(AC)29
B	Ba00454	00454_124238_F	tgtgaacaaacctaccttgacg	60.1	00454_124238_R	acagggcttattgaacacacct	59.9	281	2	perfect	(CA)16
B	Ba00457	00457_145224_F	gctctgttcctttcagcttgtt	60.1	00457_145224_R	tcaaagatgaggcttgaagaca	60.0	346	2	perfect	(AC)23
B	Ba00461	00461_72438_F	atgccaacaataatgcaaactg	59.9	00461_72438_R	tcactctgaaagcgttttgaa	60.0	164	2	imperfect with no gaps	(TG)22
B	Ba00462	00462_45158_F	attaatgagtggccttcatgct	60.0	00462_45158_R	agacaatcctgatgtttggcac	61.3	184	2	imperfect with no gaps	(CT)19
B	Ba00463	00463_73801_F	acatcagagcaacaatagcagc	59.6	00463_73801_R	cctgttcatgagtgtcctcaaa	60.2	144	2	imperfect with no gaps	(TG)20
B	Ba00464	00464_227462_F	gaaaattcaccttcagtccagg	60.0	00464_227462_R	ccccctcgtatacatcacagtt	60.1	140	2	imperfect with no gaps	(AC)18
B	Ba00466	00466_201546_F	atatcaggggaggattggagtt	60.0	00466_201546_R	tcctctgagcactgtgtttgtt	60.0	244	2	imperfect with no gaps	(CA)31
B	Ba00468	00468_62179_F	caaatccctaggttggagttga	60.3	00468_62179_R	caagcaattatccaagtgtcca	60.0	149	2	imperfect with no gaps	(GT)24
B	Ba00471	00471_29393_F	ggacacacacttctcctcacac	59.7	00471_29393_R	ttggcatcaaatgtcaccttac	59.9	399	2	perfect	(AG)35
B	Ba00477	00477_3475_F	tgatatgtatgcagcagcagtg	59.9	00477_3475_R	atgggaaagaacgtgagtgaat	59.9	252	2	perfect	(GT)16
B	Ba00479	00479_164430_F	agagacggaccaacattagcat	60.0	00479_164430_R	ngagagagagagagagtgaga-caca	60.2	116	2	perfect	(AC)25
B	Ba00481	00481_256170_F	accataaaagtgaaaaggccaa	59.9	00481_256170_R	gacctttgagtctaatgggcac	60.0	245	2	perfect	(CT)14
B	Ba00488	00488_15510_F	ctaccacagatttccacccac	59.3	00488_15510_R	ttacccctttctctcatctcca	60.1	223	2	perfect	(AC)14
B	Ba00491	00491_193325_F	aacgctgcttttgaatcatgta	59.8	00491_193325_R	gcactgctgtgttaatgaggag	59.9	140	2	perfect	(GT)15
B	Ba00492	00492_109640_F	gggatagactgcatgtgtgaaa	60.0	00492_109640_R	acaggtttggtcttgacaggtt	59.9	182	2	imperfect with no gaps	(AC)20
B	Ba00496	00496_15884_F	ggaggaggaagtcaaggttttt	60.0	00496_15884_R	ggctgcagtaccatctgtcata	60.2	149	2	imperfect with gaps	(GT)24
B	Ba00498	00498_193397_F	ttactggtgccagtttgatgtc	60.0	00498_193397_R	accagcaaatgctctgaattt	60.1	141	3	perfect	(TAA)9
B	Ba00500	00500_1665_F	gcacccacagctaataagaagg	60.2	00500_1665_R	tacatgtgctcgagtgtgtgag	60.0	146	2	imperfect with no gaps	(CA)32
B	Ba00501	00501_163327_F	gtccaccctatgacctaagcac	59.9	00501_163327_R	gctgagtgctctgggataaaat	59.8	119	2	Imperfect with no gaps	(CA)19
B	Ba00502	00502_177633_F	cactgcttgggtgatgtcata	59.6	00502_177633_R	aatttgcctacctccttccttc	60.0	148	2	imperfect with no gaps	(TG)17
B	Ba00505	00505_173542_F	tggccctgaattagaaagtcat	60.0	00505_173542_R	cagcacctttgcatttctacac	59.8	150	2	perfect	(CA)16

Continued

B	Ba00506	00506_153914_F	gtgtaaaattccccacaagctc	59.9	00506_153914_R	tcacacacacagataaacgcac	59.7	127	2	imperfect with no gaps	(TG)24
B	Ba00507	00507_138886_F	gacaggagagagatcaggcagt	60.0	00507_138886_R	aggctgataccctgtgtttgt	59.9	173	2	imperfect with no gaps	(CA)18
B	Ba00513	00513_127218_F	ttgaaagtactctgtgtgcctg	58.1	00513_127218_R	ctgtccttccctttatctccct	60.0	133	2	perfect	(TG)16
B	Ba00514	00514_61710_F	ggctacaacggtatgagaggac	60.0	00514_61710_R	catctggagacgtgacagagag	60.1	204	2	perfect	(CA)16
B	Ba00518	00518_85385_F	agtgtggccttggagatagtgt	60.1	00518_85385_R	tatttggggatgtttttggaag	60.1	352	2	perfect	(CA)13
B	Ba00519	00519_90493_F	tcaagtgagagtagggcgtaca	59.9	00519_90493_R	aggtcaaaaataacctgagcca	60.0	127	2	perfect	(GT)14
B	Ba00522	00522_93906_F	ctgcctgcatctctctctctct	60.4	00522_93906_R	ttagcattgagcacaaagcact	60.1	185	2	perfect	(TG)14
B	Ba00524	00524_24113_F	ggttattgttgccgaagttttc	59.9	00524_24113_R	ttcatgccagtatacacagcaa	59.3	111	2	perfect	(TG)12
B	Ba00525	00525_73008_F	tgtcgagatcagatcattttgc	60.2	00525_73008_R	gtcttctaacggatgttttgcc	60.0	250	2	perfect	(TG)17
B	Ba00526	00526_103784_F	gctccgtttgtttacatccttc	60.0	00526_103784_R	ttttcagtaatgagtctgctgc	57.3	145	2	perfect	(TG)20
B	Ba00528	00528_118258_F	gacggctttagttctgtcttgg	60.3	00528_118258_R	agtgtttgtaggtgtgtgggtg	59.9	150	2	imperfect with no gaps	(CA)18
B	Ba00529	00529_11236_F	ttaagtccgcaagtgctctaca	60.1	00529_11236_R	aatcgcattgacattcacaaag	60.0	220	2	perfect	(CA)13
B	Ba00530	00530_206867_F	tgaccttgagctggatgactaa	59.9	00530_206867_R	tcacagaggggtgcagtataga	59.8	134	2	imperfect with no gaps	(TG)21
B	Ba00532	00532_28858_F	agacaataaattcccccaaggt	60.0	00532_28858_R	caactgaaaaatacaaaaactgctg	59.3	122	2	perfect	(TG)16
B	Ba00539	00539_199922_F	attgcaggaaaaagggaaaaat	60.2	00539_199922_R	agggaacgggtagaggagatag	60.0	121	2	perfect	(CA)13
B	Ba00540	00540_147465_F	ccaaaaatcctaaccctaaccc	60.0	00540_147465_R	tttccagccatataccacacag	59.9	273	2	perfect	(AC)17
B	Ba00541	00541_245376_F	tttcctttgttaaagtccccct	60.2	00541_245376_R	tgtctggatatctcaagcaaaca	59.8	146	2	imperfect with gaps	(AC)39
B	Ba00542	00542_22467_F	gacagggaacacatgaagtcaa	60.0	00542_22467_R	tgtaacgcaaattgtctcatcc	60.0	118	2	imperfect with no gaps	(TG)18
B	Ba00543	00543_91589_F	acacagtccacgaaatagaataca	57.8	00543_91589_R	cttttgatctcttccagccagt	59.9	202	2	imperfect with no gaps	(AC)25
B	Ba00544	00544_183223_F	tgcagtaaaggaaaggtttgt	60.0	00544_183223_R	attgctagtggcttcgcataat	60.1	106	2	perfect	(CA)13
B	Ba00545	00545_157496_F	tgtctatctcccgctcacacta	59.9	00545_157496_R	acgtgtatgtatgcatggtggt	60.1	312	2	perfect	(CA)18
B	Ba00546	00546_227598_F	catttcagactgtttcagctcg	60.1	00546_227598_R	aaggggtcactaacctgtcaga	60.0	175	2	perfect	(TG)12
B	Ba00549	00549_102351_F	ttgtaaggtttcccacctgtct	59.9	00549_102351_R	gctttgttttcactaaatgggc	60.0	282	2	perfect	(AC)16
B	Ba00550	00550_31082_F	agtgtagccaaaatgcaggaat	60.0	00550_31082_R	atgtgccaaacatttcagagtg	60.0	124	2	perfect	(AG)14
B	Ba00551	00551_183042_F	gtgcagcacagagagaaagaaag	61.5	00551_183042_R	aaggtttgtaaaaaggcgttga	60.0	239	2	perfect	(GT)24
B	Ba00552	00552_45779_F	catcctgtcaaactgtcagctc	59.9	00552_45779_R	atgcaaagaatgtcacagcaac	60.2	259	2	perfect	(TG)19
B	Ba00554	00554_194224_F	ggagaaatgcagagaaggaaaa	59.8	00554_194224_R	tactccgaccttgtttcgattt	60.0	337	2	perfect	(TC)19
B	Ba00556	00556_116025_F	tcagacctgtaccggttttct	60.0	00556_116025_R	tgtgtgtgtgtgtgtgtgtg	61.2	221	2	perfect	(AT)16
B	Ba00559	00559_232640_F	tgaaggaacacaggagctgata	59.9	00559_232640_R	gaacaagcttttctaagcaccc	59.4	116	2	imperfect with no gaps	(TG)18
B	Ba00561	00561_195912_F	ttagcaaagggtcaattcaggt	60.0	00561_195912_R	tgctgcttctgaaaactccata	60.0	275	2	perfect	(TG)23
B	Ba00562	00562_82104_F	ngcctccctacctactgtgc	60.4	00562_82104_R	tcatcgctgtcttcctgactta	60.0	127	2	perfect	(CA)15
B	Ba00564	00564_45473_F	caggtcattctcctctgctctt	60.0	00564_45473_R	gatgcattatcctcacacatgc	60.4	163	2	perfect	(CA)14
B	Ba00568	00568_212794_F	gtttgtccagtaacccaatggt	60.0	00568_212794_R	tcaggatgctgactcctgtaaa	59.9	168	2	imperfect with no gaps	(TG)17
B	Ba00571	00571_140169_F	gccagagccaagataaagctaa	60.0	00571_140169_R	cacacacatgcaaacctaacct	60.0	139	2	perfect	(TG)13

Continued

B	Ba00577	00577_13831_F	ggcgagaaatttggtgagatag	60.1	00577_13831_R	aataaactgcaagtccgtttgc	60.5	121	2	imperfect with no gaps	(AC)19
B	Ba00578	00578_32552_F	tcctttggaaagacaacagctt	60.3	00578_32552_R	cagtggtgtgtttgtgtgtgtc	60.0	121	2	imperfect with no gaps	(AC)17
B	Ba00583	00583_197206_F	aaccaagttttcatctaggcca	60.0	00583_197206_R	taaggccaagtgtaaagccaat	60.0	105	2	perfect	(GT)18
B	Ba00587	00587_86605_F	cgtcaggtttctcatagcacaa	60.3	00587_86605_R	tgctaagagcaaaaacaccaaa	59.9	150	2	imperfect with no gaps	(GT)21
B	Ba00589	00589_151519_F	ggggaactgaatgtggagatta	60.2	00589_151519_R	cctttctttccttcatcctcct	60.1	136	2	imperfect with no gaps	(GT)27
B	Ba00591	00591_222305_F	tgttcgacacagctcctgtaat	59.8	00591_222305_R	cagtcaggtttacagtaggccc	60.1	396	2	perfect	(CA)25
B	Ba00593	00593_113620_F	ngaaaacaaaacaaaaacaagtg	57.3	00593_113620_R	tggtgttatcttgaaatgcagc	60.1	346	2	perfect	(TG)17
B	Ba00597	00597_49293_F	agggaactagcacaaagagctg	60.1	00597_49293_R	acttgtgccaaaatctgactga	59.8	201	2	imperfect with no gaps	(AC)18
B	Ba00598	00598_34944_F	atttacctcaaaccctcccatt	60.0	00598_34944_R	ctgaggactggaaaatactgcc	60.1	128	2	imperfect with no gaps	(CA)19
B	Ba00599	00599_215025_F	ccaagcagtacgactgagtgac	60.0	00599_215025_R	gctccaggaagaagacttcaaa	60.0	147	2	imperfect with no gaps	(GT)28
B	Ba00601	00601_158674_F	agcaacatccagccatgtagta	59.7	00601_158674_R	tcccattactgatccagtgaca	60.4	107	2	perfect	(GT)14
B	Ba00606	00606_117549_F	ggcactgagaaccaatctctct	59.9	00606_117549_R	gggaaaaacacacaaacactga	59.9	103	2	perfect	(TG)18
B	Ba00607	00607_205941_F	gttccttatttcctttcacccc	60.1	00607_205941_R	acaacccccaaccaacaata	60.0	176	2	perfect	(TG)16
B	Ba00608	00608_192669_F	aaagacaccaggaaaagttcca	60.0	00608_192669_R	aggacacacctcaaattacgct	60.1	235	2	perfect	(CA)20
B	Ba00609	00609_215496_F	gtgggttttcaaatgggattta	59.9	00609_215496_R	agtgtacacacatgcatcagca	60.3	144	2	perfect	(TG)19
B	Ba00611	00611_213574_F	tgcagctgagtcaagggtaata	59.9	00611_213574_R	gtttaggtccatgtggttccat	60.0	198	2	perfect	(TG)14
B	Ba00612	00612_4182_F	gtttcaggctggatttaccaag	60.0	00612_4182_R	aaaagggaaagtttagttggca	59.2	145	2	perfect	(GT)15
B	Ba00613	00613_53311_F	agagatgttgggagttcagagc	59.9	00613_53311_R	gggagatgatcagtatgaaggc	59.9	114	2	perfect	(AC)21
B	Ba00615	00615_146462_F	tttgtcacgcatacacacacat	60.0	00615_146462_R	tgtgagcaggataattgaggtg	60.1	245	2	perfect	(CA)15
B	Ba00616	00616_69185_F	actttaggtcatgcagcctgtt	60.2	00616_69185_R	gactgacaaagcagtaagcgtg	60.1	211	2	perfect	(GT)14
B	Ba00618	00618_77660_F	ttatttgtgttgcagaccttgg	60.0	00618_77660_R	acagagacaggaaggctctgac	60.1	119	2	perfect	(GT)18
B	Ba00621	00621_181178_F	gggagagctggttgtttatgac	60.0	00621_181178_R	aatgacttcatgctccaggttt	60.0	222	2	perfect	(GT)14
B	Ba00622	00622_88033_F	aaacaaggagaaatcaccctca	60.0	00622_88033_R	aagcactttgtaactgtgttttgaa	59.4	134	3	imperfect with no gaps	(ATA)19
B	Ba00623	00623_138547_F	tcccctttcacttacctgttttg	60.4	00623_138547_R	tatttacaacatggggtgtgga	60.0	167	2	perfect	(AC)19
B	Ba00627	00627_83670_F	catgtaatgcttcttaagcccc	60.0	00627_83670_R	cacatgttgactgtgtgtgtcc	60.0	347	2	perfect	(AC)16
B	Ba00631	00631_217115_F	acagatcacccattatttggct	59.7	00631_217115_R	tgtggtggagaataatcacagc	60.0	182	2	perfect	(CA)16
B	Ba00634	00634_187757_F	agtgaatgtatgtttgttgccg	59.9	00634_187757_R	ctaatgcacatcagccagagag	60.0	380	2	imperfect with no gaps	(AC)25
B	Ba00635	00635_226359_F	gctcacacaaccctgcataata	60.0	00635_226359_R	ctatcccagtgaaatgcagtga	60.1	346	2	perfect	(AC)20
B	Ba00638	00638_25913_F	gtgggagatgggtttgtatgtt	60.0	00638_25913_R	aggcagaaaccaacctctactg	59.8	126	2	imperfect with no gaps	(TG)22
B	Ba00639	00639_63945_F	gctgtgcacacatcgtctct	60.1	00639_63945_R	ctattgctgtcaccattgagga	60.1	245	2	perfect	(CA)17
B	Ba00640	00640_218522_F	tttctctatcagccaccactga	59.9	00640_218522_R	cgcgtcactctgacattagaag	60.1	182	2	imperfect with no gaps	(TA)15
B	Ba00641	00641_95262_F	atcctgcctctctctaccctct	59.9	00641_95262_R	ttaaaaacttcctgtgtgcaaacc	58.4	118	2	imperfect with no gaps	(AC)33
B	Ba00645	00645_157801_F	cgtgagagtgtgagactgaagg	60.1	00645_157801_R	atcagcactatggagcaaacct	60.2	337	2	perfect	(AC)16

Continued

B	Ba00646	00646_39958_F	atcaattgccactcactcacac	60.0	00646_39958_R	agtgtctctttggggaaaaaca	60.0	135	2	imperfect with no gaps	(CA)15
B	Ba00647	00647_18112_F	cacttcacaggaacaggatgaa	60.2	00647_18112_R	tggggattaggagctgagtaaa	60.1	336	2	perfect	(GA)18
B	Ba00649	00649_8071_F	caccagatctaggtttgcacag	59.8	00649_8071_R	aacattgattttcttccccctt	60.1	261	2	perfect	(CA)18
B	Ba00650	00650_71824_F	tctgtgaggagcacagttgatt	59.9	00650_71824_R	gacttcctcccatagtcacgtc	60.0	183	2	perfect	(GT)20
B	Ba00652	00652_95261_F	taatataggcctaccaaccccc	60.3	00652_95261_R	ccagcatcattagtgagcagac	59.9	124	2	imperfect with no gaps	(CA)24
B	Ba00654	00654_73567_F	catgtaatagcatgcaggaacaa	60.0	00654_73567_R	atcacaaggtgtggcattacag	59.9	109	2	perfect	(AC)25
B	Ba00655	00655_188487_F	aaaagcacatagatgagagggc	59.8	00655_188487_R	aagaggtgaaggcaagagacag	60.1	125	2	imperfect with no gaps	(GT)23
B	Ba00657	00657_186033_F	accatggtaactgacccagact	59.8	00657_186033_R	cacaacgtgagaaatacctgga	60.0	150	2	imperfect with no gaps	(TG)24
B	Ba00658	00658_22126_F	ttgtgtcgtgttctttgcttct	60.0	00658_22126_R	gcagcagagctagagggttaaa	60.2	281	2	perfect	(TG)15
B	Ba00659	00659_143811_F	ctgatcaggtgattagtgggtg	59.5	00659_143811_R	ctttcctccgtcctagtttcct	60.1	295	2	perfect	(CT)16
B	Ba00661	00661_199929_F	tgcacttttcatatctgcacct	59.8	00661_199929_R	gttctggaagcttttcacatcc	60.1	140	2	perfect	(AC)19
B	Ba00662	00662_10641_F	tttatgtcagcagttgggtttg	60.0	00662_10641_R	ataataaggcgcacagagtggt	60.1	183	2	perfect	(TG)15
B	Ba00663	00663_53252_F	gcaggcctagtagcaataccat	59.7	00663_53252_R	aggcctctggcataataattca	60.0	292	2	perfect	(TG)17
B	Ba00664	00664_98309_F	ataaccgcagcaatctcctaaa	60.1	00664_98309_R	gctgctgtctatgtttaaccctg	60.2	148	2	imperfect with no gaps	(GT)16
B	Ba00665	00665_91072_F	cacaagctgacaggtgacattt	60.2	00665_91072_R	cacctgtgtctgtgtgttgaga	59.8	132	2	imperfect with no gaps	(AC)19
B	Ba00672	00672_101631_F	ctttccaagtatgtgcgtgtgt	60.1	00672_101631_R	cagtcagttacggcttcattca	60.3	133	2	imperfect with no gaps	(TG)33
B	Ba00673	00673_147435_F	ctttccatcaaacccaactagc	60.0	00673_147435_R	atgaacagggacatgacatgag	59.9	141	2	imperfect with no gaps	(GA)17
B	Ba00675	00675_35983_F	agtcatggcagtgaaatgtacg	60.1	00675_35983_R	cttgtctatttccagaatgccc	60.0	169	2	perfect	(TG)16
B	Ba00677	00677_116910_F	gaaaatgatggccttaaagctg	60.1	00677_116910_R	gatggttttagtgctacctggc	60.0	127	2	imperfect with no gaps	(AC)25
B	Ba00679	00679_48521_F	atattatcgagagccccacgta	59.9	00679_48521_R	gaaatgaactggtgagaccaca	60.0	370	2	perfect	(GT)16
B	Ba00680	00680_103597_F	agcatggctcggtttttatatgt	59.9	00680_103597_R	cggagctttgaaaacaaactg	59.9	110	3	imperfect with no gaps	(TTG)16
B	Ba00681	00681_151223_F	cgtcagcatccctcttagactt	59.9	00681_151223_R	tcaaatcaccaggatagcagtg	60.1	118	2	perfect	(GT)17
B	Ba00682	00682_10180_F	agtcatttgaacttcagcccat	60.0	00682_10180_R	ttggtattagggagttggcatt	59.7	111	2	perfect	(CA)16
B	Ba00683	00683_153133_F	gacattccactttgttacccgt	60.2	00683_153133_R	tccaataaagcactccaaagtt	57.9	157	2	perfect	(CA)15
B	Ba00684	00684_16035_F	tgatccaggatgaataccagtg	59.8	00684_16035_R	agccaagatagctggcttcata	60.4	120	2	imperfect with no gaps	(TG)23
B	Ba00685	00685_2827_F	gcgtgtagcatttcatttgtgt	60.1	00685_2827_R	aagttcatttcaagcaggaagc	59.9	136	2	imperfect with no gaps	(TG)20
B	Ba00686	00686_84565_F	ccaacgaggcttatggagatag	60.1	00686_84565_R	gcctgtggcttttacagttctc	60.3	106	2	perfect	(GT)13
B	Ba00692	00692_182106_F	ggagcataacagattgctgaca	60.3	00692_182106_R	tgttgtcagtagctcgactggt	60.0	142	2	Imperfect with no gaps	(GT)19
B	Ba00693	00693_47943_F	ttaatttaaagggcaatgcag	60.3	00693_47943_R	tgatttctgttgtgctacaggc	60.3	258	2	perfect	(AC)23
B	Ba00697	00697_95618_F	accatggattaccagaaccatc	60.0	00697_95618_R	tgtcatagttgtttgaccctgc	60.0	235	2	perfect	(AC)14
B	Ba00699	00699_205382_F	caggctaccactcaactcactg	60.0	00699_205382_R	ccttttgaagccatttcatctc	60.1	178	2	perfect	(GT)15
B	Ba00700	00700_63539_F	gtagcgactccagctctctctc	59.9	00700_63539_R	tatgaagaccctggtgtgtttg	59.9	372	2	perfect	(CA)12

Continued

B	Ba00703	00703_106777_F	tttcaggggaaatctaaaacca	59.8	00703_106777_R	ccagttaattgggaaaaagctg	60.0	387	2	perfect	(AC)33
B	Ba00706	00706_63620_F	ctggtgtgcctgttgaatctta	60.2	00706_63620_R	caaactctgcagtcagttggag	60.1	210	2	perfect	(CA)18
B	Ba00707	00707_13000_F	ccttcatggaagtcttttaccg	60.0	00707_13000_R	tttcctgtattgtgattggctg	60.0	187	2	perfect	(CT)24
B	Ba00708	00708_100317_F	gtgtatgtgtgtatgtgcgtgc	60.0	00708_100317_R	gctttgtctctctttgtcaccc	60.3	282	2	imperfect with no gaps	(TG)26
B	Ba00709	00709_165201_F	ccctatgcattctgtgttttca	60.0	00709_165201_R	tacaggctgagaaagacgtcaa	60.1	262	2	perfect	(GT)14
B	Ba00711	00711_149557_F	acacagccaatttagagccatt	60.0	00711_149557_R	cttgatttgagagcccatgaat	60.5	131	2	perfect	(CA)15
B	Ba00712	00712_32975_F	actaagcatgattgcacagcag	60.5	00712_32975_R	atgaagcagagacattggtcct	60.1	143	2	imperfect with no gaps	(AC)18
B	Ba00714	00714_19543_F	tttgtgctgctgtgataaacct	59.8	00714_19543_R	ccatttaagcacaaacaggtga	60.0	175	2	perfect	(CA)15
B	Ba00729	00729_16418_F	gctgattgagcctacaagcg	61.1	00729_16418_R	gagatcacaaaggcaaaaggac	60.1	107	2	imperfect with gaps	(GT)26
B	Ba00731	00731_72616_F	tgggctggaaagtagtacctgt	60.1	00731_72616_R	aacgagatcatcaacccagact	60.0	178	2	imperfect with gaps	(CA)18
B	Ba00732	00732_205680_F	atacagctccaagtccactggt	60.1	00732_205680_R	tgagtgtgttgcctttgcttat	59.8	102	2	perfect	(AC)18
B	Ba00733	00733_52024_F	tttaaaaagcgaggctttcatc	59.9	00733_52024_R	tctaactggctctgatagccct	59.5	122	2	imperfect with no gaps	(GT)26
B	Ba00735	00735_142037_F	aggtggaaaatgagcagaatgt	60.0	00735_142037_R	gtgtgtatttagcgtagcccaa	59.2	144	2	imperfect with no gaps	(TG)29
B	Ba00736	00736_28103_F	gtattaagcagatgggacgctt	59.7	00736_28103_R	ccagctaaataaaacagggcac	60.0	132	2	imperfect with no gaps	(AC)16
B	Ba00739	00739_156044_F	ctgggaatgtgagttcattcaa	60.0	00739_156044_R	tcctgtgttagcttagctgcaa	60.2	138	3	perfect	(TTG)22
B	Ba00740	00740_129410_F	aatgcaaaaacacagcattcac	60.1	00740_129410_R	tgttccaacattcctttcagtg	60.0	359	2	perfect	(TG)18
B	Ba00741	00741_134776_F	aaaagtgtgtgtaagcgtgtgg	60.1	00741_134776_R	tgagcttcggataatggtttct	60.1	101	2	perfect	(TG)15
B	Ba00742	00742_20341_F	ataaaaccaaagccatctgcat	59.9	00742_20341_R	aaagtgccacatcatcacagag	60.2	333	2	perfect	(TG)21
B	Ba00745	00745_120874_F	caccaactgtcacaaatgacct	59.9	00745_120874_R	ggctgtgtggagaaaatacaca	60.0	238	2	perfect	(CA)33
B	Ba00746	00746_27380_F	taggaaccactggagttaggga	60.0	00746_27380_R	cagagaggctgagagacagtga	59.9	134	2	imperfect with no gaps	(CT)29
B	Ba00747	00747_77239_F	acattacccgccactattttg	60.1	00747_77239_R	tgccacctactgtactggaatg	60.1	146	2	imperfect with no gaps	(CT)20
B	Ba00749	00749_68946_F	aggatatccactgcacacactg	60.1	00749_68946_R	acttttgttccgtttccaccta	59.9	108	2	imperfect with no gaps	(GA)17
B	Ba00751	00751_167377_F	tagcagtaaaataacggcagca	59.9	00751_167377_R	tattgtgtgtctccaggtgagg	60.0	279	2	perfect	(CA)16
B	Ba00755	00755_129270_F	taaacatcttcctcgtgtggtg	60.0	00755_129270_R	ttgccactgcattttatttg	60.0	254	2	imperfect with no gaps	(TA)16
B	Ba00758	00758_136813_F	ccaataaaggcacacaaagaca	60.0	00758_136813_R	gtgtatgcagtgtgaagtgcaa	59.8	308	2	perfect	(TG)17
B	Ba00760	00760_109813_F	ttcatgagaaattgtttggcac	60.0	00760_109813_R	aatgtgcagtctgaggaacaga	59.9	180	2	perfect	(GT)19
B	Ba00761	00761_181066_F	gacaccccctctctactacacg	60.1	00761_181066_R	atgccctgcatctgtttaaagt	60.0	125	2	perfect	(AC)13
B	Ba00762	00762_180208_F	atctcaaggattgacctggttg	60.4	00762_180208_R	tggagatgagactttgatgtgg	60.1	224	2	perfect	(TG)16
B	Ba00763	00763_149998_F	gacaatttgagcaggtgtggta	60.0	00763_149998_R	atggaacctaagcaaggactca	60.1	137	2	imperfect with no gaps	(TG)17
B	Ba00764	00764_33855_F	ttttacattgccctcatcacag	60.0	00764_33855_R	ccgtgtgtctacaaattcccn	60.9	185	2	perfect	(AC)17
B	Ba00768	00768_151767_F	ggcccatattgtcttgtgatct	60.2	00768_151767_R	ttcaaaccctcgttagtgtcct	60.0	130	2	imperfect with no gaps	(CA)24
B	Ba00769	00769_24620_F	cagcaaagtggttagtcaggtg	59.8	00769_24620_R	ggaaagttatgccctctgtttg	60.0	287	2	perfect	(TG)25

Continued

B	Ba00770	00770_193378_F	gaatcttacttccagagcctgc	59.5	00770_193378_R	ttcctgccacctcagatatttt	60.0	344	2	perfect	(CA)22
B	Ba00771	00771_194722_F	gcaagtctgggaacacacataa	60.0	00771_194722_R	gtgtgtgcctctatcagtcagc	59.9	255	2	perfect	(GT)15
B	Ba00772	00772_188965_F	gttttaacagaggggaccagtg	59.9	00772_188965_R	actgccttatacaagctgcctc	59.9	327	2	perfect	(TG)27
B	Ba00773	00773_62883_F	ccctgtcacatcgtgttagtgt	60.0	00773_62883_R	tgtgtgtccttgtgaatttaaacc	60.2	144	2	perfect	(CA)19
B	Ba00776	00776_154787_F	gtctttatcagaaccacctgcc	60.0	00776_154787_R	tcaaactttaaaccgacagcaa	59.8	326	2	perfect	(TG)16
B	Ba00777	00777_98600_F	aaagccttcctcctctctgtct	60.0	00777_98600_R	aaccaatatctcacacccaacc	60.0	368	2	perfect	(AC)19
B	Ba00778	00778_204378_F	atgactgatgatgaatggcttg	60.0	00778_204378_R	gataaaggaggagggaaaagga	59.9	213	2	perfect	(GT)19
B	Ba00781	00781_193138_F	aggattctgagtgacggaacat	60.0	00781_193138_R	agccaagcaggaagtgtgag	60.6	134	2	perfect	(TG)19
B	Ba00783	00783_22974_F	caccagaagtgcttcatatcca	60.1	00783_22974_R	tcataaatatccccccacaaagc	60.0	246	2	perfect	(GT)16
B	Ba00786	00786_188276_F	gaggagaatggagaatggacag	60.1	00786_188276_R	catacacacacacacacacta-cacn	59.6	375	2	perfect	(TA)22
B	Ba00787	00787_21001_F	agacttggctctactccaggtg	59.9	00787_21001_R	ttgccagcagccttattttatt	60.1	189	2	perfect	(TG)24
B	Ba00788	00788_133172_F	ttcaaatactagccacgagacg	59.4	00788_133172_R	tcaatcatgacaaacttgcctc	60.1	182	2	perfect	(CT)16
B	Ba00790	00790_149838_F	atacagcatgaccttttgagca	59.8	00790_149838_R	gacgcatatgctttgtgtttgt	60.1	240	2	perfect	(TG)27
B	Ba00791	00791_125354_F	cattttgcacagaacaaatggt	59.9	00791_125354_R	gataaagcccagtggaaagatg	60.0	336	2	perfect	(AC)30
B	Ba00795	00795_9771_F	gctacaccgctctcgtctttat	59.9	00795_9771_R	gagcacattgtgttttggagaa	60.2	136	2	perfect	(TG)17
B	Ba00799	00799_175806_F	ctccttctgctttctttttgga	60.0	00799_175806_R	aaagagtcttagcaagcggatg	60.0	106	2	imperfect with no gaps	(AC)19
B	Ba00804	00804_765_F	tacgtcatcttgttcctgatgg	60.0	00804_765_R	tctcctccaggaaacactcact	60.3	350	2	perfect	(AC)16
B	Ba00807	00807_15806_F	aaaagccatctcatcatgtcct	60.0	00807_15806_R	cccatgtcattttccattctt	60.1	177	2	perfect	(TG)17
B	Ba00809	00809_161938_F	catttcatcaactctgcctctg	59.9	00809_161938_R	aatgtgtgtttgtcatgaagcc	59.9	103	2	imperfect with no gaps	(AC)20
B	Ba00814	00814_163533_F	gccccatggttgatgtattagt	60.0	00814_163533_R	acagtgggtggtagaggaggta	59.9	260	2	perfect	(AC)17
B	Ba00815	00815_144058_F	tagctgatgtttactgcctgga	59.9	00815_144058_R	acaccgtctggatgagagtttt	60.0	298	2	perfect	(CA)17
B	Ba00816	00816_37075_F	actgcactatcacaacaatggc	60.1	00816_37075_R	agtggctatggtcagggttaga	60.0	287	2	perfect	(AC)29
B	Ba00817	00817_131946_F	tctctgccggattcttctagtc	60.0	00817_131946_R	caccacacactcctcttgacat	60.1	264	2	perfect	(CA)23
B	Ba00819	00819_168963_F	gatattctaagggtgtcggctg	60.0	00819_168963_R	tgtaaataccccaaagtgaccc	60.0	363	2	perfect	(AC)22
B	Ba00820	00820_135582_F	ttggaagtgcagtagaggacaa	59.9	00820_135582_R	taacctgcatctgtgtggaaacac	60.0	194	2	perfect	(TG)18
B	Ba00821	00821_176782_F	cttactacacctaccctaccccctc	57.2	00821_176782_R	ttgtgttaatttgtggcaaagg	59.9	180	2	perfect	(CA)17
B	Ba00826	00826_12131_F	ggtgggctgtaggtcttagatg	60.0	00826_12131_R	atcatcacagcgtgagaagaac	59.4	335	2	perfect	(TG)20
B	Ba00828	00828_109198_F	ttggtttcaagatgaactgtgg	60.0	00828_109198_R	gtgaagaacatcctcatccacca	60.0	272	2	perfect	(AC)18
B	Ba00833	00833_77351_F	ggcagttcaaggtgcttaacat	60.5	00833_77351_R	cagctgtgtgtatttttgagctt	58.7	150	2	perfect	(AC)21
B	Ba00835	00835_35085_F	acgaggcagatgagagaaagtc	60.0	00835_35085_R	acactgtcactcaaacaccacc	60.0	127	2	imperfect with no gaps	(TG)20
B	Ba00836	00836_149429_F	atcatggaacatcacattagcg	59.9	00836_149429_R	tcatgtttgttgttgttccctctg	60.0	100	2	perfect	(GT)13
B	Ba00837	00837_71847_F	tcattttcaattctgttcgctg	60.2	00837_71847_R	taaacatagcaatgcaaatgcc	60.0	332	2	perfect	(AT)15
B	Ba00839	00839_21044_F	aaagcaggaaacacggattaaa	60.0	00839_21044_R	tcagcgtttgtctctttgtgtt	60.0	198	2	perfect	(AC)17
B	Ba00841	00841_157365_F	aaacgacatgctttcctcattt	60.0	00841_157365_R	ttatgacaacattcaagggcag	60.0	133	2	imperfect with no gaps	(GT)17
B	Ba00843	00843_27849_F	ccttgaaatacagctcaggtcc	60.1	00843_27849_R	gtttatctttccaagtccgtgc	60.0	252	2	perfect	(TG)16
B	Ba00845	00845_96881_F	gcacatgtcacacacataccag	60.0	00845_96881_R	ttggctcattagctgctttaca	60.0	209	2	perfect	(AC)16
B	Ba00846	00846_50838_F	aacaagataaagcagacggctc	59.9	00846_50838_R	agtgctgggtaggatcaacagt	60.1	281	2	perfect	(TG)16
B	Ba00847	00847_127421_F	tacatgtgtgtctgaggggtgt	60.3	00847_127421_R	tgcttgagaactggagatgaaa	60.0	124	2	perfect	(TG)19

Continued

B	Ba00854	00854_147469_F	actgtgctgtaccactctgcac	60.4	00854_147469_R	ccaaggtacaacagcactgaaa	60.2	140	5	perfect	(TAATC)8
B	Ba00856	00856_1876_F	ttcatcaccaaccaccaaaata	60.1	00856_1876_R	aatgtcagccctcactctgtct	60.3	315	2	perfect	(AC)16
B	Ba00857	00857_38754_F	atgattgccctaagtacagcgt	60.1	00857_38754_R	atatttcatccacgacacctcc	60.1	203	2	perfect	(TG)15
B	Ba00858	00858_125335_F	caaagtactgctctgcctctga	59.8	00858_125335_R	tgtcatgtgtcctgttgtgaaa	60.1	342	2	perfect	(TG)16
B	Ba00859	00859_104637_F	cctgcatgcatcacagtttaat	60.0	00859_104637_R	atgttactgagcatgttggtgc	60.1	224	2	perfect	(CA)18
B	Ba00862	00862_125083_F	ctcttctctgctccctcttcac	59.8	00862_125083_R	tgaggtaacgacacacaaaatgc	60.0	130	2	perfect	(TC)14
B	Ba00864	00864_54093_F	agctgaagaaggagaggaaggt	60.0	00864_54093_R	acagtgtagctggatgctgaga	60.1	120	2	perfect	(CA)19
B	Ba00866	00866_166922_F	gagacgtcaacaggtgaagaaa	59.4	00866_166922_R	gtacacacccatgtgcttcagt	60.0	117	2	perfect	(TG)15
B	Ba00868	00868_187920_F	aggcccaaaaataaaggaagag	60.0	00868_187920_R	agtgtgttgtgtttctgatggg	59.9	250	2	perfect	(AC)23
B	Ba00872	00872_135029_F	tacagctggcctgtcagataaa	59.9	00872_135029_R	aagcaaaatgggaccaaatcta	59.8	295	2	perfect	(AC)18
B	Ba00873	00873_188013_F	tgcataggattgtatctgcgtc	60.1	00873_188013_R	ttccagtttttctccaccatct	60.0	300	2	perfect	(GT)12
B	Ba00875	00875_106151_F	agctgtgaggggaaatatgaaa	60.0	00875_106151_R	aaataaagccatcagctgtcgt	60.2	276	2	perfect	(TG)19
B	Ba00878	00878_146379_F	gctagctcagagttgagtgggt	60.1	00878_146379_R	tgggcccagtttgttagtctac	60.4	140	2	perfect	(TC)16
B	Ba00882	00882_77228_F	caccagttcagctctgcttatg	60.1	00882_77228_R	aacaatcaaggactctgggaaa	60.0	394	2	perfect	(AC)16
B	Ba00883	00883_134414_F	nggtgcctacatactgtagatttc	57.6	00883_134414_R	cactcaaactgattttttgcagc	59.9	274	2	perfect	(GT)26
B	Ba00885	00885_143593_F	aagtgacattgcctggtctttt	60.0	00885_143593_R	catgtgcaggtgtaattgtgtg	60.0	211	2	perfect	(AC)15
B	Ba00889	00889_109127_F	tttttcacgtaaaatcctgcct	60.0	00889_109127_R	actggtaccgcttgaatgttct	60.1	287	2	perfect	(AC)20
B	Ba00892	00892_38605_F	caaactaacatcttggcaacca	60.0	00892_38605_R	caccaaactgtgcaaaaacatt	59.9	364	2	perfect	(CA)20
B	Ba00894	00894_115217_F	tgaggcagggatatttactcgt	60.0	00894_115217_R	ctccttactgagacgagcctgt	60.1	272	2	perfect	(TG)26
B	Ba00895	00895_124894_F	acaaatgaatgatgctgattgg	59.8	00895_124894_R	agattccattttcaccactgct	60.0	315	2	perfect	(AC)21
B	Ba00899	00899_61488_F	ttaaaatgaggcttcagtgggt	60.0	00899_61488_R	caggttgtaccccactgatttt	60.1	304	2	perfect	(AC)22
B	Ba00902	00902_75955_F	gcaggagtagacagacatgcac	59.9	00902_75955_R	aagcactttcgttaaaaggcag	60.0	186	2	perfect	(TA)16
B	Ba00903	00903_63693_F	ctattttgtcgtcggtttgtga	60.0	00903_63693_R	agcttttggaaaacaacagagc	59.9	163	2	perfect	(TG)15
B	Ba00905	00905_129588_F	gagaccatactacgatggcaca	60.0	00905_129588_R	ctctgcaaacaacaacacatca	59.8	304	2	perfect	(TG)25
B	Ba00906	00906_34904_F	tgtaaggaagatgcatttgtgg	60.0	00906_34904_R	agcaacatcaggaagaaggaaa	60.2	389	2	perfect	(AT)16
B	Ba00909	00909_89223_F	gtaacagccgacagactctcct	59.9	00909_89223_R	cctaaccaggatattgctgcat	60.4	202	2	perfect	(TG)13
B	Ba00910	00910_65961_F	tttataagaccatggggattgc	60.0	00910_65961_R	gaaggaaagctgtgagtgtgtg	60.0	200	2	perfect	(TG)15
B	Ba00911	00911_167209_F	ngtgtgtagtgaaaagtaattctgc	57.9	00911_167209_R	gtaagctgaatatctgtggggg	59.9	199	2	perfect	(TG)17
B	Ba00913	00913_106376_F	ttctttcatgcctttgttgaa	59.7	00913_106376_R	tcctacattggtctcgcctatt	60.0	384	2	perfect	(CT)13
B	Ba00915	00915_183244_F	gaccttgagagtcacatgacca	60.2	00915_183244_R	agggttagagtctgtctggctg	59.9	364	2	perfect	(AC)28
B	Ba00916	00916_67468_F	tctgaccaaaagtggactgaga	59.9	00916_67468_R	ctgtgctaggaagtagcctggt	60.0	280	2	perfect	(AC)13
B	Ba00917	00917_2632_F	accctaggtgggattttgtttt	60.0	00917_2632_R	gcatcggattaaagtgataggc	60.0	389	2	perfect	(AT)40
B	Ba00918	00918_35163_F	agggataagagggggtcattcat	60.0	00918_35163_R	ctcttgagcgagactgacagaa	59.9	143	2	imperfect with gaps	(CA)24
B	Ba00920	00920_111110_F	ttgcagcttcacatgctagttt	60.1	00920_111110_R	actgtgtgtggtttctgaatgg	59.9	259	2	perfect	(GT)13
B	Ba00921	00921_56424_F	tgactttcctggatcaggttt	60.0	00921_56424_R	cttttcatcaatttccagcaca	60.1	297	2	perfect	(AC)13
B	Ba00926	00926_178429_F	cttcctcaattgatatggagcc	59.9	00926_178429_R	tgtaacagtggaggttgaatgc	60.0	206	2	perfect	(GT)14
B	Ba00927	00927_74939_F	tcaagcttctccagacatttca	60.0	00927_74939_R	gtacatggggaaatcaaccagt	60.0	331	2	imperfect with no gaps	(CA)18
B	Ba00930	00930_14611_F	atgggaactgctgctaagtagg	59.8	00930_14611_R	aacaacttgacgttttcaggct	60.2	198	2	perfect	(GT)19
B	Ba00931	00931_32550_F	tctcattaagccagccaaaaat	60.1	00931_32550_R	ggtaaagccttcatttcctgtg	60.0	260	2	perfect	(CA)21
B	Ba00932	00932_179206_F	aggacagttccaacattcctgt	59.9	00932_179206_R	tgaatgtgtgtgtgtgtgtgtg	60.0	280	2	perfect	(GT)18
B	Ba00933	00933_85820_F	ttcaagctttgtttgtctccaa	59.9	00933_85820_R	ggtgtgtgtgtttatgtattgctc	58.5	123	2	perfect	(CA)20
B	Ba00934	00934_70815_F	atgtgagtgtcattatgcggag	60.0	00934_70815_R	cctctcccatcctgtttatctg	60.0	176	2	perfect	(AC)14

Continued

B	Ba00935	00935_155990_F	tccatttgtaatcaccctgtca	60.2	00935_155990_R	attccttcacgacatgtaggct	60.0	132	2	perfect	(TG)22
B	Ba00936	00936_23116_F	acgtaaaccaataaaactgcaan	57.5	00936_23116_R	tttgcagaatatgatcaatggc	59.9	270	2	perfect	(CA)26
B	Ba00937	00937_53528_F	aatgttgctgttgaaaacgatg	60.0	00937_53528_R	ctgggctctctctcgtgtgat	61.9	137	2	perfect	(AC)20
B	Ba00938	00938_145208_F	ggagataagggaactaaacgg	60.2	00938_145208_R	gaaaggaacatggaaaggagtg	60.0	179	2	perfect	(TA)29
B	Ba00940	00940_5717_F	acaagtctccagtggctctttc	59.9	00940_5717_R	caaactggtatttgaagtggca	60.0	203	2	perfect	(AG)14
B	Ba00944	00944_65398_F	ctcatgaagccattcacacaat	60.0	00944_65398_R	gagccaaacctctatgagcagt	59.9	116	2	Imperfect with no gaps	(AC)24
B	Ba00953	00953_123140_F	acactcagctggcagacattta	59.9	00953_123140_R	gtgactgctaacatgaagtcgc	60.0	108	2	perfect	(GT)12
B	Ba00955	00955_124695_F	agcagtttaactaagacaaggattg	57.5	00955_124695_R	ggataacgagaagagctaccga	59.9	235	2	perfect	(TG)20
B	Ba00956	00956_154565_F	ctcattcaaggtaatgggaagg	59.8	00956_154565_R	tagagtcgccgtcatgctaata	59.9	268	2	perfect	(GT)17
B	Ba00957	00957_84992_F	cttgctgcccaatatgtatcaa	60.0	00957_84992_R	gttgccaaagcatcaaaataca	60.0	255	2	perfect	(AC)16
B	Ba00958	00958_133110_F	ttgtcacttgtccatcctcaac	60.0	00958_133110_R	atcagtttgaatgagctggctt	60.3	284	2	perfect	(TG)21
B	Ba00962	00962_9072_F	ctagcccttcgtttccctttat	60.0	00962_9072_R	ttgtgtagcctcttgcttgtgt	60.0	285	2	imperfect with no gaps	(CA)26
B	Ba00963	00963_169877_F	tctttgcactcctgttgtgact	60.0	00963_169877_R	ctagccgaatgttacctgctct	59.9	139	2	imperfect with no gaps	(TG)15
B	Ba00966	00966_43581_F	aggtgctgtcactacccaaact	60.1	00966_43581_R	cacaaccatacagaaaagccaa	60.0	216	2	perfect	(TG)18
B	Ba00967	00967_158089_F	ctcagtctattcccaccacaca	60.0	00967_158089_R	ccacccagcagtaatactctcc	60.0	118	2	imperfect with no gaps	(CT)17
B	Ba00970	00970_154333_F	aaaaacaagcctcatcttgagc	59.9	00970_154333_R	tgtttttaaggctttatgggga	59.9	198	2	perfect	(TG)15
B	Ba00971	00971_110457_F	tgtgattaattaagccgtgtgg	59.9	00971_110457_R	acggatcacaaaaagaatttcc	59.4	192	2	perfect	(AC)15
B	Ba00973	00973_74660_F	ttacaccggttaaggagttgct	60.1	00973_74660_R	aaaacttgaaatgcgtcaaatg	59.2	192	2	perfect	(AC)16
B	Ba00974	00974_18978_F	ccaatcaaagcttatgaccctc	60.0	00974_18978_R	tagatgcctctcgtctgaaaca	60.0	113	2	imperfect with no gaps	(TG)21
B	Ba00979	00979_44555_F	gagatttgcaggtgggtttaag	60.0	00979_44555_R	cattgcttatgcaggtgagaac	59.8	121	2	perfect	(TG)12
B	Ba00981	00981_113310_F	agttgagactgagcaaaggagc	60.2	00981_113310_R	tgatagactgcaggcagaaaaa	60.0	147	2	perfect	(CA)17
B	Ba00982	00982_115106_F	gtcatcactgtgctgtctggtt	60.2	00982_115106_R	tgtgaatgtgtgtcaccagtgt	60.0	351	2	perfect	(TC)16
B	Ba00984	00984_169741_F	agtgcagtcaaatgtcaagcat	59.8	00984_169741_R	cattgaactctgaacatgcctc	59.7	378	2	perfect	(TG)18
B	Ba00988	00988_100199_F	gtcagaggacagcatcaacact	59.4	00988_100199_R	ctggtttccttctctttccctt	60.1	127	2	perfect	(AG)12
B	Ba00989	00989_7275_F	tccccttaggtctctgtaacca	60.0	00989_7275_R	caccagcacagctaaacaagag	60.1	237	2	perfect	(AC)14
B	Ba00992	00992_130518_F	agtggtggagacaggatgtttt	59.9	00992_130518_R	tcatcccaaaatttacatgcag	59.8	266	2	perfect	(TG)21
B	Ba00993	00993_79659_F	agagtcgtggagatgaaccatt	60.0	00993_79659_R	ctgtcctaccattcctactggc	60.0	261	2	imperfect with no gaps	(CA)32
B	Ba00994	00994_81046_F	ttcctctgaatacatgcgtttg	60.1	00994_81046_R	gaagatggagagagagagggtgaa	59.8	382	2	perfect	(TG)14
B	Ba00997	00997_851_F	atgcctctctaacctaatgcca	60.1	00997_851_R	aggagagaggaggagagacgn	60.3	241	2	perfect	(TG)34
B	Ba01000	01000_1001_F	tcagtagttgctgatgatgcct	59.9	01000_1001_R	cttgtactcaaggggtttggag	60.0	278	2	perfect	(CA)14
B	Ba01045	01045_146520_F	atttttgtgtgtatttgcgtgc	59.9	01045_146520_R	gggagttttaattaagggtcgg	60.1	120	2	perfect	(GT)12
B	Ba01054	01054_116762_F	tactgctgaggcaacacagtct	60.1	01054_116762_R	tgtgagtgcatacaaacagtgc	59.8	148	2	perfect	(TG)14
B	Ba01063	01063_150945_F	tgatttaggggactaagaggca	60.1	01063_150945_R	gcttctccttatctctccccat	60.1	136	2	imperfect with gaps	(AG)24
B	Ba01098	01098_106052_F	gtatgacaagccaagcagagtg	59.9	01098_106052_R	ctgattaggtggaggatgaagg	60.0	129	2	perfect	(AC)13
B	Ba01217	01217_118109_F	tccctctcttctctcacacaca	60.0	01217_118109_R	actccaagttcatcctctgctc	59.9	114	2	perfect	(AC)16
B	Ba01223	01223_104303_F	aatgacacatgcaggaacagag	60.2	01223_104303_R	ctttcctgttttccttctccct	60.1	141	2	perfect	(GT)19

Continued

B	Ba01263	01263_44111_F	tccctgtttaacattcaccaaa	59.4	01263_44111_R	taaggcagcgctttagttcttt	59.7	143	2	imperfect with no gaps	(CA)22
B	Ba01267	01267_129645_F	tgtggtgtcagagtaatttggg	59.9	01267_129645_R	agggagtggtacatctgctcat	60.0	142	2	imperfect with no gaps	(CA)31
B	Ba01354	01354_47986_F	gacgaacctgtgagataggtga	59.2	01354_47986_R	agcaaagagctggagagagaga	60.0	116	2	perfect	(TG)18
B	Ba01561	01561_90042_F	acaacatgtccctgcagctc	61.3	01561_90042_R	tttacagtgtgtgcatccatcc	60.8	139	2	imperfect with no gaps	(CA)23
B	Ba01564	01564_12423_F	aagcagtgtatgggtcaaaggt	59.9	01564_12423_R	tgtgaatgtgcatcagtgtgtt	60.1	319	2	perfect	(AC)20
B	Ba01632	01632_2485_F	accctctctccaagaagactcc	60.2	01632_2485_R	agaggagctgagtagcacatcc	60.1	149	2	perfect	(TG)13
A	Ba01645	01493_2405_F	tagtgaaggaggcgtagagagg	60.0	01493_2405_R	gagctcatgagtgtgactgctt	59.7	281	2	perfect	(AC)13
B	Ba01757	01757_83020_F	gccgctaatgaaaagaataagc	59.4	01757_83020_R	ctttcgtccctaaccagcatac	60.0	122	2	perfect	(GT)19
B	Ba01850	01850_84397_F	tgggcttcagttttcttgttt	60.1	01850_84397_R	ctccgaatctcgttttaaatgc	60.1	140	2	perfect	(TG)15
B	Ba01894	01894_59038_F	ctttccctgaaccaatgttctc	60.0	01894_59038_R	gaaaatcacgctgtgtaatcca	60.0	188	2	imperfect with no gaps	(AC)18
A	Ba02786	04610_3871_F	agtgaaagaggtggatgcattt	60.0	04610_3871_R	gatcgacgtgtttcagcttatg	59.8	289	3	perfect	(CAT)17
A	Ba03183	04429_2197_F	actctggtgcagtgcatcttta	59.9	04429_2197_R	aggatgcttggagtggtaagaa	60.1	188	3	imperfect with gaps	(TAT)12
A	Ba03465	00485_3129_F	attttgtgactgcaatggactg	60.0	00485_3129_R	gtggtggtttaaaaggcaattc	59.8	397	5	imperfect with no gaps	(AATTC)19
A	Ba04221	00190_1837_F	gtcagacgtgaattagtgctgc	60.0	00190_1837_R	tgaatagacaccgtctcacctg	60.2	240	3	perfect	(CAA)14
A	Ba06853	02017_617_F	tgaactaacagcggatgatttg	60.1	02017_617_R	tggacatcaagacaacatgaca	60.0	259	2	imperfect with no gaps	(GT)18
A	Ba13816	03504_798_F	ataactgccctggagatgtgat	59.9	03504_798_R	tttaagtgaaacggtagcagca	60.0	391	3	imperfect with no gaps	(TGA)11
A	-	00190_460_F	tttgtgataacactgctgaccc	60.0	00190_460_R	gtggtctttgccagtcttttct	59.8	107	2	imperfect with gaps	(CA)22
A	-	03929_814_F	agagcagcctgacagttagacc	60.1	03929_814_R	taatggcaccaacatctacagg	59.9	381	2	perfect	(TG)12

Table S2. Result of parentage test.

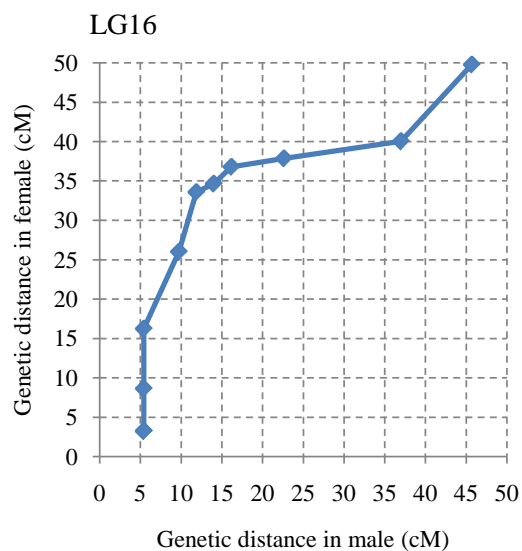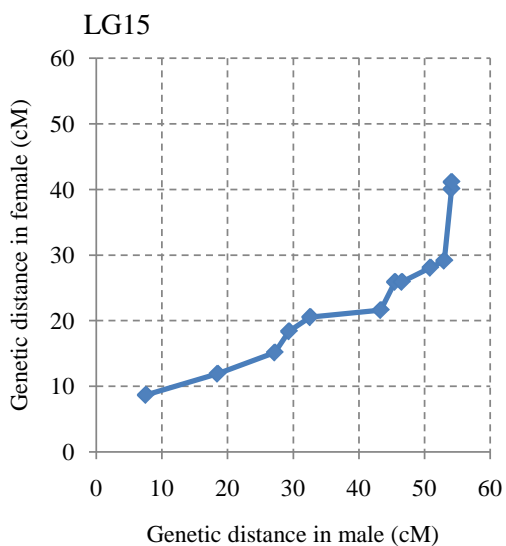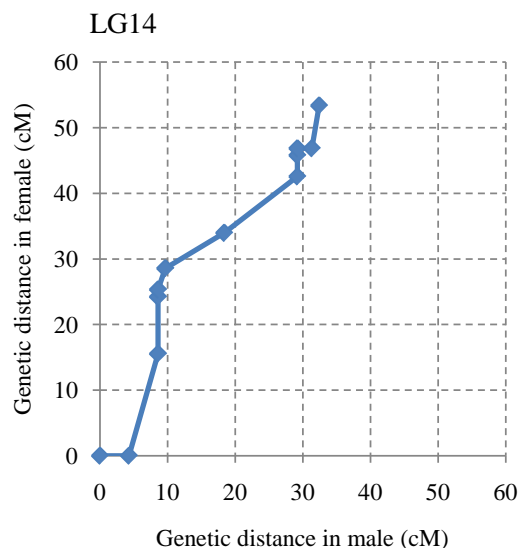| The number of offspring	23	27	138	43	194	26	2	1	46
Group number of estimated full-sib population	No. 1	No. 2	No. 3	No. 4	No. 5	No. 6	No. 7	No. 8	ND
Male Parent No.	♂No. 1	♂No. 2	♂No. 3	♂No. 4	♂No. 5	♂No. 6	♂No. 7	♂No. 8	-
Female Parent No.	♀No. 1		♀No. 2			♀No. 3		♀No. 4	-
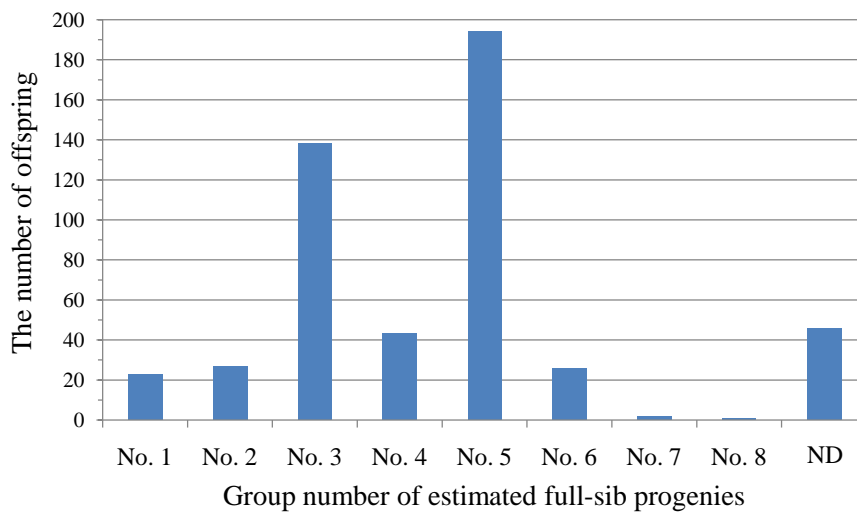
Figure S1. Composition of the full-sib population estimated from about 500 Pacific bluefin tuna progeny.

(a)

LG7
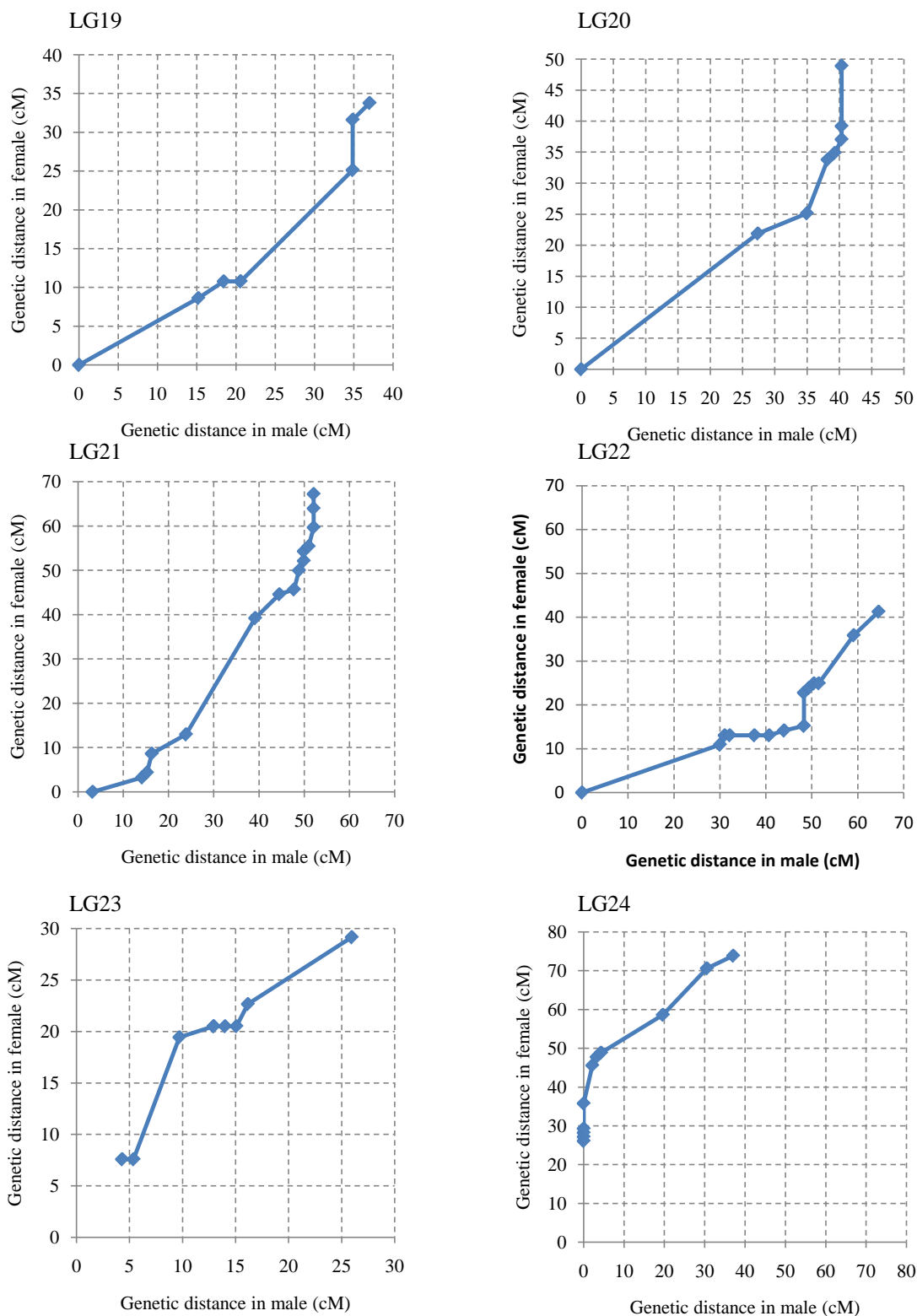
LG8

LG9

LG10

LG11

LG12

(b)

LG13

LG14

LG15

LG16

LG17

LG18

(c)
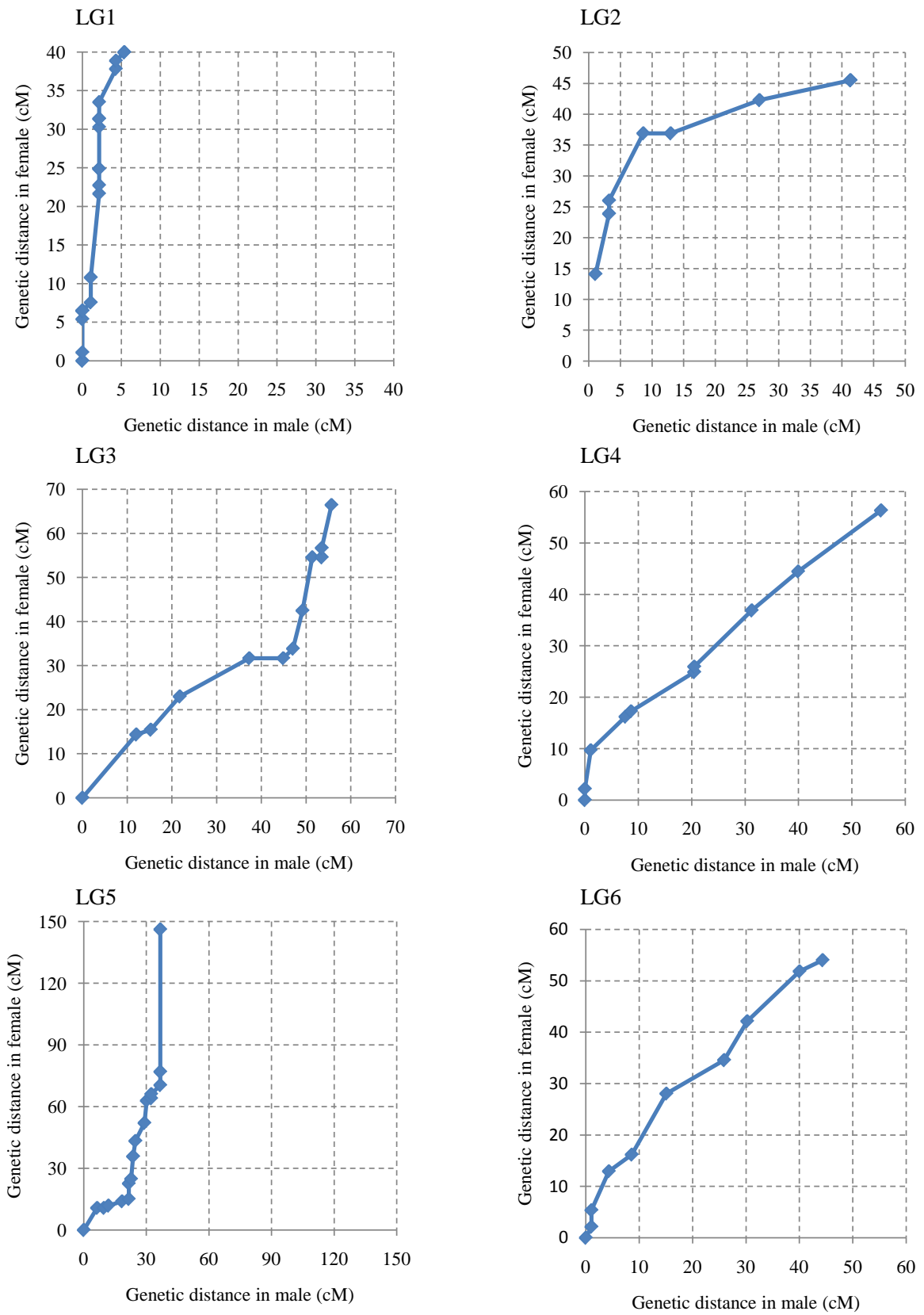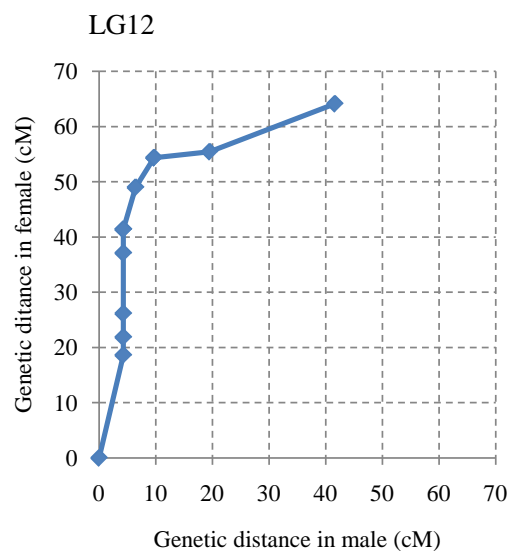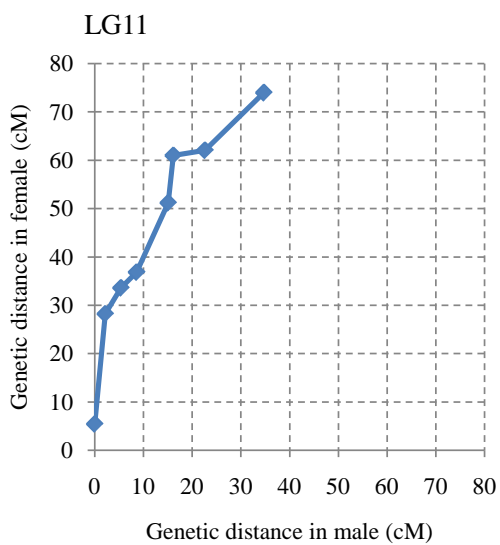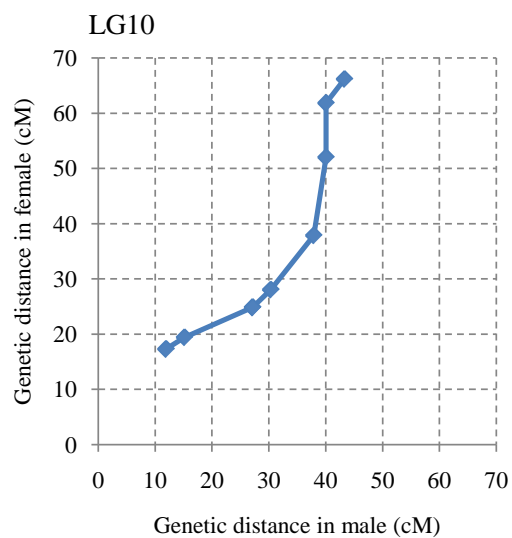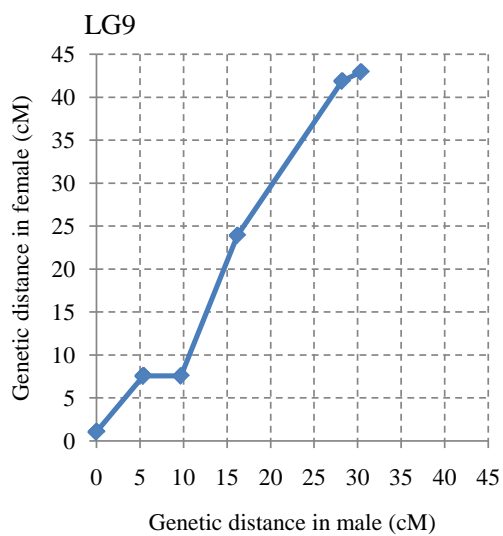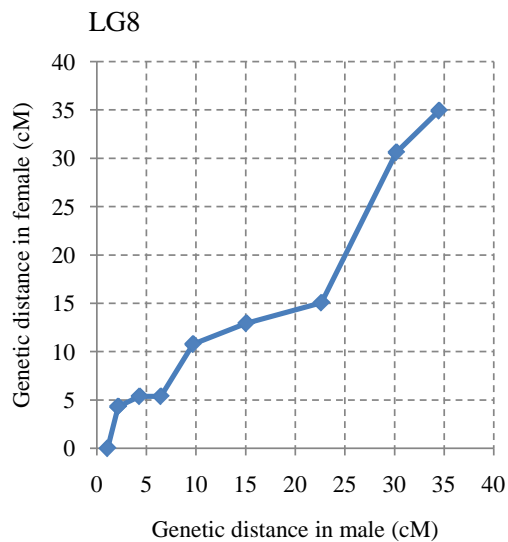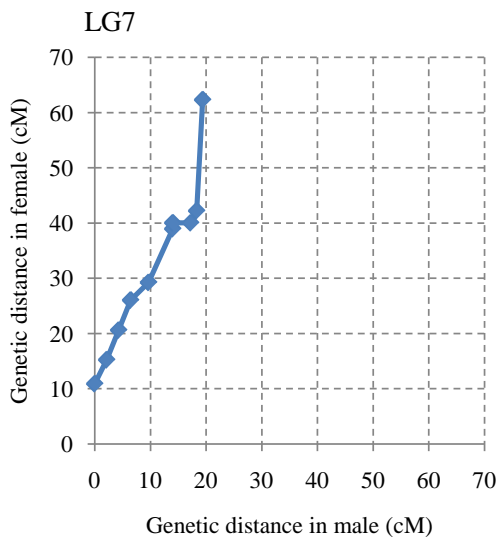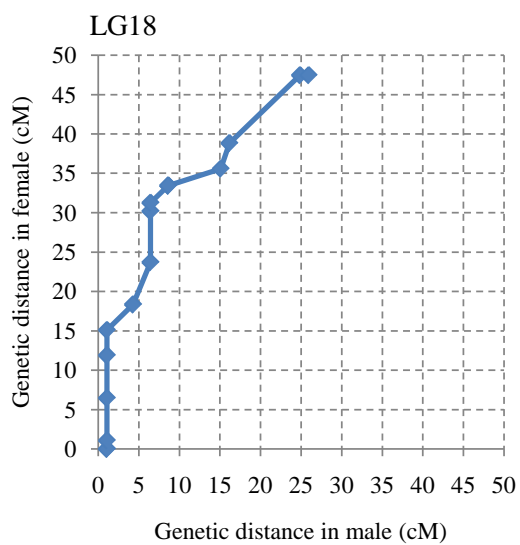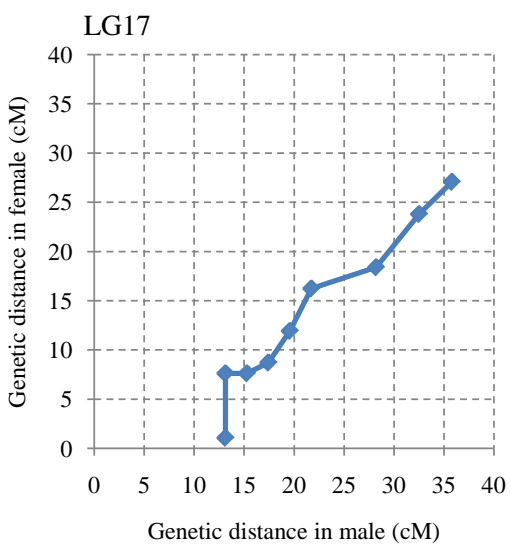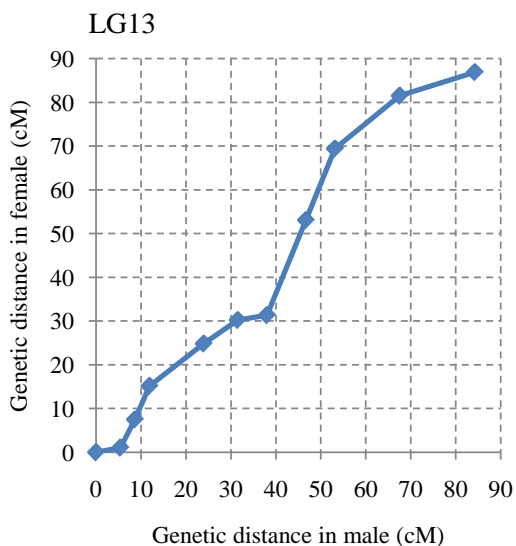
Figure S2. The intervals of between contiguous common marker in male linkage map and female linkage map. Contiguous common markers between both linkage group were plotted by dot. X axis and Y axis show cumulative genetic distance of linkage group of male and female, respectively. (a) LG 1-LG6; (b) LG7-LG12; (c) LG13-LG18; (d) LG19-LG24.
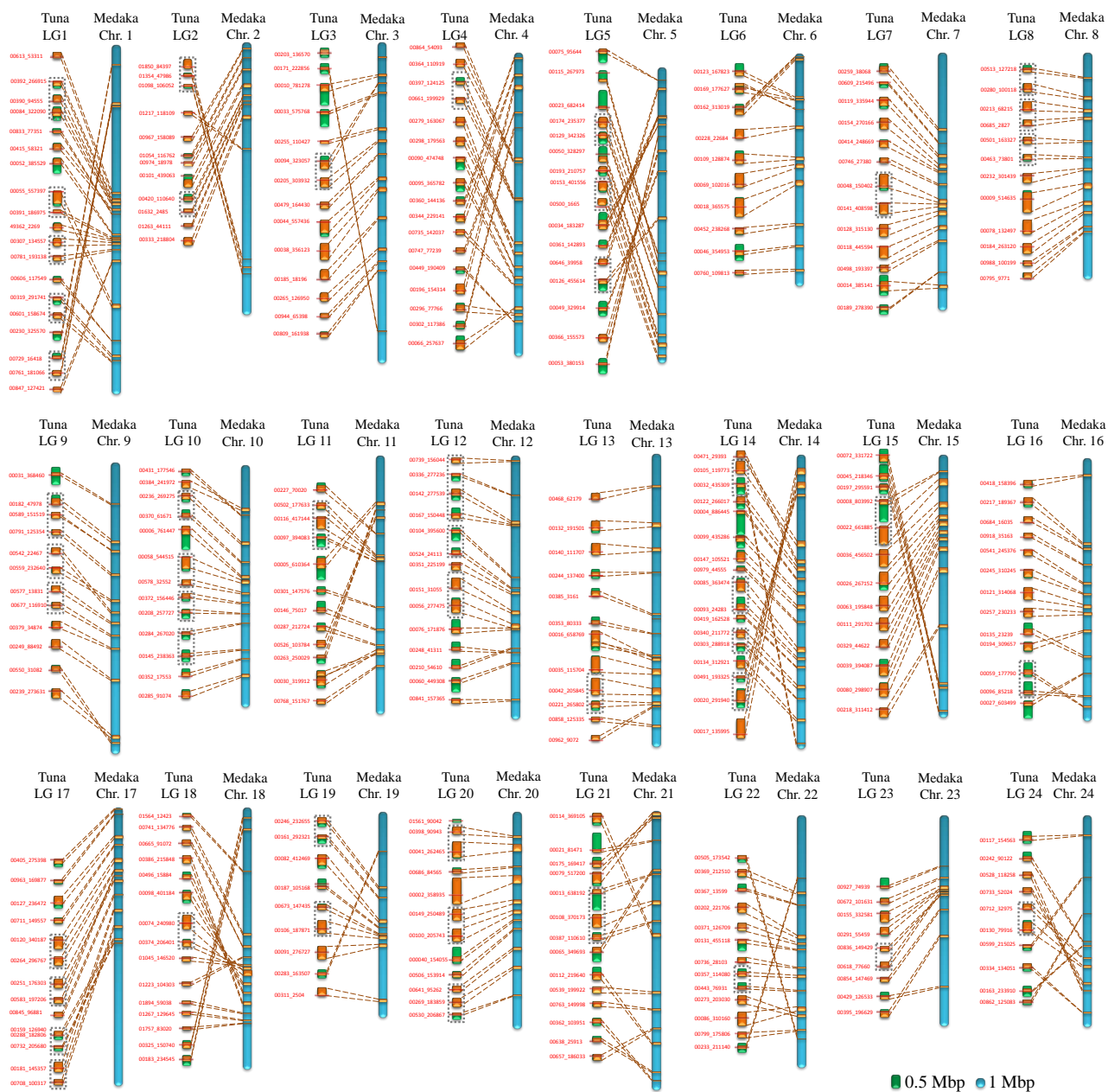
Figure S3. Comparison of chromosome structure between bluefin tuna and medaka. Red number indicates MS marker name, orange square indicates homologous region between tuna and medaka. Boxes with dotted lines indicate areas in which marker order is uncertain.