Supplmental Table 1. Nuclear SSR markers mentioned in Xu *et al*. (2013) applpied to Shiikuwasha

Marker	Forward	Reverse	Remark
Csin.0384	ACAGCAACAGCAACAGCAAC	TGAGAATTGTGGAGCAAGCA	NA (not amplified)
Csin.0384	ACAGCAACAGCAACAGCAAC	TGAGAATTGTGGAGCAAGCA	NA
Csin.0479	GGGGCCATCTCTTGAGACTA	ATGGTGGCATCTCGAACAAT	NA
Csin.0543	CCTTAGTTGATTATTGTCGTTTGTT	TTGCTGTTGTTTTTGTTGATGA	NA
Ma6_29	CACTTCTAAACCCGAACCCA	TTGGAGGAATCAAGAGGGTG	NA
Ma3_5	CACGCACGCATAATGAGTTT	GGAGATTGCTACCAATAAATCCC	(polymorphic*)
Ma3_18	ACGTATGGATACTGCGACCC	TAAAGGGATTCCACAGCGTC	NA
Ma3_33	GGCCGTAACATCACAGTCAA	GTATCGGGAACCACCATCAC	NA
Ma3_35	CTCCATTACCACCACTCCTCA	TGACCCATGTCAACCATTTG	NA
Ma3_44	TTTCAGTTTCTGCTGACCCC	GGATTGTGACTGTGGCTGTG	NA
Ma3_64	CGTCCGGAATAATCAACCAA	GGAAGAATAGCGAACACCCA	NA
Ma3_68	CTGAGGAGAGTGTGAGTGCG	AACCCAAAGGCAGAACCTG	NA
Ma3_80	TGATGGCTTTCGAGTCACTG	CCTATGTAAAGCCTCGCTGC	NA
Ma3_98	GATCACCACAAGCAGCACAC	TCTCAAGAGCCCAGTTCGAT	polymorphic
Ma3_112	ACGCGTCCGAAGTAAAGAAA	TCTGGATGGAGTCGTAAGGC	NA
Ma3_117	TCCGGGACACACTTCTAACC	TGGTATGCAGCATGACGTTT	NA
Ma3_122	ACACAAATCTGCCCACATCA	GTGTGTGCATGGATGAGGAG	NA
Ma3_130	TCTTTGTCTTTCTGGCCTCTG	ATGTCCATCTCGAAGCTCGT	NA
Ma3_142	TTTCTTCGTCAACCCCAAAG	TAGAAGAAGGACCCCGAACC	polymorphic
Ma3_151	TTTTGCCACTGCACTCAATC	TAAAGGTTTAGGCGGGAGGT	NA
Ma3_161	GCATGCAAAACAGCTTGAAA	CTTGATGGGTAGTTGTGCCA	NA
Ma3_166	TCCGGTACCAAATCACAAATC	GGCATAATAGCTTTGAGCCG	NA
Ma3_168	GATTCTTCTTTCGGCTGCTG	GCTCGACAGGTTGTTGGTTT	polymorphic
Ma3_178	TTTCGCGGGATTAATTGAAG	CCAAGTTTTCGACTTCAGGC	NA
Ma3_179	GGCTTCGATTCTGGATGCTA	GCAACCTTTTCTTCTTGTTGG	NA
Ma3_191	GATGGCGGGAATAGCAATAA	CAAGAACCGAGAGGCAAAAG	NA
Ma3_200	ATGTCGACGTTGACCAATGA	TTTCGCTTCTCAGGTGGACT	polymorphic
Ma2_582	GACATGTCACACAAGCAGGC	GCAAAATACAGTTGAAAATGCG	polymorphic
Ma2_1710	TGGAACATTGAAGTGGGTGA	ACTTGAGATTAGGGCCGGTT	polymorphic

*This marker showed unstable amplification. Thus, it was not applied to estimate diversity.

Supplemental Table 2. List of SNPs presumed from NGS data obtained from MM2 accession

Chromosome	Region	Type	Reference	Allele
SNP1	282	SNV	G	T
SNP2	3078	SNV	T	A
SNP3	3086	SNV	C	A
SNP4	5568	SNV	C	T
SNP5	6309	SNV	A	G
SNP6	7320	SNV	G	A
SNP7	9559	SNV	A	C
SNP8	11041	SNV	T	C
SNP9	12653	SNV	C	G
SNP10	12806	SNV	A	C
SNP11	14040	SNV	C	A
SNP12	17470	SNV	T	C
SNP13	23257	SNV	T	G
SNP14	23363	SNV	T	C
SNP15	27243	SNV	C	A
SNP16	33340	SNV	T	G
SNP17	35351	SNV	C	A
SNP18	36140	SNV	A	C
SNP19	38215	SNV	A	C
SNP20	41051	SNV	A	T
SNP21	44357	SNV	A	C
SNP22	45627	SNV	A	C
SNP23	49450	SNV	C	A
SNP24	49898	SNV	T	A
SNP25	50074	SNV	G	T
SNP26	54420	SNV	G	A
SNP27	55629	SNV	T	G
SNP28	56377	SNV	C	G
SNP29	68608	SNV	G	A
SNP30	69566	SNV	C	A
SNP31	69726	SNV	C	G
SNP32	69997	SNV	G	T
SNP33	71966	SNV	C	A
SNP34	74586	SNV	A	C
SNP35	75266	SNV	T	C
SNP36	76225	SNV	A	C
SNP37	76319	SNV	G	A
SNP38	78113	SNV	T	G
SNP39	78452	SNV	G	A
SNP40	78954	SNV	T	C
SNP41	83814	SNV	C	G
SNP42	84450	SNV	T	G
SNP43	86719	SNV	A	T
SNP44	114697	SNV	C	A
SNP45	115100	SNV	A	G
SNP46	117267	SNV	A	C
SNP47	118376	SNV	C	A
SNP48	118676	SNV	A	G
SNP49	119636	SNV	C	A
SNP50	120227	SNV	A	T
SNP51	123024	SNV	G	T
SNP52	124007	SNV	A	C
SNP53	125276	SNV	T	G
SNP54	127176	SNV	G	T
SNP55	130204	SNV	T	G
SNP56	130332	SNV	T	G
SNP57	131104	SNV	C	A
SNP58	132216	SNV	A	C
SNP59	132396	SNV	T	G
SNP60	132915	SNV	A	C
SNP61	133177	SNV	G	T
SNP62	136291	SNV	G	A
SNP63	136306	SNV	A	T
SNP64	136320	SNV	C	T
SNP65	136333	SNV	C	A
SNP66	136344	SNV	A	T
SNP67	136347	SNV	A	G
SNP68	136352	SNV	C	A
SNP69	136354	SNV	C	A
SNP70	136357	SNV	G	A
SNP71	136359	SNV	G	A

Supplmental Table 3. List of INDELs presumed with NGS data obtained from MM2 accession

Region	Type	Reference	Allele	Markers
4201^4202	Insertion	-	ATATTTA	MM2-cpINDEL1
4485^4486	Insertion	-	A	
8129..8132	Deletion	AAAA	-	
8833^8834	Insertion	-	AAT	
8915..8926	Deletion	TTCTATATTCTC	-	MM2-cpINDEL 2
9002^9003	Insertion	-	T	
13413	Deletion	A	-	
15255^15256	Insertion	-	T	
17532..17540	Deletion	CTCTTTTTT	-	MM2-cpINDEL 3
29290	Deletion	C	-	
29544^29545	Insertion	-	T	
31113	Deletion	T	-	
31348^31349	Insertion	-	A	
37371..37372	Deletion	GG	-	
37387	Deletion	T	-	
38371^38372	Insertion	-	T	
39335^39336	Insertion	-	A	
46206^46207	Insertion	-	T	
46668	Deletion	T	-	
46718	Deletion	T	-	
47956	Deletion	A	-	
48025..48028	Deletion	AAAA	-	
48532^48533	Insertion	-	A	
49034^49035	Insertion	-	T	
49924	Deletion	T	-	
51930^51931	Insertion	-	T	
54911^54912	Insertion	-	T	
64311^64312	Insertion	-	T	
64506^64507	Insertion	-	AATTTG	MM2-cpINDEL 4
69015..69018	Deletion	TTTT	-	MM2-cpINDEL5
70634^70635	Insertion	-	A	
70959^70960	Insertion	-	AA	
71471^71472	Insertion	-	AAAC	MM2-cpINDEL 6
72550^72551	Insertion	-	A	
74562^74563	Insertion	-	T	
74823^74824	Insertion	-	AA	
78459	Deletion	C	-	
81067..81068	Deletion	TT	-	
82054..82055	Deletion	TT	-	
83618	Deletion	A	-	
84146	Deletion	T	-	
85198^85199	Insertion	-	A	
86806^86807	Insertion	-	GTTCTTT	MM2-cpINDEL 7
117908..117915	Deletion	TTTTAACA	-	MM2-cpINDEL 8
118545^118546	Insertion	-	A	
118605^118606	Insertion	-	AA	
119083..119086	Deletion	TTTT	-	

Supplmental Table 4. Genetic diversity measured by number of plastid types and nuclear haplotyes

	Ogimi		Nago		Kunigami	
Genotypes	Dom.	Wild	Dom.	Wild	Dom.	Wild
Plastid types	1	13	2	8	9	5
n=	29	73	20	42	114	67
Nuclear haplotypes	1	13	5	11	9	22
n=	29	71	20	42	114	67