

**Supplemental Table 1** Summary of Illumina NextSeq sequencing and alignment data of bulked Y-bulk, S-bulk and L-bulk\*

Sample	Number of bulked individuals	Total read number <sup>a</sup>	Total read data (Gb)	Aligned percent(%) <sup>b</sup>	Average depth <sup>c</sup>	Accession number in DDBJ
Y-bulk	22	67,352,430	5.05	96.74	7.76	DRR089343
S-bulk	32	90,010,280	6.75	91.25	6.39	DRR089342
L-bulk	33	65,973,982	4.95	96.99	10.06	DRR089341

\*Sequence reads of each sample were aligned to the Yuikogane consensus sequence

<sup>a</sup> The short reads in which more than 20% of sequenced nucleotide exhibited a phred quality score of < 20 were excluded from the analysis

<sup>b</sup> Percentage of total genomic region of Yuikogane reference sequence aligned by shot reads.

<sup>c</sup> Average of read depth in the whole genome.

**Supplemental Table 2** Characterization of 24 genetic markers developed by this study

Name	Left primer (5'-3')	Right primer (5'-3')	Chr_Positions (bp)	Restriction enzyme
Indel2_1	CTGGGGGAAGTGAAACAG	CTCGCACTGTCGCCATCT	Chr.2_36322253	
CAPS2_1	TGGAAAGAGTGGCTTGCTCT	TCCCAACTTGAACACTCT	Chr.2_36976261	Dde I
Indel2_2	CGCAAAGGGGACGGTAAATC	TGCCAGCACAGTAATTTGGC	Chr.2_37731894	
Indel2_3	AGGTGATGAAATTCAAAGATGCA	CTGTGGCGGGGAACATAAGT	Chr.2_38480665	
Indel2_4	TTCACAAATACAAACGAAACGCT	AGTTGCGCACACACTTTCTC	Chr.2_39712914	
Indel2_5	AAGTCATCGTCTTGCTTGCT	ACTTGCATCAGCTAGCTTCC	Chr.2_40076876	
CAPS2_2	TCGAGGCATCGATATCCTTT	CAGAGGTGCGTGTAGATGC	Chr.2_40407154	BamH I
CAPS2_3	GCGTGCTGATGATTGAATTG	TTCAGACGTTGCTTTGCTTG	Chr.2_41193277	Hae III
Indel2_6	CTGCTGTTTCATGCTCTTGCT	TTTACGCAATGCGGCTAAAT	Chr.2_41825982	
Indel3_1	ATCTCACCTCCCTCTTCATCC	AACCGCTCCTCTCACTCTCA	Chr.3_46556440	
Indel3_2	AGCCTGAACTCGTTCCAAAA	TGCTGAAACTGAAAAATTTGGA	Chr.3_47386968	
Indel3_3	GCGATCCGAATACCCCTGTA	TAGGGAGGATGGTTGGAACG	Chr.3_48548835	
Indel3_4	GACCTATATCGTGTCCGCCC	CCGTAGTGTGGGCTAAAGAAG	Chr.3_48831423	
Indel3_5	CCTGCGTTAGAGGCAAACCTC	CTTTTGGCGAGGCATACATA	Chr.3_50549891	
Indel7_1	ATAGGGCACGTTTGGACAGA	CTGCGCAGTTCATTTTCG	Chr.7_28590261	
Indel7_2	ATATAGCGAGGGCCGAGAGA	CCGTGTGAAAGCCGAAC	Chr.7_29204015	
CAPS7_1	TGTTCTTCCCAGAACATTGCT	TCATGTGCAGCAAACAATGA	Chr.7_29599705	Taq I
CAPS7_2	GTTTGCTTGTGCCAGAGCTT	GCCAGCAAAAGAAGTTCAGG	Chr.7_29886373	Xsp I
Indel7_3	TGTCACTGCCAGTACCAGACA	AAAGGAGAGTGGGTTTGGTG	Chr.7_30158868	
CAPS7_3	GCAGTGTCCCGCTATACAT	TGGTTTCCTTATTGACATCTCTTG	Chr.7_30419207	Taq I
Indel7_4	CCCCAATTTCTTCGCTGGTT	TTGGTGAGCGAGGAAGAGAG	Chr.7_30522602	
CAPS7_4	CTGCGTCGCGTGAATATC	TACTGCGGGTACTTGTGTGC	Chr.7_30709835	Bcn I
CAPS7_5	TCTCCTCCGTGAGGTAACCA	CTGCACACGAGAGGTTTGAA	Chr.7_31055253	BciI130 I
CAPS7_6	TGTTCTCGTTCCTTGTTCC	CGTGCAACAGCCTCTGCT	Chr.7_31563393	Dde I