Supplementary Figures

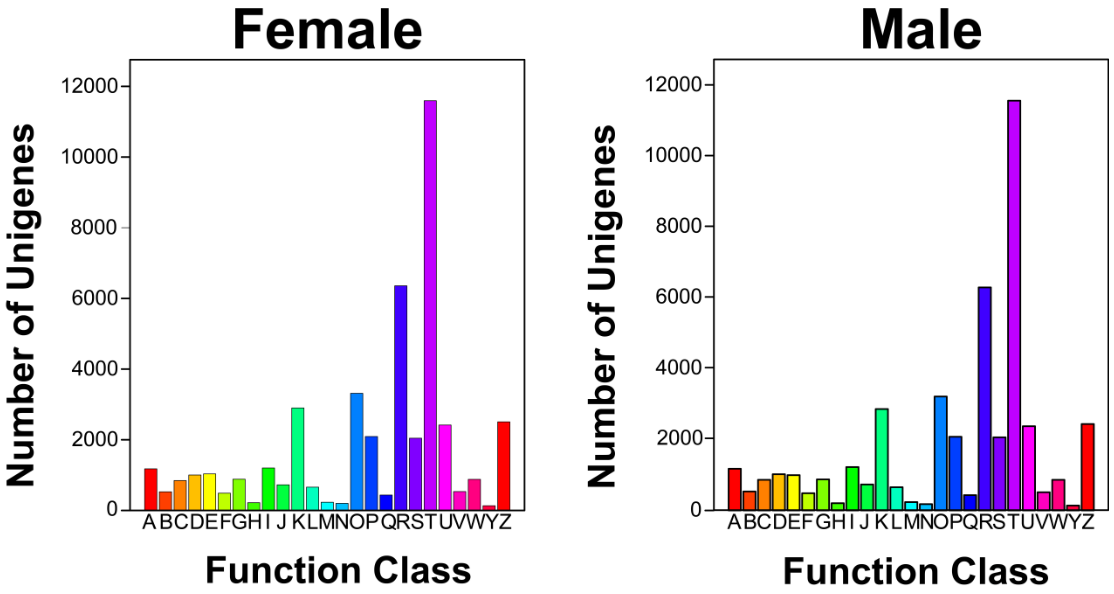

Figure. S1. KOG function classification of predicted genes in *S. argus.* The different color code (A–Z) represented different category as listed at right of the histogram. A: RNA processing and modification. B: Chromatin structure and dynamics. C: Energy production and conversion. D: Cell cycle control, cell division, chromosome partitioning. E: Amino acid transport and metabolism. F: Nucleotide transport and metabolism. G: Carbohydrate transport and metabolism. H: Coenzyme transport and metabolism. I: Lipid transport and metabolism. J: Translation, ribosomal structure and biogenesis. K: Transcription. L: Replication, recombination and repair. M: Cell wall/membrane/envelope biogenesis. N: Cell motility. O: Posttranslational modification, protein turnover, chaperones. P: Inorganic ion transport and metabolism. Q: Secondary metabolites biosynthesis, transport and catabolism. R: General function prediction only. S: Function unknown. T: Signal transduction mechanisms. U: Intracellular trafficking, secretion, and vesicular transport. V: Defense mechanisms. W: Extracellular structures. Y: Nuclear structure. Z: Cytoskeleton.

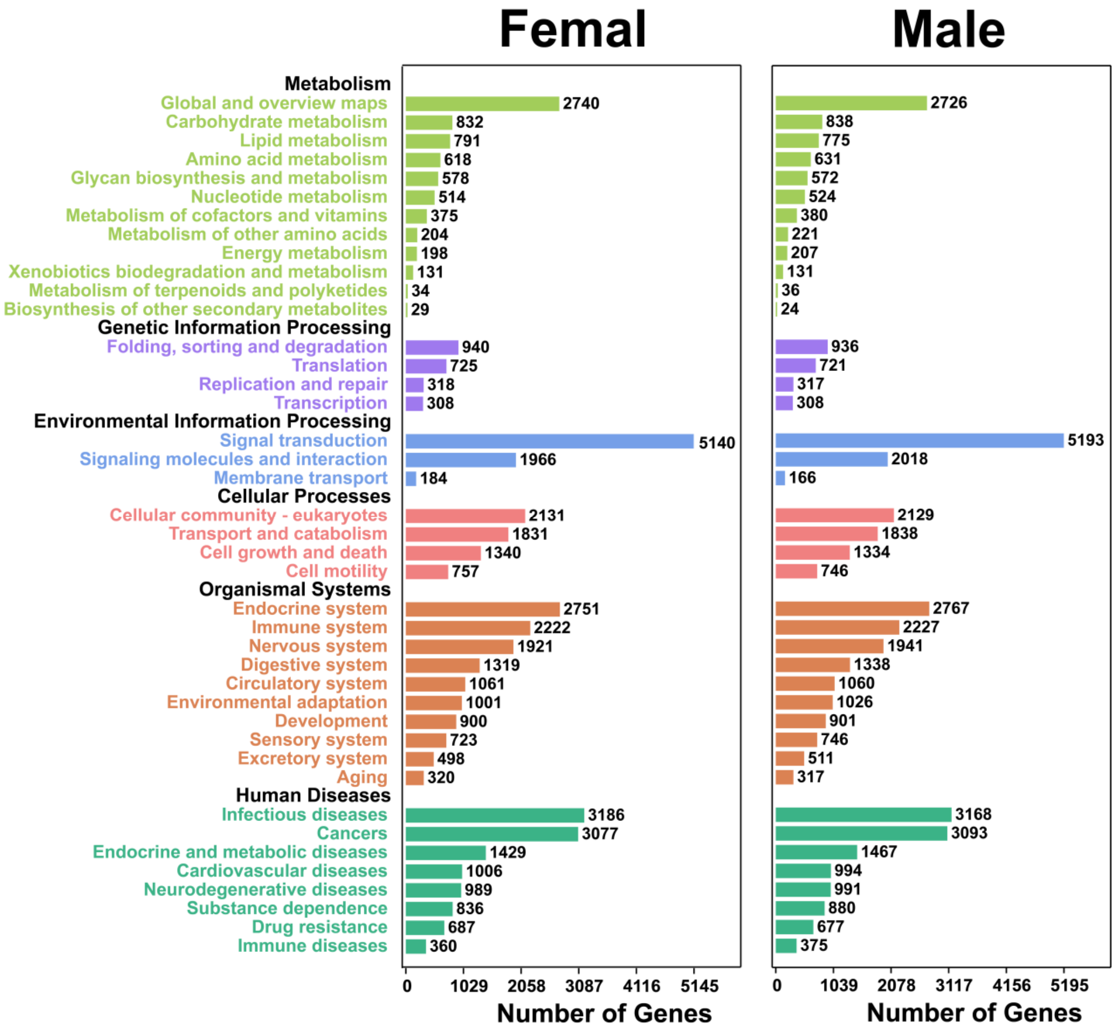

Figure. S2. KEGG pathway annotation of predicted genes in *S. argus*. The different color code represented different category.

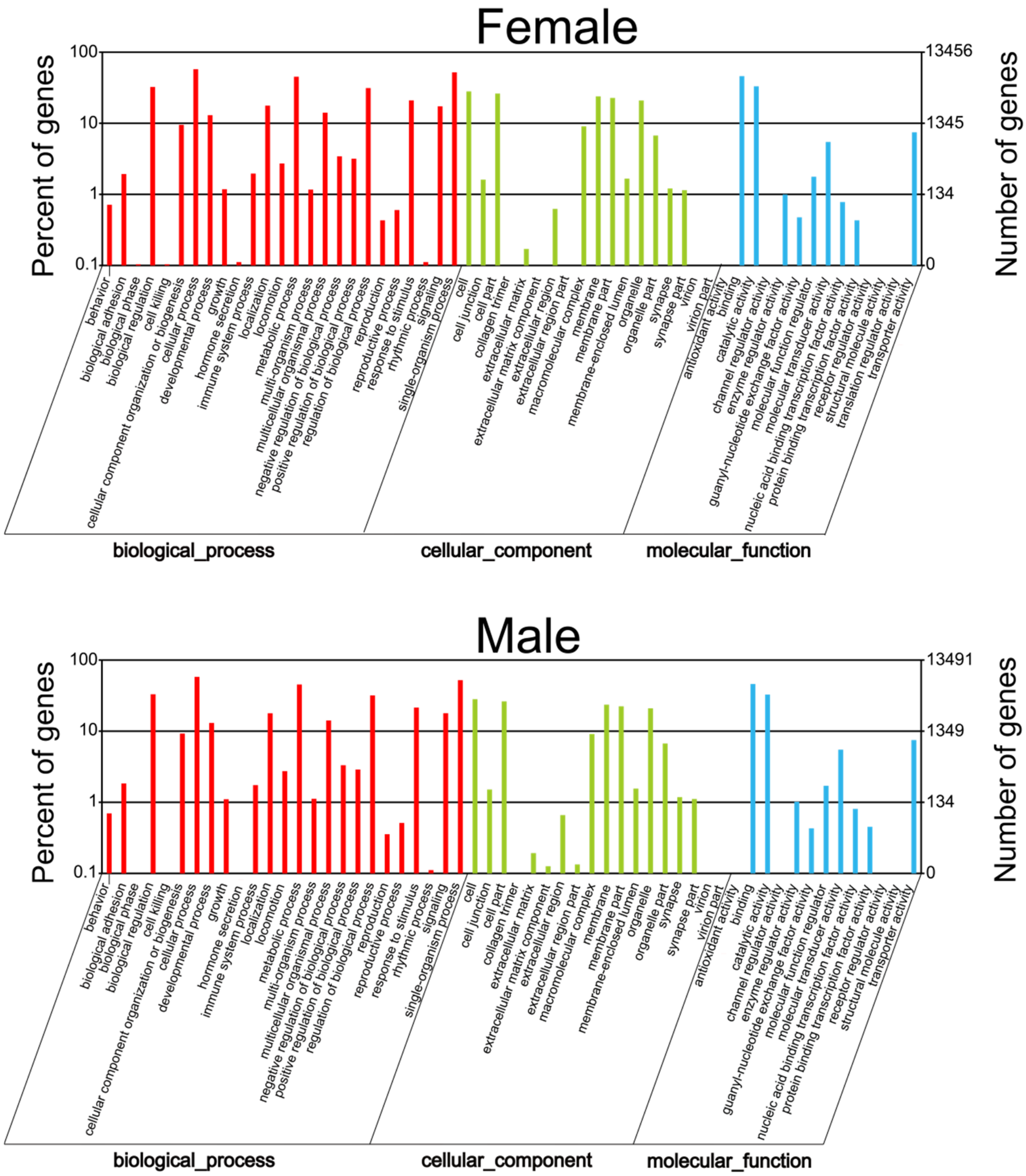

Figure. S3. Gene Ontology classification of predicted genes in *S. argus*. Genes were assigned to three categories: biological process, cellular component and molecular function.

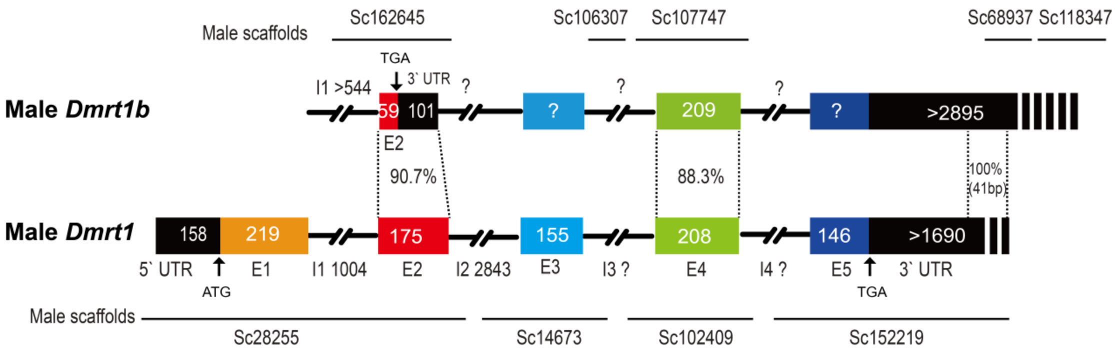

Figure. S4. The *Dmrt1b* gene from male genome. Numbers indicate base pairs (loci) of exon and intron sequences. Percentages indicate the similarity of *Dmrt1* and *Dmrt1b*. Arrows indicate the start and stop codons. Different colored rectangles represent different exons.

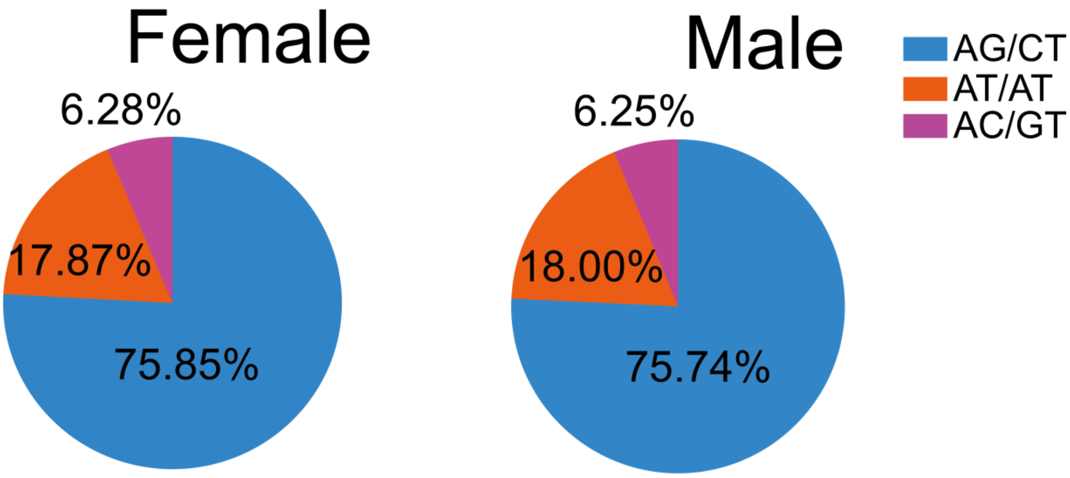

Figure. S5. Percentage of different motifs in di-nucleotide repeats of female and male *S. argus* genome.

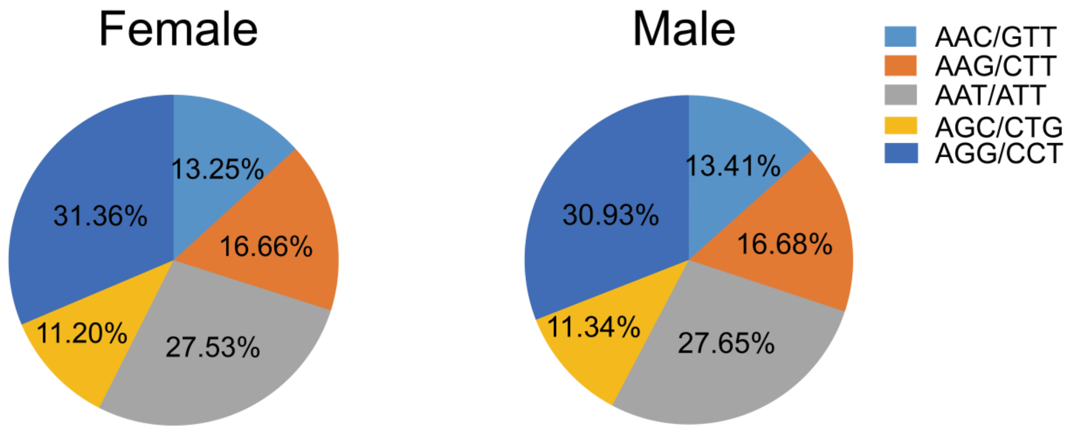

Figure. S6. Percentage of different motifs in trinucleotide repeats of female and male *S. argus* genome.

Supplementary Tables

Table S1. Statistics of top 4 similar species blasted against the NCBI nonredundant nucleotide database.

Species	**Percentage (female/male)**
Dicentrarchus labrax	0.91 / 0.91
Scatophagus argus	0.49/0.19
Haplochromis burtoni	0.36 / 0.37
Oreochromis niloticus	0.26 / 0.30

Note: Percentage of the similarity more than 90% reads in 5000 reads of female and male *S. argus*.

Table S2. Statistics of KOG function classification of predicted genes in *S. argus*

KOG code	KOG code description	Gene number (female/male)
A	RNA processing and modification	1178/1193
B	Chromatin structure and dynamics	528/543
C	Energy production and conversion	846/877
D	Cell cycle control, cell division, chromosome partitioning	1003/1037
E	Amino acid transport and metabolism	1035/1011
F	Nucleotide transport and metabolism	489/493
G	Carbohydrate transport and metabolism	884/889
H	Coenzyme transport and metabolism	219/208
I	Lipid transport and metabolism	1201/1242
J	Translation, ribosomal structure and biogenesis	725/744
K	Transcription	2901/2904
L	Replication, recombination and repair	659/665
M	Cell wall/membrane/envelope biogenesis	232/239
N	Cell motility	201/181
O	Posttranslational modification, protein turnover, chaperones	3315/3262
P	Inorganic ion transport and metabolism	2092/2110
Q	Secondary metabolites biosynthesis, transport and catabolism	436/438
R	General function prediction only	6357/6386
S	Function unknown	2045/2094
T	Signal transduction mechanisms	11595/11733
U	Intracellular trafficking, secretion, and vesicular transport	2418/2412
V	Defense mechanisms	535/521
W	Extracellular structures	880/877
X	Mobilome: prophages, transposons	0/0
Y	Nuclear structure	134/140
Z	Cytoskeleton	2507/2474

Table S3. Assessment of *S. argus* genome assembly and completeness using BUSCO (Benchmarking Universal Single-Copy Orthologs).

	Genome BUSCO **(female / male)**	**Percentage (female / male)**
Complete BUSCOs	3,055/3,108	66.6%/67.8%
Complete Single-Copy BUSCOs	2,990/3,042	65.2%/66.4%
Complete Duplicated BUSCOs	65/66	1.4%/1.4%
Fragmented BUSCOs	881/838	19.2%/18.3%
Missing BUSCOs	648/638	14.2%/13.9%

Supplementary Sequences

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TCTTGTCTCCGTGGCTTCACTTTTCAGACACAGGGGCACAGTCCATTTATTATACTGTCT
ATGGTCAGCACCTGCTTCTCTTTGAAATATTGTCATTAAAATGCTGTTGAAACAACGGT
TAGGAGCAACTGTCTTGTCAACAATACTGTAACCCAACAGATGCTGTTACTGATATACT
GATATTTCAGAGTACAGTACAGTATAGAGTGTAAAATTCTGATAATTGTTCATACATACT
TTTTTTCTTACAATTTGATAGGGAAAACATTTTAAATAATTGTAACCATTGTAC

>Predicated amino acid sequence of *Dmrt1*
MNKDTQRKQVPESTGTLSPSKHQKPSRMPKCSRCRNHGYISPLKGHKHFCNWRDCQCPK
CKLIAERQKVMAAQVALRRQQDQEEELGICSPVILPGPEVMVKDEAGADCMLSAEGRSPT
PTSTSNFSLAATGSCSMSSSLSTGARAHTEEPSDLLLENSYYNFHRPLCYPTYYGNLYNYQ
QYQQMPHDDGLLSSHNMSSQYYMHSYYPAATYLTQSLVSTPCVPGVFNLEDNNSNKNNN
NNNDNNCSEAMAASFSPSHISIVHDSACRTPLNSEVNVECEASDEMPNFTVSSIIDGDAAK.

>Female scaffold83349 (Exon1 and 2 of *Dmrt1b*)
atatatatactgtcaataaagctgattcttcttcttctttactccactttatttatttgctaacttttgtcactttgcagaatgggattaataatgccaaatca
atcaacatacaaattattattattattatgtttagtattaatgggtaatgtttattatatttattattatcataatatatagtatccattttcaccaggtgcaac
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CAAGCAGGTGCCGGAGTCCACCGGAACTCTCTCCCCATCCACGGGCCAGAAACACCG
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ACAAACGCTTCTGCAAGTGGAGGGACTGCCAGTGTCCCAAATGTAAACTGACAGCTG
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aaaacatgcaatgaaaacatgaaaagaaaacttcagacctgcgactgcatgccataattacaaaaacaaacaaacaaaaaaaaaaaccaaca
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>Predicated amino acid sequence of *Dmrt1b*
MNKDTQSKQVPESTGTLSPSTGQKHRRIFKCSLCRNHGCIIPVKGHKRFCKWRDCQCPKC
KLTADLTDIQEGKKKEASSAGKARYFARA.

> Female scaffold545689 （Contains homologous sequences to the exon 3 and 4 of *Dmrt1*)
tagcatattttattgttctgttatttagtgatgtaaagaaattaaataaatccacaggacatgagtactttcatagggactgtaaataccatagataag
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gtggtggaatgaatagaagaatcttatgaagttcatggtttcttttcctatcaactgtccgatcaatagatttgaggcaagcctagatctatacaattt
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> Female scaffold49157 (Contains homologous sequences to the 3` UTR of *Dmrt1*)
GAAGGCCAGGCTTATAAAGTGGAGTGAATAGATAGAACTTATGTTGTGATAAAACACCT
GACAGAACTCAGGTGTGCCTCAGCTGCCAACAGGAGGAGTCAGCCACACCCCCTGCC
ACCCACAGGCTCTGCAAAAGGAACAGAAAATGGAAAGGTAAACAGAGAGAGCACAA
AAAGAAAAGCACAACAGAAAACATACTACACCAAACCATAACAACAATAAAGCCTTG
TCTCCATGGCTTCACTTTTCAGACATTTATTATACTGTCTATGGTCAGCACCTGCTTCTCT
TTGAAATATTGTCATTAAAATGCTGCTGAAACAACGGTTAGGAGCAACTGTCTTGTCAA
CAAAACTGTCACCCAACAGATGCTGTTACTGATATATTGATATTTCAGAGTACAATAGTA
TAGAGTGTAAAACTCTGATAATCATTCATACGTACTTTTTTTCTTACAATTTTGATAGGG
AAAACATTTTAAATAATTGTAACCATTGTACTGAGCAGGATAATTCATCAGACCATTTGT
TTCTAAATGAGCTCAAACATGTCTTGTCTTTTCTGTACAATAATTCCATGTCAGTCATCA
GGTGACACATACAAATATATCTGCAATAAGCTATTTTTTCTTGTACAATTTATTGGTGGAT
GACAAGACACCTTTTGACTTGCAACATTGGAAAGTACTCTGAATTAAATACTGTGATTT
ACCTCAAACAACGATCGGATCAATGGGAAAATCAGATGATTGCGAAGCTGCTGAAACT
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CCTGTCTGACAGAGTGTCTCCTCCTGCAGGACAATGTGCAATTCGAGGGTTAGGGGGG
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ACTGCTTATTTATGGCGCTGATCCGGCAGCACCGTTTATACCACAGAATTTGCATGTCTG
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ACTTTGGTACTGCCTCGTAGATACAGCAGAGGATGAGGGGGTGAATCTGTAGCAGTGA
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CATTTTATAGTTTCAGCATCTCTTTGGATTTGCTGTTTTTTCTTGTCCTGAGTTGTAGTAA
ATTGAATATCTTTGAGTTCTGGACTGTTGGGATCTGGCCATTTTTCATGTTTGTTTTGTG
ATGATTTACAGACCCAGTAACATTAATCAAACCCCAAATCAAACTAAAGTTGTTTTTTA
CTTCATGAACTAATGATAGTAATCCTGTTTTGCCCACTTATGAGTTGTGTTGTTTAAGTG
TTAATTAAAAAACAACACAGATGAGATTTTGCCAATTTCTCTGCATTGTGAAGCTGACT
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GCCCTCCCATAATAGATAAAATCTGCTCGGATCCCACCGTGACACCTCCTGGTGGAGTG
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GAACATGTTCAATAAGACAAAAATTGGTCTGAAATGTGTACCACTTGAAGTTTAGGCA
ACATGATCTGCAACTTATTTGCATTCTCTCCTTTTATTCCTCTTTACCTTTTTTTGGTGAA
AATCTGTAACAGCATACTTAATGCTGAGCCTTAGGTTAAAGTTTAGTATATACCTTGTTT
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TGACAAGGCCTGTTAATGTTGACAGACATCTTCTTTGGCTAAATACAACTGATTGAATG
ATTCAGATATTAATAAATATTATTCTGTTTTCCAAGGTTTGATTATTGTGTGTATTTGTTCC
AAATATTTATATGAAGAAAGATCTGCTTTTCTTTTTTATGACGTGATCTGTTGTGGGTTC
AATACCTCAGCGTTTACTGTGATATATTCAGATTTTTTGAATGAGAGATCAGAAATATCA
GTTTATCGTGATAGATCTACTGGCGGATTTTGGCATGTTT

>Male scaffold162645 (Exon 2 of *Dmrt1b*)
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>Male scaffold106307 (Contains homologous sequences to the intron 3 of *Dmrt1*)
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>Male scaffold107747 (Contains homologous sequences to the exon 4 of *Dmrt1*)

ctcagtgccatgaaaatgcatttagaaacaggctctggagaggtctttttatcaagttatcatcctctcatctgtgatttctgcagaacacctctttg
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atatgataaaaaaaacaatcgtacaatgcatgactcggatgttgtctgtgaaatacagcacatgACGACAATTCTTTATATCAG
CCTCCTGTCGAGCCGCAACATGTCCTCTCGGTACTGCATGCATTCCTACTACCCAGCAG
ACACCTACTCGGCTCAGAGACTGGATTCCACCCCCTGTGTGCCAAGTGTCTTCAACCT
GGAGGACAACAACAGCAACAACAACAATGACAACAATGACAACAACTGCTCTGAGG
CCATGGCTGCATGTNNnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn
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gggctttatccacagtgtagttaagtgcgttcaagggagaat

>Male scaffold68937   (Contains homologous sequences to the 3` UTR of *Dmrt1*)
TTTGATAGGGAAAACATTTTAAATAATTGTAACCATTGTACTGAGCAGGATAATTCATCA
GACCATTTGTTTCTAAATGAGCTCAAACATGTCTTGTCTTTTCTGTACAATAATTCCATG
TCAGTCATCAGGTGACACATACAAATATATCTGCAATAAGCTATTTTTTCTTGGACAATT
TATTGGTGGATGACAAGACACCTTTTGACTTGCAACATTGGAAAGTACTCTGAATTAAA
TACTGTGATTTACCTCAAACAACGATCGGATCAATGGGAAAATCAGATGATTGCGAAGC
TGCTGAAACTGCACACGTTCTTTCTTTTTCTGGTATAGATGAAAGTTAATTAAAGCTCA
GAGCAGGGAACCTGTCTGAGTGTCTCCTCCTGCAGGACAATGTGCAATTCGAGGGTTA
GGGGGGACAAAAAGCCAAACATGAATCATATTTCCCTTTGTTGTGTTGGTGTGTGATGA
GCAACGACTGCTTATTTATGGCGCTGATCCGGCAGCACCGTTTATACCACAGAATTTGC
ATGTCTGTTGTATATTTAACCCCTTCTGGCCAGGAGTTTTGCTGTGCACACGGGTTACTC
TTTACACACTTTGGTACTGCCTCGTAGATACAGCAGAGGATGAGGGGGTGAATCTGTAG
CAGTGATGTGTAGAGCAGGAATATTTGAGTTTATTATCTGATTAAGTCATCTAGAAAATG
AGTCAGCATCTAATTCGAGTCGTTGGTCAGTCATTTAAGGCATTTTCCAAGACAAAAAA
GTAAAACATTTTATAGTTTCAGCATCTCTTTGGATTTGCTGTTTTTTCTTGTCCTGAGTTG
TAGTAAATTGAATATCTTTGAGTTCTGGACTGTTGGGATCTGGCCATTTTTCATGTTTGT
TTTGTGATGATTTACAGACCCAGTAACATTAATCAAACCCCAAATCAAACTAAAGTTGT
TTTTTACTTCATGAACTAATGATAGTAATCCTGTTTTGCCCACTTATGAGTTGTGTTGTTT
AAGTGTTAATTAAAAAACAACACAGATGAGATTTTGCCAATTTCTCTGCATTGTGAAGC
TGACTAGTACATGGCTGTATTGTATATTGCTTGTGTTTTATGGAGATTCATTTCAAACTGC
ATGCTTTGAA

>Male scaffold118347   (Contains homologous sequences to the 3` UTR of *Dmrt1*)
GACTTAATTGGATTTTACAGAAGATTGAGTTTTATTGCCCCGTGCTTTACGAGTTTAGTT
AAGGAAGGCCATTTTATCATGGTTGTCAGGGGTGAGCTGCTGTGCTGCCTTGTCCTTCT
GTAGCTGCTGCTGCCCTGTGTACAGCGCAGGGGAGAAAGTGTCACAGGATTGGTTTTC
CTTGAGCTGCCTCCACCTCCATGAATCATGCCCTCCCATAATAGATAAAATCTGCTCGGA
TCCCACCGTGACACCTCCTGGTGGAGTGATGGCCGCTCGACACAGACGAGAAGTGTG
GAAGAGGACGCCGTAAGATGTTGGTGTATACTTGTGTATACTTTGGATGTAGTTTCATCT
GAGTGATGTAGATGAAATATGTGTGATGAGGTCATCATACAGGATCATACAGGATTTTG
GGAAGCTCTTTATGCCTGTAGGTAGGGCTGAACATGTTCAATAAGACAAAAATTGGTCT
GAAATGTGTACCACTTGAAGTTTAGGCAACATGATCTGCAACTTATTTGCATTCTCTCCT
TTTATTCCTCTTTACCTTTTTTTGGTGAAAATCTGTAACAGCATCCTTAATGCTGAGCCTT
AGGTTAAAGTTTAGTATATACCTTGTTTAAATGTTGAAGATTAGTTAGCAAACCAGTACA
AACTATATGCTCATTCAATAAAGTACGTGACAAGGCCTGTTAATGTTGACAGACATCTT
CTTTGGCTAAATACATCTGATTGAATGATTCAGATATTAAGAAATATTATTCTGTTTTCCA
AGGTTTGATTATTGTGTGTATTTGTTCCAAATATTTATATGAAGAAAGATATGCTTTTCTT
TTTTATGACGTGATCTGTTGTGGGTTCAATACCTCCGCGTTTACTGTGATATATTCAGATT
TTTCGAATAAGAGATCAGAAATATGAGTTTATCGTGATAGATCTACTGGCGGATTTTGGC
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TCCGCTTCACCCGGGACCGGGTCGTGGGGGCAGCAGCTTGAGCAGGGATGCCCAGAC
TTTCCTCTCCCCAGACACTCTCTCCAGCTCTTCCGGGCAGACCCCAAGGCGTTCCCAG
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TATTTTTCACAACATAAGTGGAGAGTCAAGCTACATTATTTCATTTATAGAAAACAACTC
GTTTCAGGAACCTTTTAGAAATGAGACAGTAAAACAGAATAAGGGATAGCTGCTTTAG
ACTCAAGAGAAGTGTGACTTAATCCCAGAAAATAGTTTCCTCCTGTTAAAACAAGCTG
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TAATCTGAAACTAATCTGTATCGACAATTAAAGCAACAGGGGCACATATTTTGCAGAAC
CCCTAAACAAAATCGAACACTTCAAAATCATACAGCAGTTTTATCAGCATCTTTTATATG
CTGAGATGCTGATTTGTACAATTTTATCCAATATTAAATCATTTTGGCCACTTTCCTGTCC
ACTTCCCTAACAAATAAGATAAATGTCAATCATGTGTTTCATAGGGTTTTGGTCAAGTC
AAGTCAAGTCAAGTCAACTTTATTTGTACA