Supplemental Table S18. Assignment of inter-assembly collinear genes of ten breeds based on the Large White assembly.

		Hampshire	Berkshire	Landrace	Piétrain	Large White	Bamei	Jinhua	Meishan	Rongchang	Tibetan wild boar	
Genes in whole assembly												
Gene number		20,850	20,842	20,792	20,842	20,724	20,943	20,830	20,898	20,646	20,453	
	1 (Singleton)	1,230	1,194	1,225	1,279	244	1,381	1,314	1,401	1,135	1,220	
	2	12	19	11	17	136	11	18	13	13	22	
	3	44	22	33	38	151	35	30	28	27	45	
Number of	4	66	62	53	48	168	62	56	42	55	60	
assemblies	5	92	100	83	89	195	91	84	75	76	90	
shared with	6	165	147	144	130	249	125	141	132	130	131	
the collinear	7	250	263	250	233	362	241	234	239	239	223	
genes	8	392	409	389	403	496	403	379	388	376	333	
	9	1,277	1,304	1,282	1,283	1,401	1,272	1,252	1,258	1,273	1,007	
	10, 17,322											
	10	1	17,042 (98.38%) out of 17,322 are also been determined by the Rongchang assembly-based alignment ^a .									
Missing genes												
Missing gene number		1,105	1,092	1,093	1,096	1,105	1,104	1,090	1,116	1,064	1,094	
	1 (Singleton)	67	63	65	60	14	83	65	95	49	85	
	2	1	0	2	2	7	0	0	1	0	1	
Number of	3	5	3	3	7	16	2	3	3	0	6	
assemblies	4	0	1	2	3	5	1	2	0	3	3	
shared with	5	7	7	5	7	12	4	4	3	3	8	
the collinear	6	15	12	8	11	20	9	11	11	10	13	
missing	7	22	18	22	19	30	21	20	22	18	18	
genes	8	30	32	29	34	39	28	32	30	26	32	
	9	87	85	86	82	91	85	82	80	84	57	
	10	10 871										

^a To confirm the assignment of inter-assembly collinear genes using the Large White assembly-based alignment, we also determined the pairwise collinear relationships of gene pairs among ten assemblies using the Rongchang assembly-based alignment which has the second longest scaffold N50 size (2.36 Mb), and found that out of 17,322 inter-assembly collinear genes that were shared in all ten assemblies using the Large White assembly-based alignment, 17,322 (98.38%) were identified using the Rongchang assembly-based alignment.