Supplemental Table S1. Summary of sequencing data.

Breed	Insert size length	Raw data (Gb)	High quality data			
			Base (Gb)	Proportion of Q20 (%)	Proportion of Q30 (%)	Sequence coverage (×) [a]
Berkshire	180 bp	113.08	106.75	97.51	92.80	47.12
	500 bp	59.47	54.52	96.64	90.81	24.06
	2 kb	57.19	51.44	96.98	91.74	22.71
	5 kb	20.50	18.70	97.10	92.04	8.25
	6 kb	28.32	25.67	96.56	90.33	11.33
	Total	**278.55**	**257.09**	**97.09**	**91.86**	**113.47**
Hampshire	180 bp	101.11	97.56	96.83	91.27	41.86
	500 bp	49.61	46.26	92.93	83.65	19.85
	2 kb	45.12	41.44	95.82	89.29	17.78
	5 kb	27.65	25.62	96.37	89.84	10.99
	6 kb	26.70	24.23	95.58	87.87	10.40
	Total	**250.18**	**235.12**	**95.70**	**88.91**	**100.88**
Landrace	180 bp	87.18	82.18	96.25	89.16	35.22
	500 bp	56.69	51.68	94.16	84.65	22.15
	2 kb	49.55	44.97	95.50	88.54	19.27
	5 kb	19.20	17.36	95.46	88.96	7.44
	6 kb	18.49	16.68	95.39	89.27	7.15
	Total	**231.11**	**212.88**	**95.45**	**87.92**	**91.23**
Large White	180 bp	86.65	82.39	96.15	88.85	35.12
	500 bp	56.28	51.60	94.60	85.66	22.00
	2 kb	46.77	42.69	95.61	88.77	18.20
	5 kb	17.96	16.80	96.55	90.58	7.16
	6 kb	25.29	23.60	96.36	90.10	10.06
	10 kb	7.53	6.88	97.20	92.44	2.93
	Total	**240.48**	**223.95**	**95.77**	**88.47**	**95.48**
Piétrain	180 bp	87.97	83.45	94.91	86.89	36.00
	500 bp	53.28	46.85	93.23	83.21	20.21
	2 kb	41.73	36.52	97.17	92.43	15.75
	5 kb	30.17	27.68	95.79	88.38	11.94
	6 kb	30.73	28.58	96.55	90.23	12.33
	Total	**243.88**	**223.08**	**95.24**	**87.64**	**96.22**
Bamei	180 bp	88.53	84.44	95.28	87.76	36.85
	500 bp	52.43	46.42	93.39	83.47	20.26
	2 kb	34.80	30.94	96.25	90.46	13.50
	5 kb	18.98	17.59	95.59	88.68	7.68
	6 kb	25.23	23.91	96.78	91.28	10.44
	Total	**219.97**	**203.29**	**95.20**	**87.68**	**88.72**
Jinhua	180 bp	107.31	103.57	97.01	91.44	45.28
	500 bp	56.29	52.96	94.62	86.41	23.15

	2 kb	44.18	40.32	95.65	88.65	17.63
	5 kb	26.28	24.20	95.76	88.34	10.58
	6 kb	30.81	28.41	95.78	88.33	12.42
	Total	**264.87**	**249.45**	**96.02**	**89.26**	**109.05**
Meishan	180 bp	117.31	111.39	96.99	91.31	50.02
	500 bp	54.58	51.69	95.22	87.66	23.21
	2 kb	41.51	37.99	95.50	88.34	17.06
	5 kb	22.09	20.33	96.51	89.87	9.13
	6 kb	28.52	26.07	96.41	89.73	11.71
	Total	**264.02**	**247.47**	**96.29**	**89.80**	**111.13**
Rongchang	180 bp	97.93	94.32	97.18	92.12	41.36
	500 bp	50.72	46.48	92.37	82.38	20.38
	2 kb	45.32	41.67	95.91	89.57	18.27
	5 kb	12.08	10.97	96.95	91.37	4.81
	6 kb	13.51	12.13	97.02	91.63	5.32
	10 kb	8.15	7.75	97.11	92.10	3.40
	Total	**227.71**	**213.32**	**95.86**	**89.43**	**93.54**
Tibetan wild boar[b]	180 bp	136.57	130.05	96.80	91.42	54.66
	500 bp	88.64	86.19	96.20	91.01	36.22
	2 kb	27.13	20.84	94.44	88.06	8.76
	5 kb	33.72	13.08	95.58	90.62	5.50
	10 kb	33.23	28.07	96.71	91.16	11.80
	Total	**319.29**	**278.23**	**95.946**	**90.454**	**116.94**

Short-insert (180 and 500 bp) and long-insert (2, 5 and 6 kb) DNA libraries were constructed, and read lengths were 100 bp. For Large White and Rongchang pigs, long-insert DNA libraries in 10 kb length were constructed. In total an average of 246.75 ± 19.43 Gb of sequence data were obtained for *de novo* assembly for each of nine individuals. After filtering reads based on quality, an average of 229.52 ± 18.74 Gb of high-quality data for each individual were retained for subsequent analysis. [a]The estimated genome size (revised) is listed in **Supplemental Table S2**. The estimated genome size of Tibetan wild boar is 2,379.31 Mb. [b] The unassembled sequencing reads of Tibetan wild boar were downloaded from the NCBI sequence read archive (SRA) under accession code SRA065461.