Supplemental Table S4. Comparison of characteristics of ten *de novo* assemblies and the reference genome.

Genomic features	Rongchang	Bamei	Jinhua	Meishan	Large White	Berkshire	Hampshire	Landrace	Piétrain	Duroc[a]	Tibetan wild boar[b]	Tibetan wild boar (improved)
Assembled genome size (Gb) [c]	2.48	2.49	2.48	2.49	2.47	2.46	2.45	2.46	2.45	2.52	2.43	2.44
Number of 'N' (Mb) (unidentified nucleotides)	29.40	27.21	20.75	28.84	27.09	20.13	19.19	20.55	23.38	289.54	75.39	63.02
N content of whole genome (%)	1.17	1.08	0.83	1.14	1.08	0.81	0.78	0.83	0.94	10.31	3.01	2.52
Repeat rate (%)[d]	38.36	38.35	38.27	38.23	38.38	38.56	38.52	38.54	38.77	38.05	39.47	37.74
Number of Contigs	164,130	173,646	156,849	211,377	156,159	148,496	131,882	149,882	142,850	73,524 (placed) | 168,358 (unplaced)	370,587	219,353
Contig N50 (kb)[e]	36.52	36.01	39.70	28.99	38.66	39.29	42.66	39.57	40.75	69.67	20.69	22.54
Average contig length (kp)	14.67	13.89	15.39	11.45	15.45	16.23	18.25	16.08	16.84	11.61	10.18	10.99
Largest contig length (kp)	361.38	337.37	321.77	288.40	352.32	361.68	404.46	493.58	360.68	1.60	278,361	291.06
Number of Scaffolds	44,905	52,722	48,572	61,929	42,258	38,799	32,657	39,994	36,591	5,343 (placed) | 4,562 (unplaced)	163,276	164,315
Number of Scaffolds over 2 kb	5,992	7,534	7,403	9,154	5,730	6,486	6,321	6,820	6,243	3,754	8,678	9,569
Scaffold N50 (Mb) [d]	2.36	1.54	1.49	1.26	2.45	1.68	1.56	1.42	1.67	0.58	1.06	0.88
Average scaffold length (kb)	54.28	46.27	50.12	39.54	57.74	62.64	74.28	60.77	66.38	283.54	87,98	84.49
Largest scaffold length (Mb)	15.39	13.41	10.06	8.22	11.39	8.41	9.17	13.57	9.96	3.86	6.12	5.46
GC content (%)	41.89	41.89	41.89	41.93	41.87	41.88	41.87	41.87	41.85	41.70%	41.82%	41.83%

[a] From Supplemental ref. [41]. [b] From Supplemental ref. [42]. [c] The fragments of the ungapped genome assembly. [d] The repeat rate (%) was calculated by the total length of the non-redundant consensus of the combined TEs divided by the size of the assembled genomes (with 'N, unidentified nucleotides). [e] N50 (50% of the genome is in fragments of this length or longer) of genome assembly was calculated using fragments longer than 500 bp.