**Table S1.** Abbreviation and measurement method description in this study.

|  |  |  |
| --- | --- | --- |
| **Abbreviation** | **Description** | **Measurement** |
| CW-Left (kg) | Left half carcass weight | The left half of the carcass weight of the pig shall be removed from the head, hoof, tail and viscera (to retain the suet and kidney) after bleeding and stretching. |
| LD | Longissimus dorsi | At the 6th to 12th ribs of the left carcass. |
| COL (cm) | Carcass oblique length | The oblique length from the front edge of pubic symphysis to the junction of the first rib and sternum measured by tape measure. |
| CL (cm) | Carcass length | Linear length from the front of pubic symphysis of the carcass to the front of the first cervical vertebra measured by tape measure. |
| BFT (mm) | Backfat thickness | The fat thickness of the carcass at the waist to sacrum junction measured by vernier caliper. |
| L.LD (%) | Longissimus dorsi (Brightness) | This trait was measured by colorimeter (SR-64). Repeat the measurement after slaughtering 45 minutes for three times to calculate the mean value. |
| a.LD (%) | Longissimus dorsi (Redness) | This trait was measured by colorimeter (SR-64). Repeat the measurement after slaughtering 45 minutes for three times to calculate the mean value. |
| b.LD (%) | Longissimus dorsi (Yellowness) | This trait was measured by colorimeter (SR-64). Repeat the measurement after slaughtering 45 minutes for three times to calculate the mean value. |
| pH45min | pH after 45 minutes (Longissimus dorsi) | This trait was measured by Portable hand-held pH meter (HI-9025). Repeat the measurement after slaughtering 45 minutes for three times to calculate the mean value. |
| pH24h | pH after 24 hours (Longissimus dorsi) | This trait was measured by Portable hand-held pH meter (HI-9025). Repeat the measurement after slaughtering 24 hours for three times to calculate the mean value. |

**Table S2.** Distribution of SNPs before, and after quality control and the average distance between adjacent SNPs on each chromosome.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **CHR** | **NSNP1** | **NSNP2** | **Physical distance (bp)3** | **SNP/bp4** |
| 1 | 4,753 | 3,327 | 274,018,613 | 82,386.83 |
| 2 | 3,212 | 2,204 | 151,322,033 | 68,689.08 |
| 3 | 2,840 | 1,861 | 132,538,400 | 71,257.2 |
| 4 | 2,938 | 1,691 | 130,756,997 | 77,371 |
| 5 | 2,239 | 1,459 | 103,541,477 | 71,016.1 |
| 6 | 3,338 | 2,439 | 170,514,723 | 69,940.41 |
| 7 | 2,697 | 2,219 | 121,206,582 | 54,646.79 |
| 8 | 2,857 | 1,644 | 138,698,852 | 84,418.05 |
| 9 | 3,081 | 1,869 | 139,185,075 | 74,510.21 |
| 10 | 1,453 | 946 | 69,170,958 | 73,196.78 |
| 11 | 1,810 | 1,115 | 78,978,619 | 70,896.43 |
| 12 | 1,276 | 877 | 60,934,130 | 69,559.51 |
| 13 | 3,573 | 2,557 | 207,996,524 | 81,375.79 |
| 14 | 3,214 | 2,164 | 141,617,056 | 65,472.52 |
| 15 | 2,834 | 1,754 | 140,055,764 | 79,894.90 |
| 16 | 1,774 | 1,124 | 79,253,250 | 70,572.80 |
| 17 | 1,376 | 1,027 | 61,598,438 | 60,037.46 |
| 18 | 1,235 | 829 | 55,566,607 | 67,109.43 |
| X | 2,192 | — | — | — |
| Y | 215 | — | — | — |
| Unknown | 1,790 | — | — | — |
| Total | 50,697 | 31,106 | 2,256,954,098 | 71,797.29 |

1 The original number of GGP50K chip.

2 Extracting criteria: MAF > 1%, HWE < 10-6, SNP call rate > 90%, autosomes. After quality control, we removed 537 SNPs due to HWE test, and 14,812 SNPs were removed due to MAF threshold.

3 Chromosome region length.

4 Average distance between SNPs.

**Table S3.** Enrichment of KEGG pathway in Homo Sapiens dataset

|  |  |  |  |
| --- | --- | --- | --- |
| **Trait** | **KEGG pathway** | **ID** | ***P-adj*** |
| a.LD | Proteasome | hsa03050 | 1.15E-2 |
| BFT | Apoptosis | hsa04210 | 3.42E-2 |
| CL | Amyotrophic lateral sclerosis (ALS) | hsa05014 | 1.94E-2 |
| Kaposi sarcoma-associated herpesvirus infection | hsa05167 | 2.84E-2 |
| Human immunodeficiency virus 1 infection | hsa05170 | 3.18E-2 |
| GnRH signaling pathway | hsa04912 | 3.18E-2 |
| Human cytomegalovirus infection | hsa05163 | 3.43E-2 |
| Inflammatory mediator regulation of TRP channels | hsa04750 | 3.43E-2 |
| AGE-RAGE signaling pathway in diabetic complications | hsa04933 | 3.43E-2 |
| C-type lectin receptor signaling pathway | hsa04625 | 3.53E-2 |
| Platelet activation | hsa04611 | 4.48E-2 |
| Osteoclast differentiation | hsa04380 | 4.68E-2 |
| Oocyte meiosis | hsa04114 | 4.68E-2 |
| Dopaminergic synapse | hsa04728 | 4.87E-2 |
| DNA replication | hsa03030 | 4.97E-2 |
| Spliceosome | hsa03040 | 4.97E-2 |
| Apoptosis | hsa04210 | 4.97E-2 |
| COL | Apoptosis | hsa04210 | 6.18E-3 |
| Phosphatidylinositol signaling system | hsa04070 | 4.11E-2 |
| Protein processing in endoplasmic reticulum | hsa04141 | 4.11E-2 |
| Kaposi sarcoma-associated herpesvirus infection | hsa05167 | 4.20E-2 |
| Human immunodeficiency virus 1 infection | hsa05170 | 4.20E-2 |
| Human cytomegalovirus infection | hsa05163 | 4.29E-2 |

**Table S4.** Top 10 traits with the highest enrichment QTLs number.

|  |  |  |
| --- | --- | --- |
| **Trait** | **Related Trait Name** | **NQTL** |
| CL | Average daily gain | 13 |
| Average backfat thickness | 10 |
| Head Wight | 9 |
| Loin muscle area | 7 |
| Adipocyte diameter | 6 |
| Conductivity 45 minutes post-mortem | 6 |
| Backfat at last lumbar | 5 |
| Backfat at last rid | 5 |
| NADP-malate dehydrogenase activity | 4 |
| Carcass length | 3 |
| COL | Average daily gain | 14 |
| Average backfat thickness | 11 |
| Head Wight | 11 |
| Loin muscle area | 7 |
| Mean corpuscular volume | 7 |
| Adipocyte diameter | 6 |
| Conductivity 45 minutes post-mortem | 6 |
| Backfat at last lumbar | 5 |
| Backfat at last rid | 5 |
| Carcass Length | 4 |
| BFT | Average daily gain | 5 |
| Carcass weight(hot) | 3 |
| Average backfat thickness | 2 |
| Body weight | 2 |
| Fat-cuts percentage | 2 |
| Head weight | 2 |
| Intramuscular fat content | 2 |
| Loin muscle area | 2 |
| Loin muscle depth | 2 |
| Muscle moisture percentage | 2 |
| a.LD | Average daily gain | 4 |
| Average backfat thickness | 2 |
| Body weight | 2 |
| Ham weight | 2 |
| Intramuscular fat content | 2 |
| Leaf fat weight | 2 |
| 3 hr-24 hr pH decline | 1 |
| Meat color a\* | 1 |
| Meat color b\* | 1 |
| Meat color L\* | 1 |