Supplemental Table S7. The concordance between SNPs identified by the porcine 60K BeadChip genotyping array (Illumina) and the assembly-versus-assembly method.

SNP type	Category	Berkshire	Hampshire	Landrace	Large White	Piétrain	Bamei	Jinhua	Meishan	Rongchang	Tibetan wild boar
Homozygous	SNPs identified by the chip	11,594	12,592	12,224	11,913	13,102	16,479	18,890	17,908	17,723	17,983
	Validated by the assembly-based method	11,347	12,432	12,076	11,805	12,917	16,311	18,735	17,687	17,526	17,739
	Concordance ratio (%)	97.87	98.73	98.79	99.09	98.59	98.98	99.18	98.77	98.89	98.64
Heterozygous	SNPs identified by the chip	13,712	11,390	14,555	16,337	13,211	11,317	7,989	9,234	9,804	9,464
	Validated by the assembly-based method	13,384	11,161	14,254	16,040	12,952	10,976	7,753	8,929	9,532	9,175
	Concordance ratio (%)	97.61	97.99	97.93	98.18	98.04	96.99	97.05	96.70	97.23	96.95
Total	SNPs identified by the chip	25,306	23,982	26,779	28,250	26,313	27,796	26,879	27,142	27,527	27,447
	Validated by the assembly-based method	24,731	23,593	26,330	27,845	25,869	27,287	26,488	26,616	27,058	26,914
	Concordance ratio (%)	97.73	98.38	98.32	98.57	98.31	98.17	98.55	98.06	98.30	98.06
Identified specifically by assembly-based method	Common loci with the chip	2,328	2,197	2,458	2,545	2,416	3,060	2,967	2,991	3,124	3,062
	Validated by the chip	2,253	2,146	2,398	2,507	2,358	2,962	2,873	2,881	3,021	2,952
	Concordance ratio (%)	96.78	97.68	97.56	98.51	97.60	96.80	96.83	96.32	96.70	96.41