Table S1: The profiles of 15 SSR markers amplified in the five Japanese quail lines in this study.

Locus	n_a	n_e	H_o	H_e	H_a	F_{IS}	F_{IT}	F_{ST}	PIC
GUJ0006	7.00	3.89	0.59	0.74	0.63	0.06	0.20	0.15	0.58
GUJ0013	6.00	4.02	0.32	0.75	0.69	0.54	0.58	0.09	0.63
GUJ0023	9.00	4.60	0.33	0.78	0.63	0.46	0.57	0.20	0.58
GUJ0027	5.00	1.27	0.04	0.21	0.20	0.78	0.79	0.06	0.18
GUJ0031	5.00	2.29	0.10	0.56	0.60	0.81	0.83	0.10	0.41
GUJ0033	10.00	3.78	0.15	0.74	0.65	0.77	0.80	0.12	0.60
GUJ0036	5.00	2.08	0.22	0.52	0.44	0.51	0.58	0.14	0.39
GUJ0037	10.00	6.09	0.48	0.84	0.71	0.32	0.42	0.15	0.69
GUJ0052	6.00	3.24	0.45	0.69	0.60	0.26	0.36	0.13	0.53
GUJ0054	8.00	3.24	0.25	0.69	0.58	0.57	0.64	0.17	0.53
GUJ0055	6.00	3.04	0.33	0.67	0.61	0.45	0.51	0.10	0.51
GUJ0063	2.00	1.33	0.17	0.25	0.22	0.19	0.31	0.16	0.18
GUJ0071	9.00	4.38	0.32	0.77	0.68	0.53	0.59	0.12	0.63
GUJ0087	6.00	3.21	0.64	0.69	0.62	0.03	0.08	0.10	0.55
GUJ0097	8.00	2.51	0.33	0.60	0.51	0.37	0.46	0.15	0.47

H_o: Observed heterozigosity. H_e: Expected heterozigosity, H_a: Average heterozigosity. n_a: allele number. n_e: effective allele number, F_{IS}, F_{IT} ,F_{ST}: Fixation indices (F_{IS}: inbreeding coefficient of an individual relative to the subpopulation, F_{IT}: the inbreeding coefficient of an individual relative to the total population, F_{ST}: effect of subpopulations compared to the total population), PIC: Polymorphic Information Content.