**Figure S1.** Ring diagram of lipid subclass composition, 18 samples of subcutaneous adipose from six Ningxiang pigs, six Berkshires and six $F_1$ pigs, respectively, were used to detect lipidomic profile.
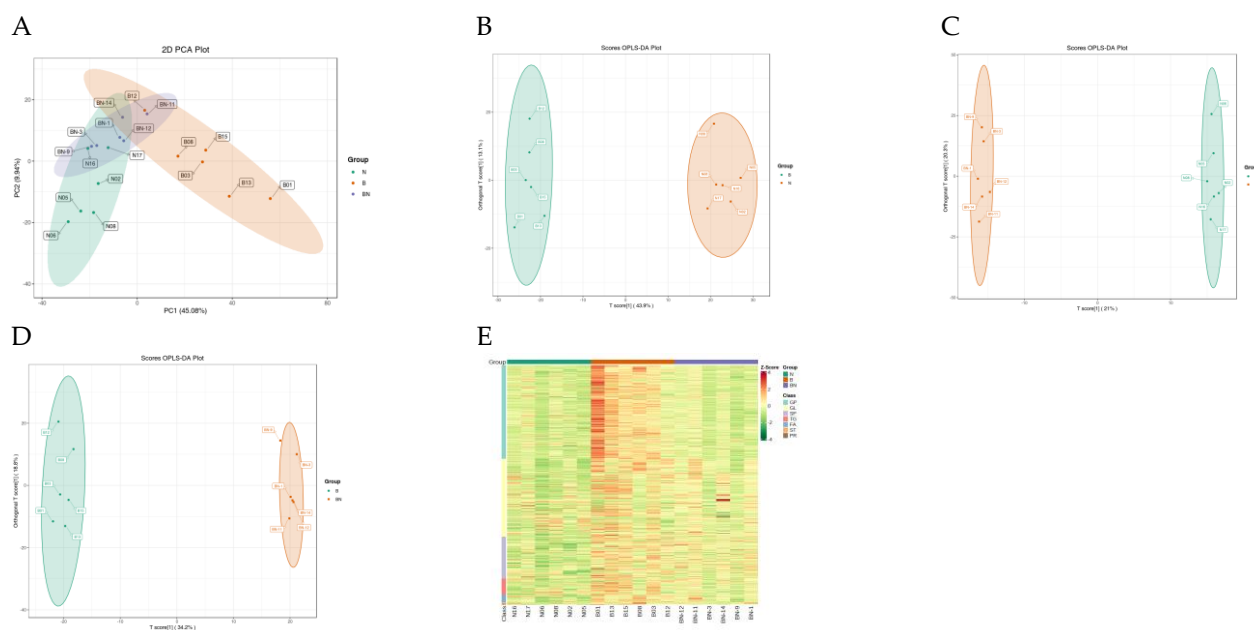


**Figure S2.** The subcutaneous adipose tissue lipid composition. (A) PCA of the subcutaneous adipose tissue from Ningxiang pigs, Berkshires and $F_1$ offspring. (B) OPLS-DA of the subcutaneous adipose tissue from Ningxiang pigs and Berkshires. (C) OPLS-DA of the subcutaneous adipose tissue from Ningxiang pigs and $F_1$ offspring. (D) OPLS-DA of the subcutaneous adipose tissue from Berkshires and $F_1$ offspring. (E) Overall cluster heat map of the samples. Eighteen samples of subcutaneous adipose from six Ningxiang pigs, six Berkshires and six $F_1$ pigs, respectively, were used to detect lipidomic profile.
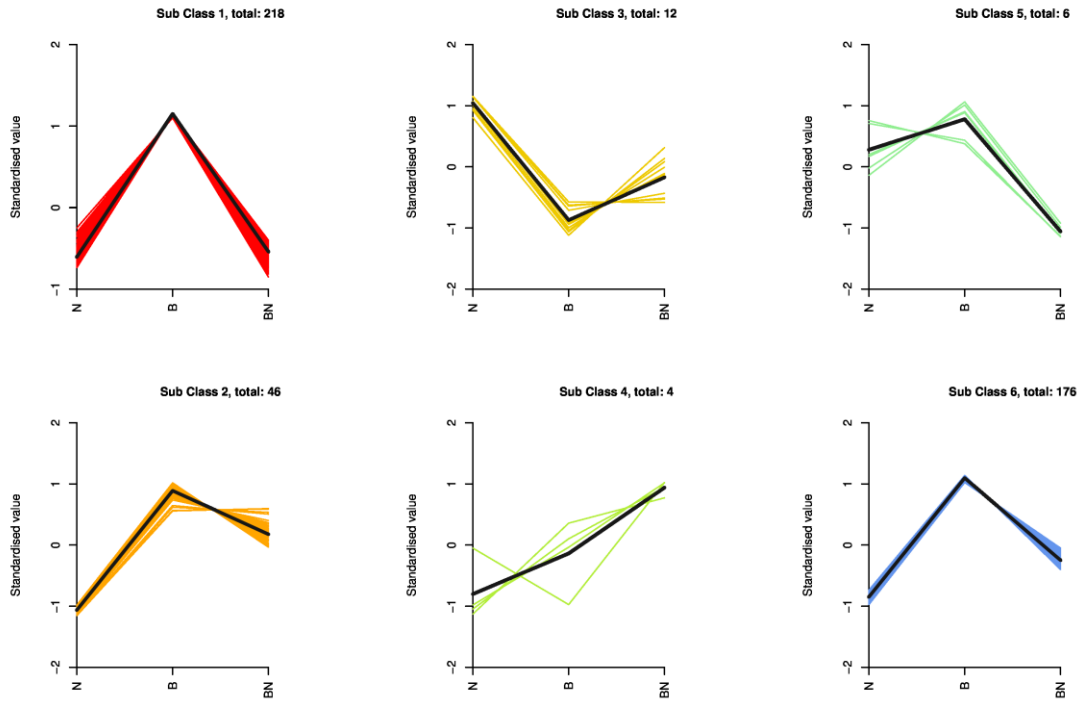
**Figure S3.** K-Means of SCLs. The horizontal ordinate represents sample groups, the Y-axis represents standardized relative lipid content, and Sub Class represents lipid class numbers with the same trend of change. Twelve samples of subcutaneous adipose from four Ningxiang pigs, four Berkshires and four $F_1$ pigs, respectively, were used to detect transcriptomic profile. B, Berkshires; N, Ningxiang pigs; BN, $F_1$ offspring.



**Figure S4.** Transcriptome profiles diverse in the subcutaneous adipose tissue. (A) Transcriptome correlation analysis, B, Berkshire; N, Ningxiang pig; BN, $F_1$ offspring; (B-D) Cluster heat map of DEGs for the subcutaneous adipose tissue in the groups of Berkshires vs Ningxiang pigs (B), Ningxiang pigs vs $F_1$ offspring (C), Berkshires vs $F_1$ pigs (D). Twelve samples of subcutaneous adipose from four Ningxiang pigs, four Berkshires and four $F_1$ pigs, respectively, were used to detect transcriptomic profile. B, Berkshire; N, Ningxiang pig; BN. $F_1$ offspring.
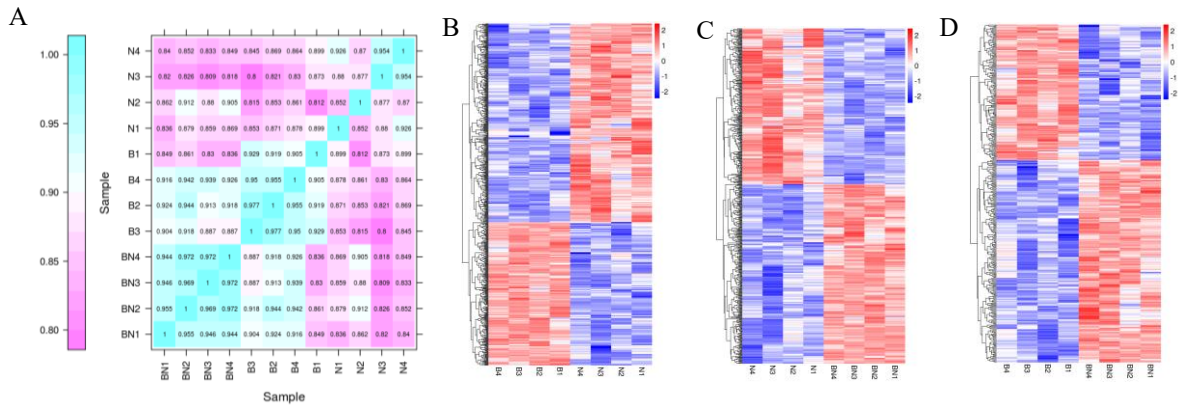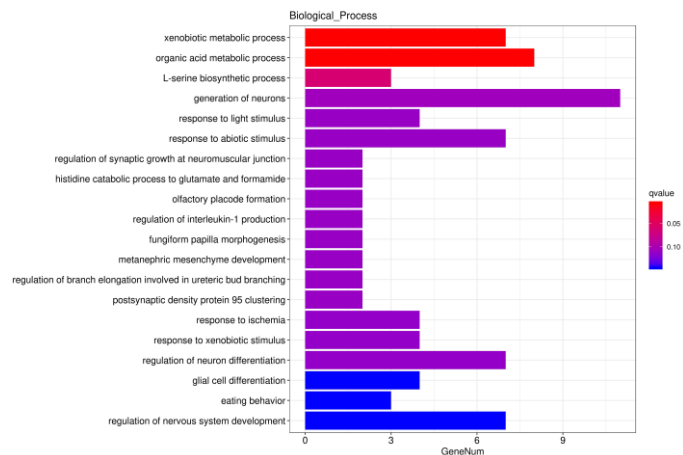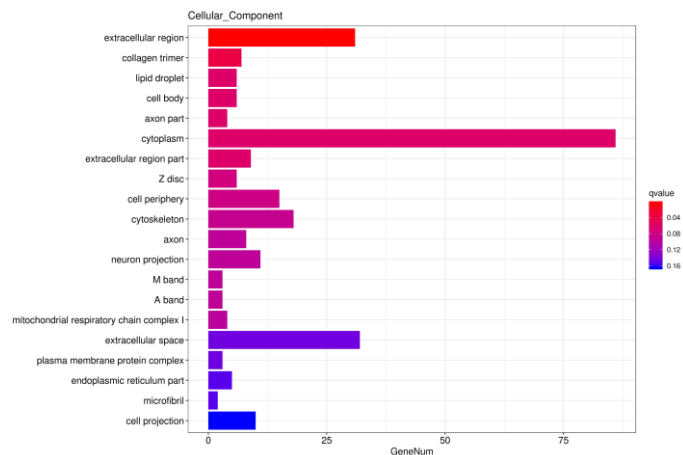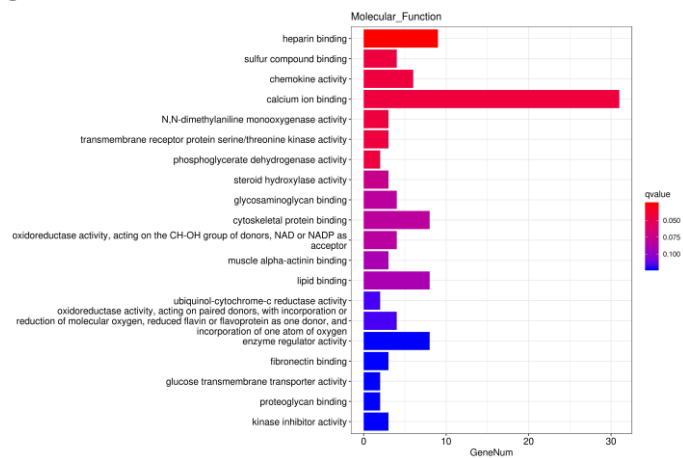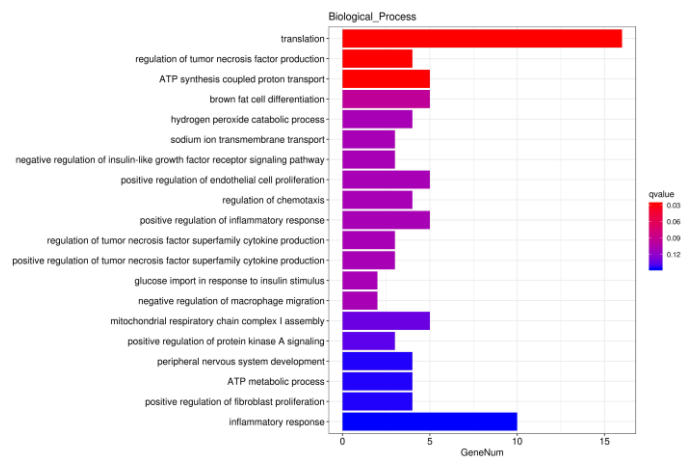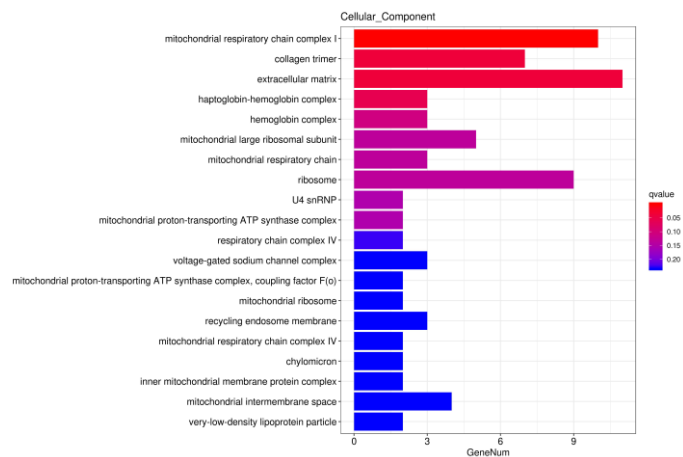
A

**Biological_Process**

- xenobiotic metabolic process
- organic acid metabolic process
- L-serine biosynthetic process
- generation of neurons
- response to light stimulus
- response to abiotic stimulus
- regulation of synaptic growth at neuromuscular junction
- histidine catabolic process to glutamate and formamide
- olfactory placode formation
- regulation of interleukin-1 production
- fungiform papilla morphogenesis
- metanephric mesenchyme development
- regulation of branch elongation involved in ureteric bud branching
- postsynaptic density protein 95 clustering
- response to ischemia
- response to xenobiotic stimulus
- regulation of neuron differentiation
- glial cell differentiation
- eating behavior
- regulation of nervous system development

qvalue 0.05 / 0.10

GeneNum: 0 3 6 9

B

**Cellular_Component**

- extracellular region
- collagen trimer
- lipid droplet
- cell body
- axon part
- cytoplasm
- extracellular region part
- Z disc
- cell periphery
- cytoskeleton
- axon
- neuron projection
- M band
- A band
- mitochondrial respiratory chain complex I
- extracellular space
- plasma membrane protein complex
- endoplasmic reticulum part
- microfibril
- cell projection

qvalue 0.04 / 0.08 / 0.12 / 0.16

GeneNum: 0 25 50 75

C

**Molecular_Function**

- heparin binding
- sulfur compound binding
- chemokine activity
- calcium ion binding
- N,N-dimethylaniline monooxygenase activity
- transmembrane receptor protein serine/threonine kinase activity
- phosphoglycerate dehydrogenase activity
- steroid hydroxylase activity
- glycosaminoglycan binding
- cytoskeletal protein binding
- oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
- muscle alpha-actinin binding
- lipid binding
- ubiquinol-cytochrome-c reductase activity
- oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen
- enzyme regulator activity
- fibronectin binding
- glucose transmembrane transporter activity
- proteoglycan binding
- kinase inhibitor activity

qvalue 0.050 / 0.075 / 0.100

GeneNum: 0 10 20 30

D

**Biological_Process**

- translation
- regulation of tumor necrosis factor production
- ATP synthesis coupled proton transport
- brown fat cell differentiation
- hydrogen peroxide catabolic process
- sodium ion transmembrane transport
- negative regulation of insulin-like growth factor receptor signaling pathway
- positive regulation of endothelial cell proliferation
- regulation of chemotaxis
- positive regulation of inflammatory response
- regulation of tumor necrosis factor superfamily cytokine production
- positive regulation of tumor necrosis factor superfamily cytokine production
- glucose import in response to insulin stimulus
- negative regulation of macrophage migration
- mitochondrial respiratory chain complex I assembly
- positive regulation of protein kinase A signaling
- peripheral nervous system development
- ATP metabolic process
- positive regulation of fibroblast proliferation
- inflammatory response

qvalue 0.03 / 0.06 / 0.09 / 0.12

GeneNum: 0 5 10 15

E

**Cellular_Component**

- mitochondrial respiratory chain complex I
- collagen trimer
- extracellular matrix
- haptoglobin-hemoglobin complex
- hemoglobin complex
- mitochondrial large ribosomal subunit
- mitochondrial respiratory chain
- ribosome
- U4 snRNP
- mitochondrial proton-transporting ATP synthase complex
- respiratory chain complex IV
- voltage-gated sodium channel complex
- mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)
- mitochondrial ribosome
- recycling endosome membrane
- mitochondrial respiratory chain complex IV
- chylomicron
- inner mitochondrial membrane protein complex
- mitochondrial intermembrane space
- very-low-density lipoprotein particle

qvalue 0.05 / 0.10 / 0.15 / 0.20

GeneNum: 0 3 6 9

F

**Molecular_Function**

- cytochrome-c oxidase activity
- structural constituent of ribosome
- frizzled binding
- NADH dehydrogenase (ubiquinone) activity
- dopachrome isomerase activity
- intramolecular oxidoreductase activity, interconverting keto- and enol-groups
- intramolecular oxidoreductase activity, transposing C=C bonds
- phenylpyruvate tautomerase activity
- interleukin-2 binding
- rRNA binding
- oxygen transporter activity
- ubiquinol-cytochrome-c reductase activity
- organic acid binding
- chemorepellent activity
- oxygen binding
- collagen binding
- glucose transmembrane transporter activity
- protein tag
- voltage-gated sodium channel activity
- microtubule motor activity

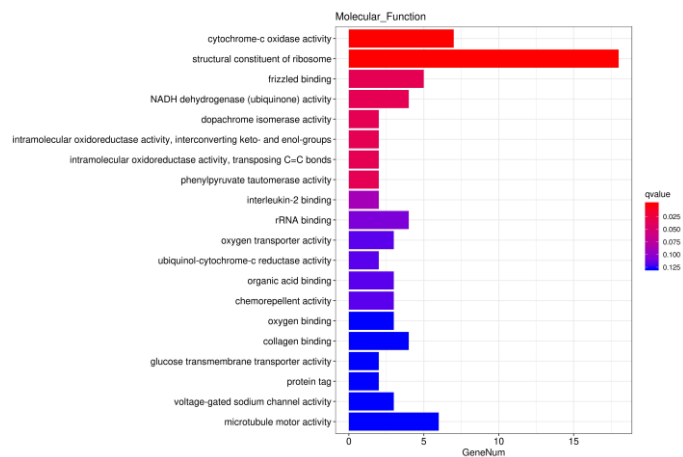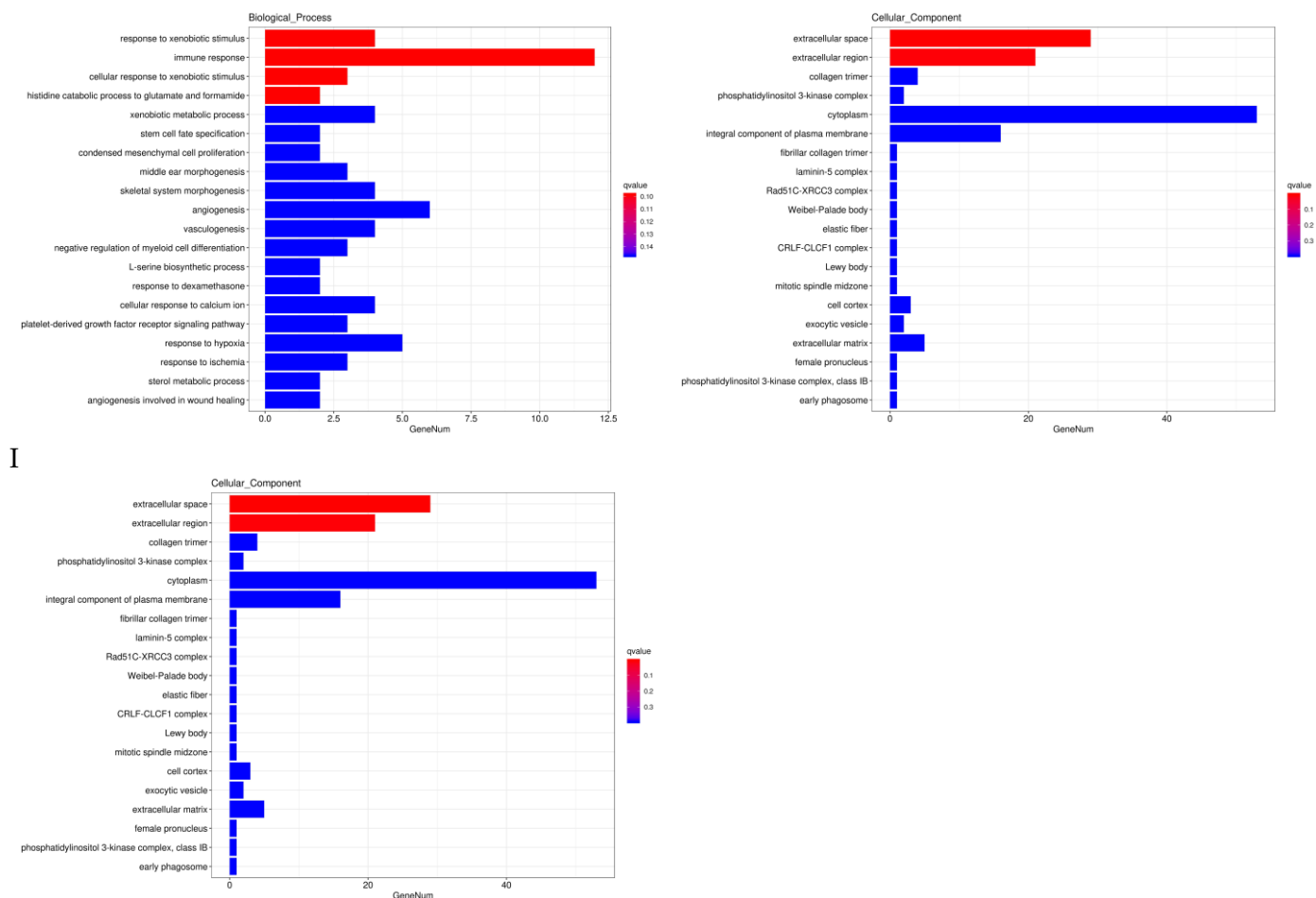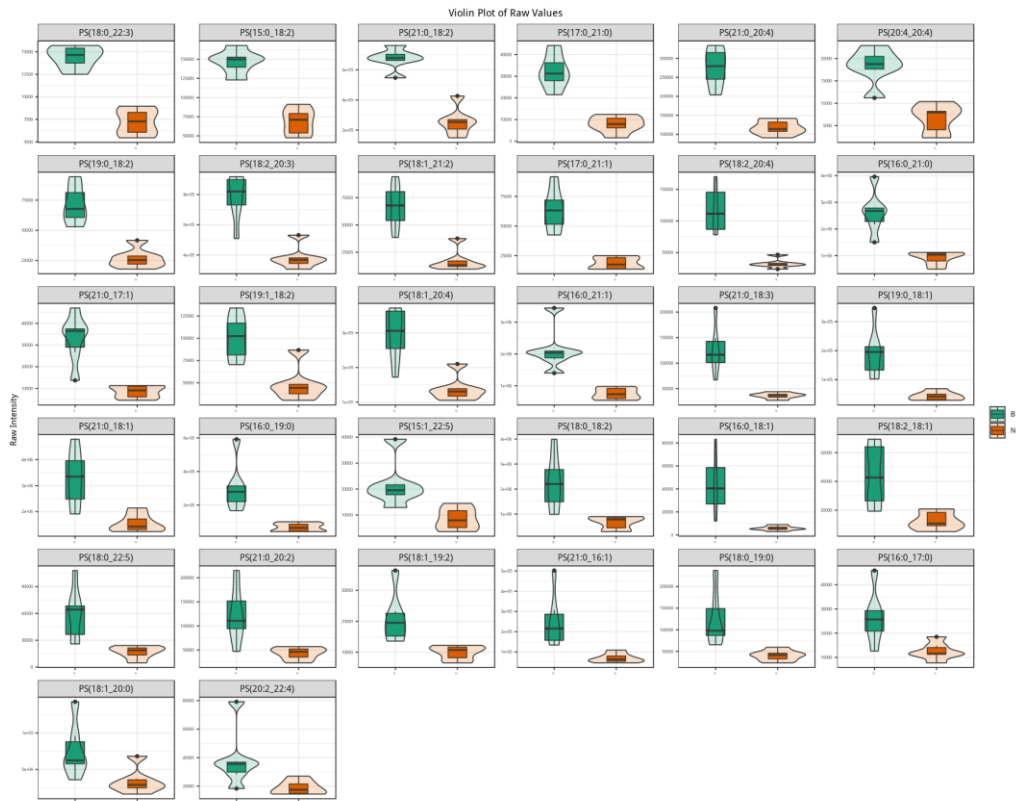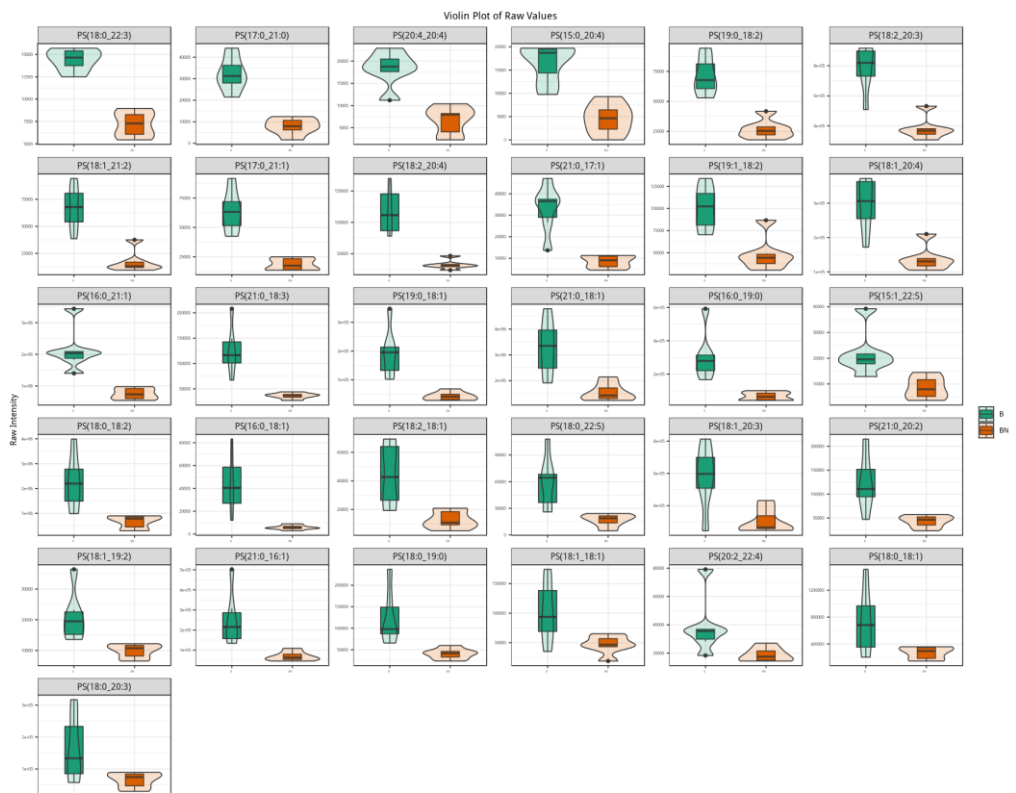qvalue 0.025 / 0.050 / 0.075 / 0.100 / 0.125

GeneNum: 0 5 10 15

G

H

**Figure S5.** A partial list of bioinformatics analysis results using DEGs of the subcutaneous adipose tissue. (A-C) The column diagrams for the analysis of biological processes (A), cellular components (B), and molecular functions (C) of DEGs in Berkshires vs. Ningxiang pigs; (D-F) The column diagrams for the analysis of biological processes (D), cellular components (E), and molecular functions (F) of DEGs in Ningxiang pigs vs. $F_1$ offspring; (G-I) The column diagrams for the analysis of biological processes (G), cellular component (H), and molecular function (I) of DEGs in Berkshires vs. $F_1$ offspring. Twelve samples of subcutaneous adipose from four Ningxiang pigs, four Berkshires and four $F_1$ pigs, respectively, were used to detect transcriptomic profile.

A



B



**Figure S6.** The violin chart of the SCLs related to kO00260 pathway. The violin chart of Phosphatidylserines in Berkshires vs. Ningxiang pigs (A) and Berkshires vs F₁ offspring (B), respectively. B, Berkshires; N, Ningxiang pig; BN. F₁ offspring. .

**Figure S7.** Dynamic distribution map of lipid content differences in the subcutaneous adipose tissue from Berkshires vs. Ningxiang pigs. The horizontal ordinate represents the different multiples of substances, the Y-axis represents the log₂FC. Each point represents a substance, green dots represent the substances in the top 10 of the downward ranking, and red dots represent the substances in the top 10 of the upward ranking.

**Figure S8.** The correlation heat map for significantly different lipids with the top VIP value in the subcutaneous adipose tissue in Berkshires vs. Ningxiang pigs. Red represents positive correlations, green represents negative correlations.

A



B



**Figure S9.** Bar chart of different lipids in the subcutaneous adipose tissue in Berkshires vs. $F_1$ offspring (A) and in Ningxiang pigs vs. $F_1$ offspring (B). The horizontal ordinate represents the $log_2FC$ of different lipids. The Y-axis represents differential lipids. Red represents an increase in lipid content, while green represents a decrease in lipid content.

**Table S1.** DEGs in Berkshires vs. Ningxiang pigs enriched in partial KEGG pathways (P < 0.05).

| Gene name | FPKM | | FDR | Log₂FC | regulate | Gene annotated |
|---|---|---|---|---|---|---|
| | BKX | NX | | | | |
| **kO00260 glycine, serine and threonine metabolism** | | | | | | |
| *PHGDH* | 28.12 | 4.17 | $2.27E^{-11}$ | -2.64 | down | phosphoglycerate dehydrogenase |
| *LOC100156167* | 8.84 | 1.44 | $3.84E^{-7}$ | -2.41 | down | phosphoglycerate dehydrogenase like protein |
| *SHMT1* | 86.01 | 26.98 | $9.92E^{-4}$ | -1.56 | down | glycine hydroxymethyltransferase |
| *PSPH* | 12.56 | 52.64 | $9.42E^{-6}$ | 2.21 | up | phosphoserine phosphatase |
| *LOC110256000* | 3.37 | 19.40 | $9.12E^{-08}$ | 2.49 | up | membrane primary amine oxidase-like |
| **KO00590 arachidonic acid metabolism** | | | | | | |
| *CYP2B22* | 69.83 | 17.85 | $1.32E^{-3}$ | -1.85 | down | cytochrome P450 family 2 subfamily B22 |
| *LOC110255237* | 6.63 | 22.28 | $2.09E^{-4}$ | 1.86 | up | cytochrome P450 4F6-like |
| *GGT5* | 8.43 | 23.69 | $1.70E^{-3}$ | 1.54 | up | gamma-glutamyltranspeptidase |
| *PTGES* | 3.91 | 13.12 | $4.47E^{-8}$ | 1.86 | up | microsomal prostaglandin-E synthase 1 |
| *SAL1* | 25.78 | 134.40 | $3.37E^{-6}$ | 2.45 | up | salivary lipocalin |
| *GPX1* | 334.05 | 1411.35 | $3.60E^{-7}$ | 2.20 | up | glutathione peroxidase 1 |
| *GPX3* | 2304.61 | 1055.47 | $4.01E^{-7}$ | -1.01 | down | |
| **KO00061 fatty acid biosynthesis** | | | | | | |
| *FASN* | 1320.46 | 2689.93 | $1.19E^{-3}$ | 1.15 | up | fatty acid synthase |
| *ACACA* | 26.60 | 73.44 | $5.13E^{-9}$ | 1.58 | up | acetyl-CoA carboxylase |
| *CBR4* | 3.87 | 7.46 | $9.83E^{-6}$ | 1.06 | up | carboxyl reductase 4 |
| *MCH* | 0.19 | 0.82 | $6.33E^{-3}$ | 2.20 | up | medium chain acyl hydrolase |
| **KO01212 fatty acid metabolism** | | | | | | |
| *EHHADH* | 8.54 | 16.07 | $2.70E^{-3}$ | 1.03 | up | enoyl-CoA hydratase |
| *FASN* | 1320.46 | 2689.93 | $1.19E^{-3}$ | 1.15 | up | fatty acid synthase |

| Gene name | FPKM | | FDR | Log$_2$FC | regulate | Gene annotated |
|---|---|---|---|---|---|---|
| | BKX | NX | | | | |
| ACACA | 26.60 | 73.44 | 5.13E$^{-9}$ | 1.58 | up | acetyl-CoA carboxylase |
| CBR4 | 3.87 | 7.46 | 9.83E$^{-6}$ | 1.06 | up | carboxyl reductase 4 |
| HACD | 98.60 | 42.53 | 7.91E$^{-6}$ | -1.10 | down | very long-chain (3R)-3-hydroxyacyl-CoA dehydratase |
| ELOV6 | 182.38 | 428.54 | 9.82E$^{-5}$ | 1.36 | up | very long chain fatty acids protein 6 |
| SCD | 1184.93 | 3625.88 | 5.31E$^{-5}$ | 1.75 | up | stearoyl-CoA desaturase |
| **kO00561 glycerolipid metabolism** | | | | | | |
| GK | 23.72 | 8.19 | 5.06E$^{-9}$ | -1.37 | down | glycerol kinase |
| MGLL | 192.95 | 383.22 | 7.45E$^{-10}$ | 1.04 | up | monoglyceride lipase |
| LPIN1 | 127.44 | 44.92 | 5.42E$^{-4}$ | -1.40 | down | lipin 1 |
| DGKB | 3.62 | 1.58 | 1.28E$^{-3}$ | -1.07 | down | diacylglycerol kinase beta |
| DGAT2 | 109.71 | 518.44 | 8.38E$^{-20}$ | 2.36 | up | diacylglycerol O-acyltransferase 2 |
| **ko04070 phosphatidylinositol signaling system** | | | | | | |
| NTMR7 | 0.26 | 1.43 | 1.36E$^{-3}$ | 2.54 | up | myotubularin-related protein 7 |
| PLCB1 | 4.49 | 2.06 | 1.14E$^{-6}$ | -1.01 | down | phospholipase C beta 1 |
| PIK3C2G | 9.04 | 3.31 | 4.24E$^{-14}$ | -1.30 | down | phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 gamma |
| DGKB | 3.62 | 1.58 | 1.28E$^{-3}$ | -1.07 | down | diacylglycerol kinase beta |
| PLCE1 | 0.45 | 0.19 | 4.25E$^{-3}$ | -1.11 | down | phospholipase C epsilon 1 |
| CALML5 | 2.09 | 0.13 | 6.52E$^{-6}$ | -3.91 | down | calmodulin like 5 |
| LOC102157965 | 0.15 | 1.53 | 2.35E$^{-4}$ | 4.36 | up | parvalbumin beta-like |
| **kO04973 carbohydrate digestion and absorption** | | | | | | |
| ATP1A1 | 83.22 | 34.41 | 2.93E$^{-7}$ | -1.17 | down | sodium/potassium-transporting ATPase subunit alpha1 |
| HK3 | 4,41 | 9.39 | 6.21E$^{-3}$ | 1.24 | up | hexokinase3 |
| SLC2A5 | 12.86 | 32.20 | 5.91E$^{-3}$ | 1.44 | up | Solute carrier family 2 member 5 |
| PLCB1 | 4.49 | 2.06 | 1.14E$^{-6}$ | -1.01 | down | phospholipase C beta 1 |
| **kO04714 thermogenesis** | | | | | | |
| MGLL | 192.95 | 383.22 | 7.45E$^{-10}$ | 1.04 | up | acylglycerol lipase |
| ATP5MC1 | 79.10 | 148.15 | 7.42E$^{-3}$ | 1.02 | up | ATP synthase membrane subunit c locus 1 |
| UQCR10 | 63.91 | 150.00 | 2.65E$^{-4}$ | 1.35 | up | ubiquinol-cytochrome c complex III subunit X |
| NDUFA3 | 11.52 | 25.38 | 8.14E$^{-3}$ | 1.26 | up | NADH:ubiquinone oxidoreductase subunit A3 |
| UQCRQ | 47.93 | 108.01 | 2.28E$^{-6}$ | 1.29 | up | ubiquinol-cytochrome c reductase complex III subunit VII |
| COX7C | 134.91 | 329.31 | 2.04E$^{-3}$ | 1.34 | up | cytochrome c oxidase subunit 7C |
| NDUFA11 | 45.34 | 85.17 | 9.02E$^{-5}$ | 1.03 | up | NADH:ubiquinone oxidoreductase subunit A11 |
| NDUFB2 | 39.84 | 81.82 | 2.27E$^{-3}$ | 1.20 | up | NADH:ubiquinone oxidoreductase subunit B2 |
| NDUFA2 | 33.06 | 62.73 | 7.84E$^{-8}$ | 1.04 | up | NADH:ubiquinone oxidoreductase subunit A2 |
| COX17 | 41.24 | 105.00 | 4.63E$^{-7}$ | 1.47 | up | cytochrome c oxidase copper chaperone COX17 |
| UQCR11 | 1.27 | 7.07 | 2.71E$^{-3}$ | 2.58 | up | ubiquinol-cytochrome c reductase, complex III subunit XI |

**Table S2.** Primers for real-time fluorescent quantitative PCR.

| Gene | Primer sequence (5'-3') |
|---|---|
| *β-actin* | sense: CCAGGTCATCACCATCGG |
| | Antisense: CCGTGTTGGCGTAGAGGT |
| *FASN* | sense: GGGCCCAGCATCACCATAGACA |
| | Antisense: GTTCGTGCCCGCATTGAGGAT |
| *SCD* | sense: CTTCCTGATCATTGCCAACA |
| | Antisense: GCAAACCACCCTTCTCTTTG |
| *PSPH* | sense: GATGCTGTGTGTTTTGATGTTGAC |
| | Antisense: CTTGACTTGTTGCCTGATCACATT |
| *ACACA* | sense: GTCCTCTGCCAGTTTCCC |
| | Antisense: TCCATCACCACAGCCTTC |
| *ELOV6* | sense: CCGGAAGTTTGCCATGTTCA |
| | Antisense: GCAGAAGAGCACAAGGTAGC |
| *HACD2* | sense: CAGACCGGAGCTCTTCTGG |
| | Antisense: TGTCTTCATTCTGGACCTCTCG |
| *GPX1* | sense: CAAGAATGGGGAGATCCTGA |
| | Antisense: GATAAACTTGGGGTCGGTCA |
| *GPX3* | sense: CTCGGAGATTCTGTCCACTCTCA |
| | Antisense: CCGTTCACGTCCCCTTTCT |
| *LPIN1* | sense: GATCATCTCCGACATTGACG |
| | Antisense: TGGTACAGCTTGGCTATGC |
| *MGLL* | sense: TATGAGGGTGCCTACCAC |
| | Antisense: GTCCTTTGGGAGACCCAT |
| *CYP2B22* | sense: AGTGTGGAGAAGCACCGTGAA |
| | Antisense: GCAAAGAAGAGCGAAAGGACAGT |
| *DGAT2* | sense: TGGCTCTTTCCATTTCATCC |
| | Antisense: CGTAAGCACGATCAGAACGA |