Supplemental Table S14. Summary of missing sequences.

Assemblies	Missing sequences [a]			Missing sequences vs. non-aligned fragments [b]		Missing sequences overlapped with insertions (Mb) [c]	Missing sequences vs. gaps	
	Number	Maximum length (bp)	Total length (Mb)	Overlap with non-aligned fragments (Mb)	Non-aligned fragments (Mb)		Filled in gaps (length, Mb)	Filled in gaps (number)
Hampshire	82,824	64,152	136.33	136.03	300.90	0.93	16.42	9,497
Berkshire	82,958	55,058	136.40	136.11	311.62	0.99	16.15	9,376
Landrace	82,741	51,559	135.86	135.54	313.61	0.89	15.57	9,097
Piétrain	82,472	62,679	135.75	135.45	309.33	0.84	16.48	9,507
Large White	82,987	64,657	136.04	135.73	329.75	0.86	21.08	11,872
Bamei	84,336	53,097	137.49	137.14	354.07	0.97	15.25	8,921
Jinhua	84,031	88,247	137.34	137.06	335.97	1.01	15.77	9,148
Meishan	85,197	53,126	138.65	138.32	362.49	1.03	15.90	9,221
Rongchang	84,062	55,209	137.88	137.57	350.36	1.05	19.61	10,838
Tibetan wild boar	86,592	25,985	138.42	137.89	348.92	0.55	15.44	8,262

[a] To obtain high confident sequences absent in the reference genome, only sequences of lengths ⩾ 500bp aligned by at least four orphan reads per based for each assembly were selected as 'missing sequences'. [b] Most missing sequences (136.68 of 137.02 Mb, or 99.76%) have also been identified as non-aligned fragments by aligning the ten assemblies to the reference genome using the LASTZ program. [c] The small- and intermediate-scale (1-50 kb) insertions detected by assembly-versus-assembly method are listed in **Supplemental Tables S9 and S10**.