Supplemental Table S15. Summary of copy number gains against the reference genome using read-depth method.

Breed	Total length (Mb)	Total number	Average length (kb)	Maximum length (kb)	Mapping ratio (%) of reads in copy number gains against the missing sequences
Hampshire	10.03	2,275	4.41	42.0	4.06
Berkshire	19.74	3,956	4.99	62.4	4.84
Landrace	15.07	3,400	4.43	40.6	3.57
Piétrain	11.97	2,935	4.08	37.2	3.75
Large White	16.95	3,631	4.67	58.7	3.53
Bamei	31.10	6,114	5.09	86.5	4.21
Jinhua	33.00	5,733	5.76	99.0	5.41
Meishan	35.19	6,155	5.72	108.6	4.18
Rongchang	37.06	6,855	5.41	112.8	3.75
Tibetan wild boar	19.92	4,340	4.59	44.6	4.31