

Supplemental Table S5. Assessment of sequence coverage of pig genome assemblies using the CDS regions of the reference genome.

Breeds	Gene coverage by genome assemblies (%)					Gene coverage by reads (%)			
	Length of unigenes	Number	Length	With > 90% sequence in one scaffold (Number)	With > 50% sequence in one scaffold (Number)	Number	Length	With > 90% sequence in one scaffold (Number)	With > 50% sequence in one scaffold (Number)
Berkshire	> 0 bp	99.94	99.10	95.60	99.09	99.52	99.96	98.31	99.87
	> 1 kb	99.97	99.29	95.52	99.33	99.56	99.96	98.85	99.93
	> 5 kb	100	98.88	92.94	99.09	99.64	100	99.54	99.77
Bamei	> 0 bp	99.94	99.12	95.00	99.06	99.45	99.92	98.10	99.80
	> 1 kb	99.97	99.28	94.90	99.13	99.50	99.95	98.65	99.87
	> 5 kb	100	99.00	91.57	98.41	99.60	100	99.54	99.77
Hampshire	> 0 bp	99.95	99.07	95.66	99.08	99.47	99.92	98.09	99.84
	> 1 kb	99.97	99.24	95.66	99.31	99.51	99.94	98.59	99.92
	> 5 kb	100	98.97	92.71	99.54	99.61	100	99.54	99.77
Jinhua	> 0 bp	99.94	99.17	95.38	99.23	99.46	99.94	98.15	99.79
	> 1 kb	99.97	99.24	95.09	99.16	99.54	99.95	98.79	99.90
	> 5 kb	100	98.64	91.80	98.86	99.60	100	99.54	99.77
Landrace	> 0 bp	99.96	99.17	95.31	99.27	99.47	99.94	98.09	99.85
	> 1 kb	99.97	99.28	95.22	99.37	99.51	99.94	98.64	99.92
	> 5 kb	100	98.78	91.80	98.86	99.60	100	99.32	99.77
Large White	> 0 bp	99.95	99.17	95.46	99.17	99.46	99.94	98.04	99.85
	> 1 kb	99.97	99.34	95.44	99.43	99.49	99.95	98.57	99.90
	> 5 kb	100	98.99	94.08	99.32	99.61	100	99.54	99.77
Meishan	> 0 bp	99.95	99.07	94.19	99.05	99.52	99.96	98.38	99.84
	> 1 kb	99.97	99.22	93.93	99.15	99.56	99.96	98.91	99.91
	> 5 kb	100	99.09	94.53	98.86	99.62	100	99.54	99.77
Piétrain	> 0 bp	99.95	99.17	95.41	99.14	99.43	99.94	97.97	99.82
	> 1 kb	99.97	99.35	95.47	99.36	99.47	99.94	98.48	99.90
	> 5 kb	100	98.97	92.48	98.86	99.58	100	99.09	99.77
Rongchang	> 0 bp	99.94	99.13	95.36	99.06	99.47	99.93	98.14	99.82

Tibetan wild boar	> 1 kb	99.97	99.29	95.52	99.23	99.53	99.95	98.70	99.90
	> 5 kb	100	99.11	94.31	98.86	99.60	100	99.32	99.77
	> 0 bp	99.93	98.51	90.43	98.48	99.37	99.95	97.89	99.87
	> 1 kb	99.95	98.90	89.98	99.02	99.40	99.96	98.29	99.91
	> 5 kb	100	99.33	89.75	99.54	99.55	100	99.32	99.77

The CDS sequences of the reference pig genome (Sscrofa 10.2) were mapped to the ten assemblies and high-quality short-insert reads (180 and 500 bp) by BWA software (v.0.7.12)⁴³.