Supplemental Table S2. Estimation of the genome size using *K*-mer analysis.

K mer	Breed	*K* mer number	*K* mer depth	Genome size (Mb)	Revised genome size[a] (Mb)	Heterozygous rate (%)	Repetition rate (%)[b]
17	Berkshire	1.23E+11	54	2280.90	2265.71	0.34	53.68
	Hampshire	1.10E+11	47	2348.76	2330.61	0.25	55.04
	Landrace	1.01E+11	43	2356.34	2333.33	0.35	55.89
	Large White	1.02E+11	43	2367.87	2345.59	0.33	55.55
	Piétrain	9.85E+10	42	2344.98	2318.44	0.33	55.68
	Bamei	9.27E+10	40	2317.78	2291.44	0.45	54.68
	Jinhua	1.20E+11	52	2304.71	2287.44	0.40	53.48
	Meishan	1.26E+11	56	2242.39	2226.95	0.47	52.29
	Rongchang	1.08E+11	47	2301.73	2280.54	0.43	54.05

[a] 'Revised genome size' is the accurate estimation without error *K*-mers. [b] 'Repetition rate' is the proportion of the same *K*-mer fragments in all *K*-mers.