

Characterization of Microsatellite Distribution in Siamese Fighting Fish Genome to Promote Conservation and Genetic Diversity

Pish Wattanadilokchatkun ^{1,2}, Thitipong Panthum ^{1,3,4}, Kitipong Jaisamut ^{1,3}, Syed Farhan Ahmad ^{1,3,5}, Sahabhop Dokkaew ⁶, Narongrit Muangmai ^{1,7}, Prateep Duengkae ^{1,3}, Worapong Singchat ^{1,3} and Kornorn Srikulnath ^{1,2,3,4,5,8,9,10*}



Figure S1. Types of microsatellites or simple sequence repeats: perfect microsatellite (a), imperfect microsatellite (b), and compound microsatellite (c).

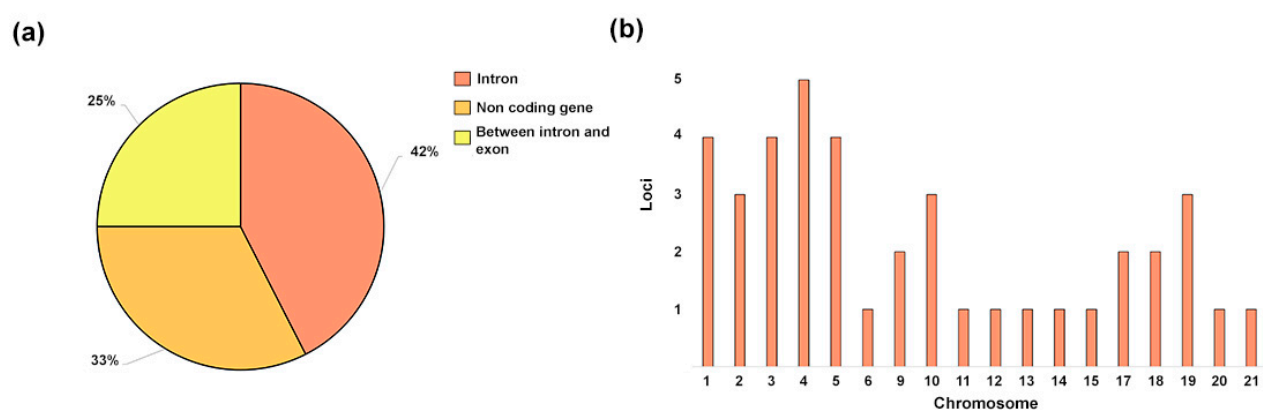


Figure S2. Pie chart showing the percentage of primer regions designed in this study (a) and bar chart of the primer loci number on Siamese fighter fish chromosomes (b).

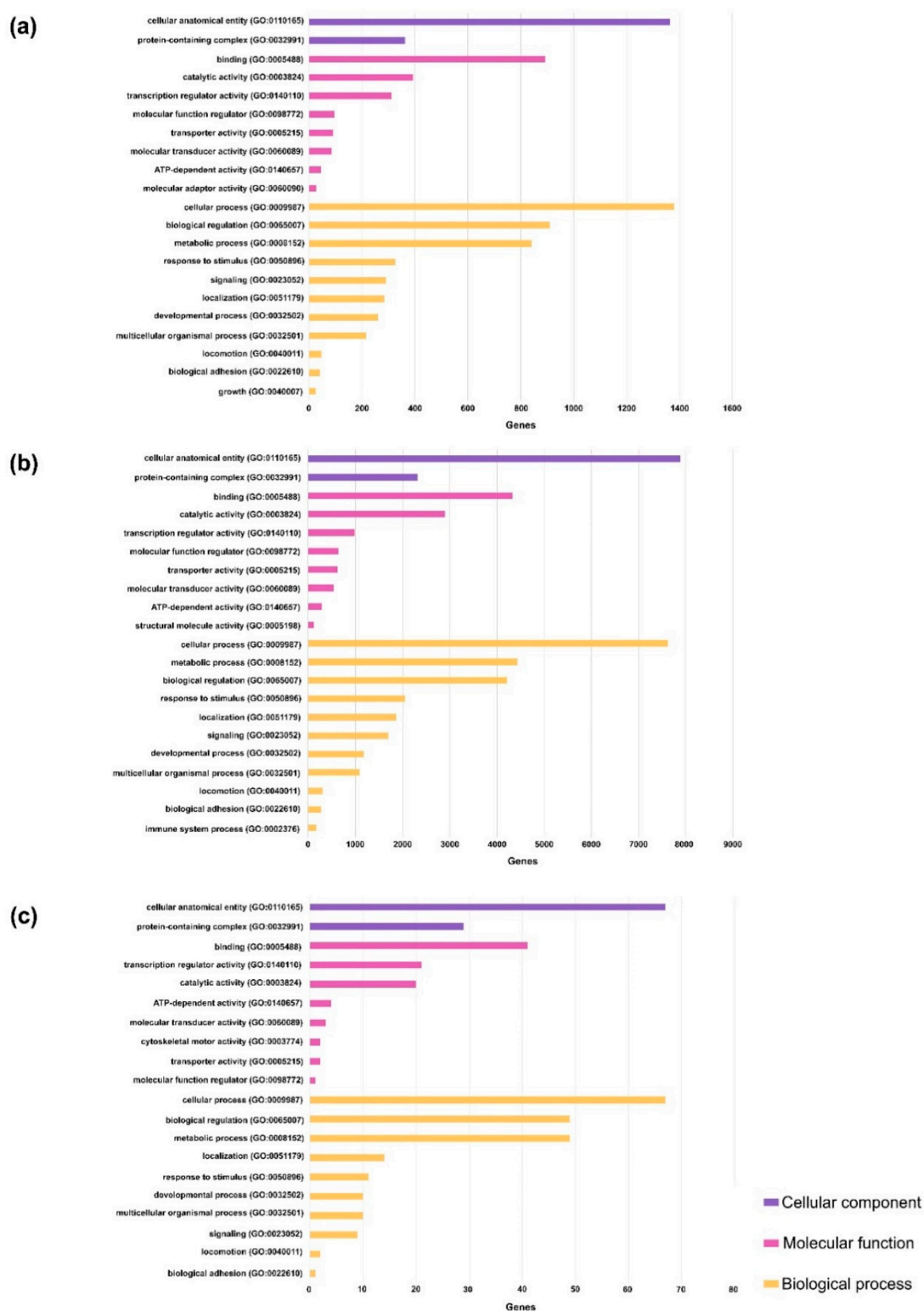


Figure S3. Gene ontology (GO) functional classification of genes containing perfect (a), imperfect (b), and compound (c) microsatellites.

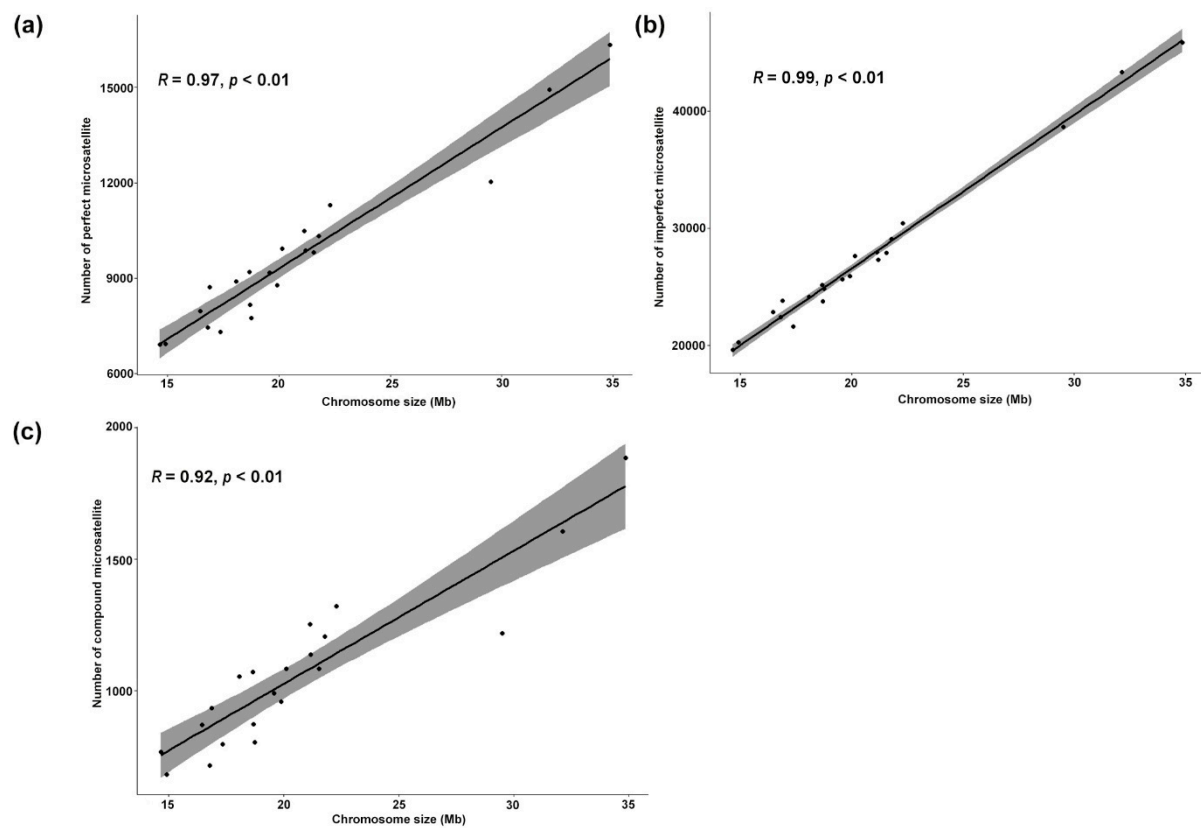


Figure S4. Scatter plots showing the correlation (R) between chromosome size and numbers of perfect (a), imperfect (b), and compound (c) microsatellites.

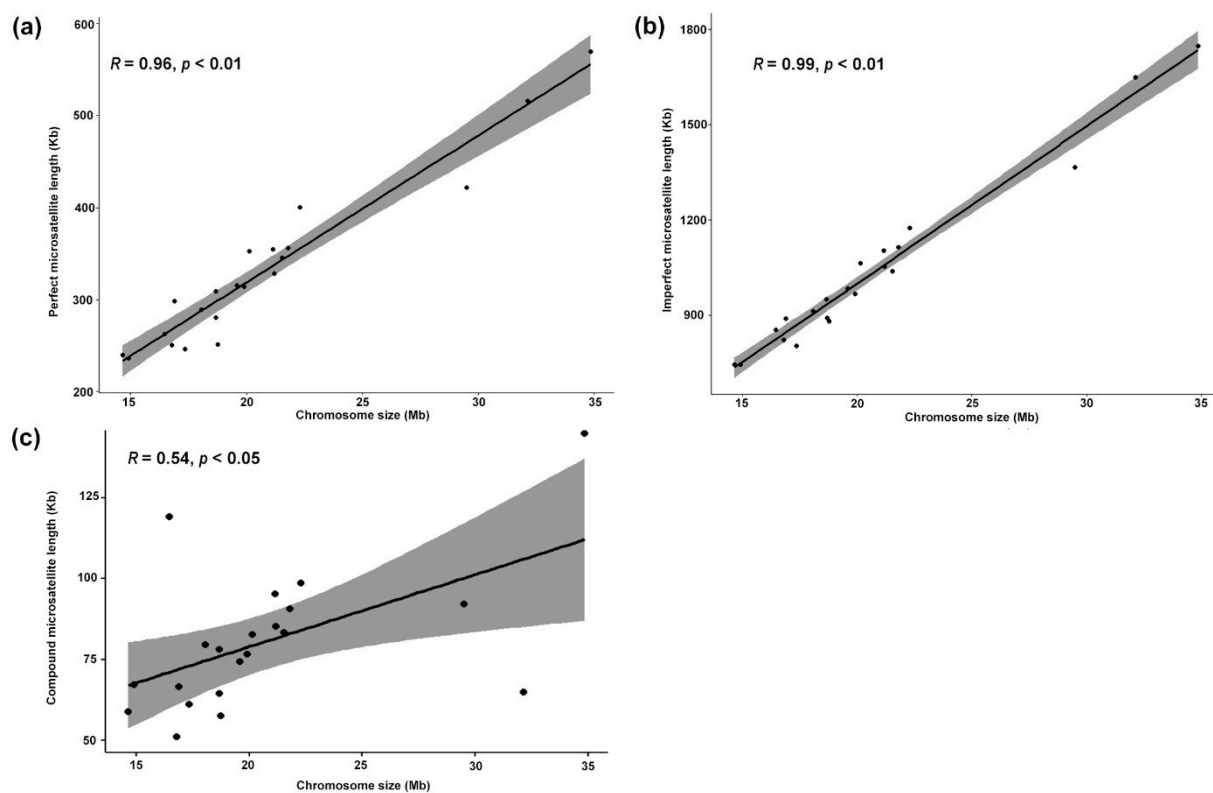


Figure S5. Scatter plots showing correlation (R) between chromosome size and lengths of perfect (a), imperfect (b), and compound (c) microsatellites.

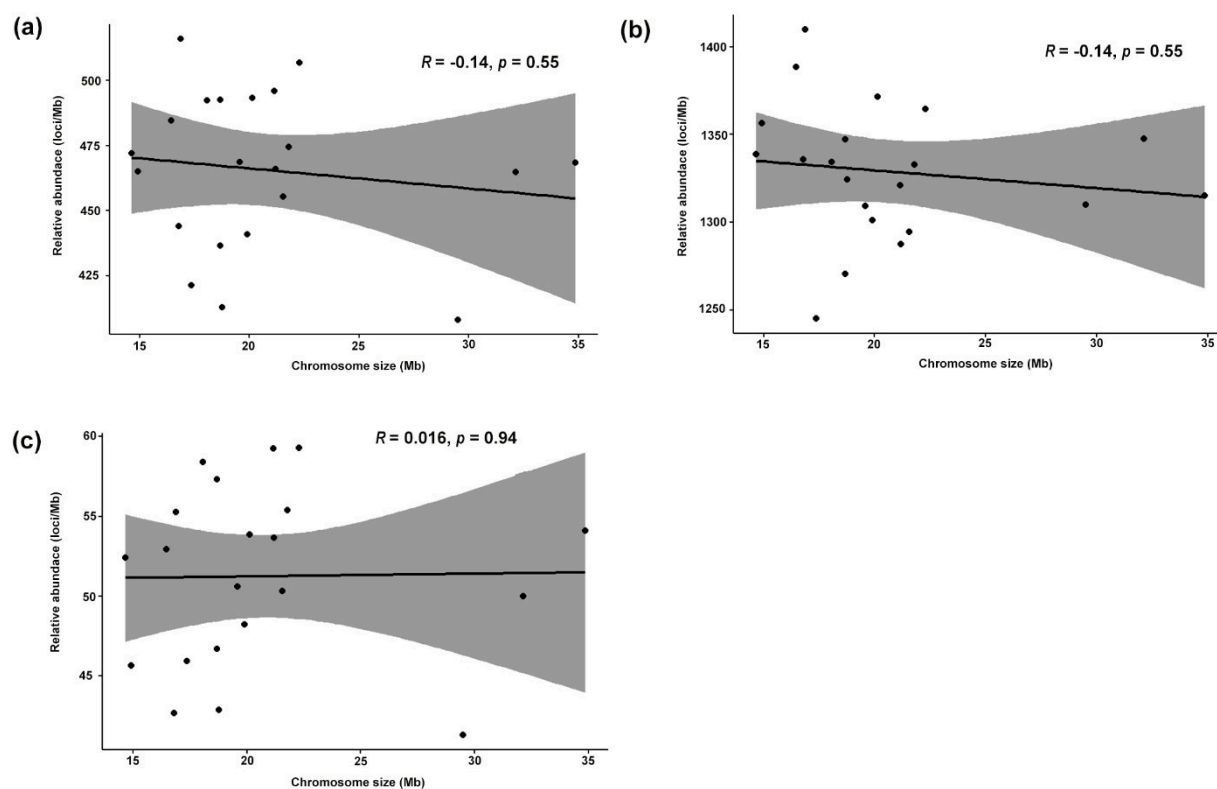


Figure S6. Scatter plots showing correlation (R) between the total number of microsatellites and the relative abundances of perfect (a), imperfect (b), and compound (c) microsatellites.

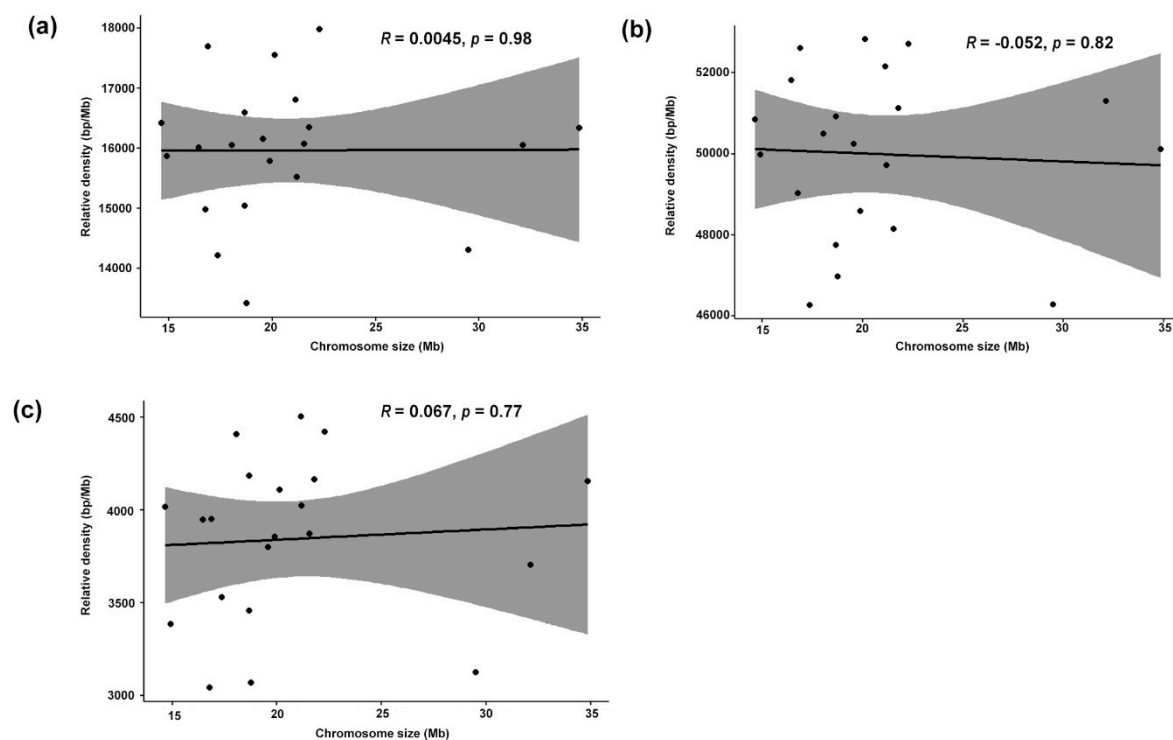


Figure S7. Scatter plots showing the correlation (R) between chromosome size and relative densities of perfect (a), imperfect (b), and compound (c) microsatellites.