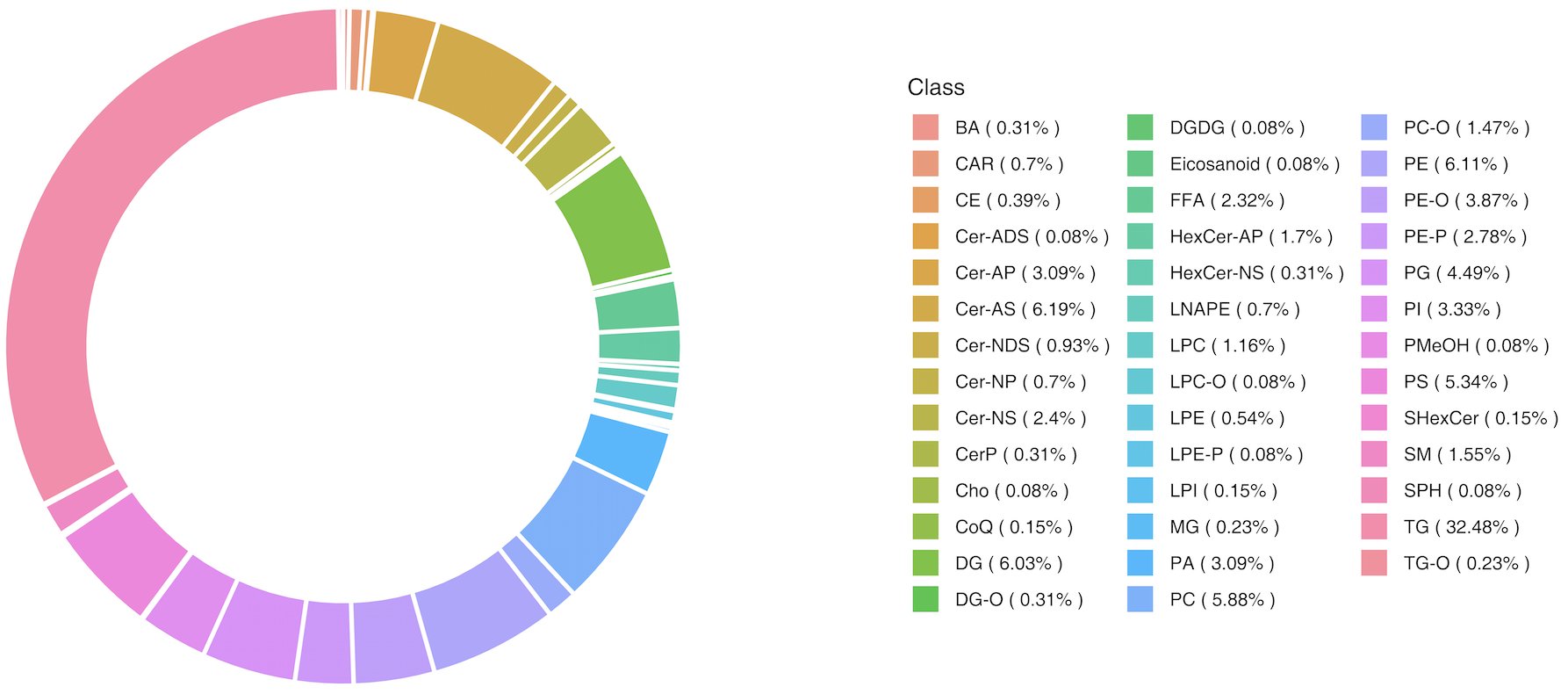
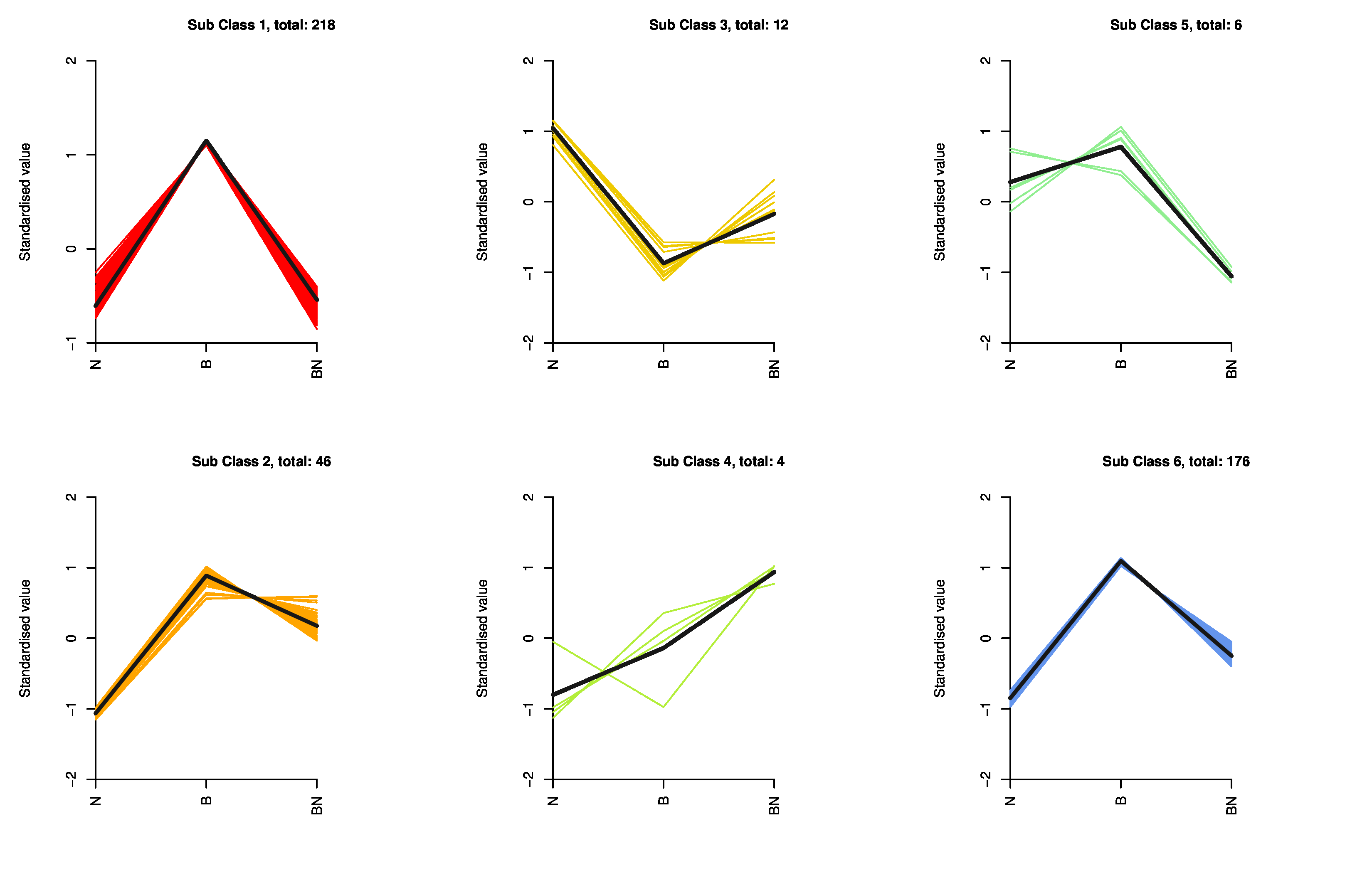
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**Figure S1.** Ring diagram of lipid subclass composition

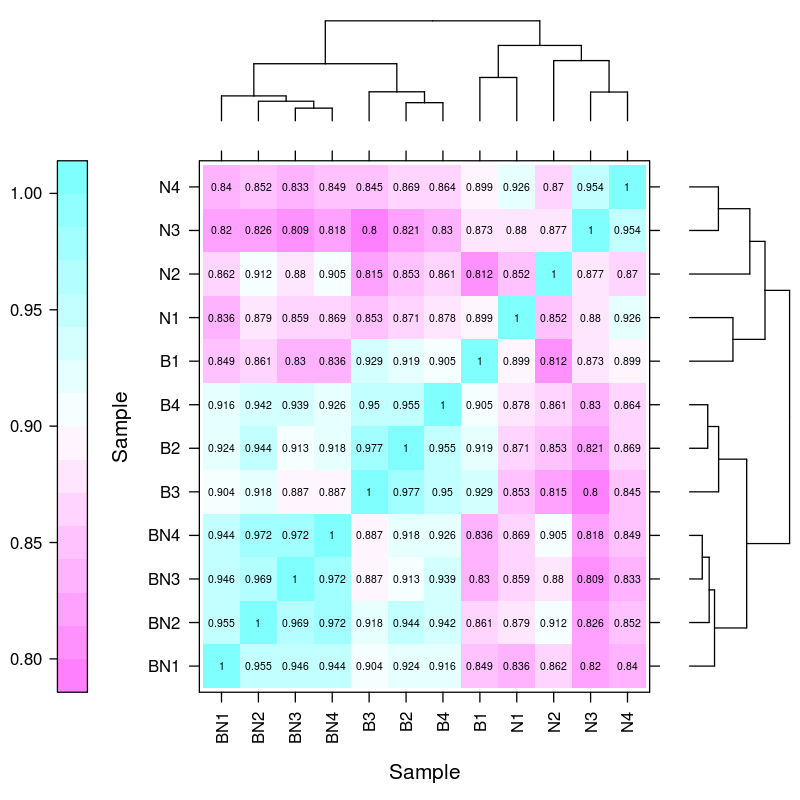
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**Figure S2.** K-Means of SCLs. The horizontal ordinate represents sample groups, the Y-axis represents standardized relative lipid content, and Sub Class represents lipid class numbers with the same trend of change. B represents Berkshire pigs, N represents Ningxiang pigs, BN represents F1 pigs.

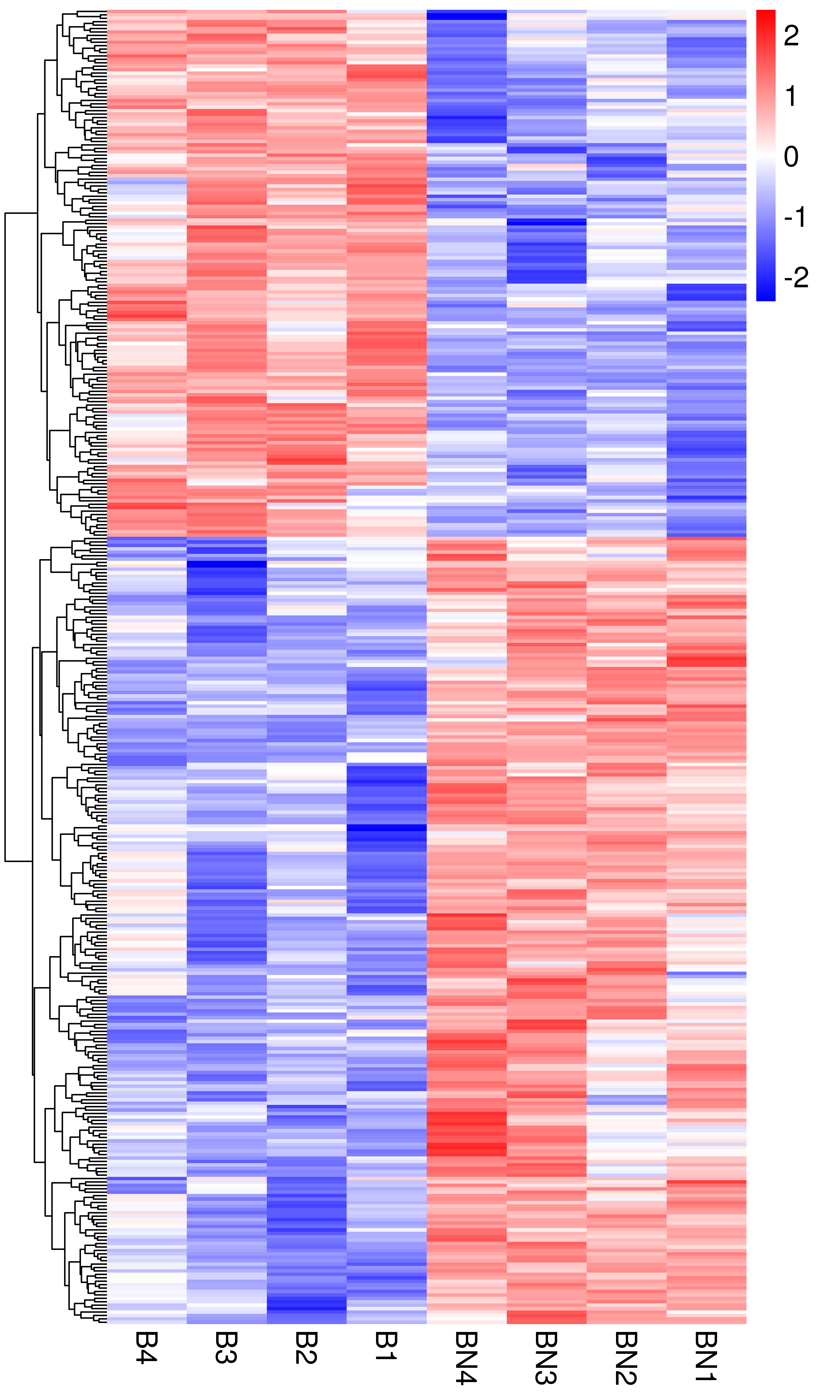
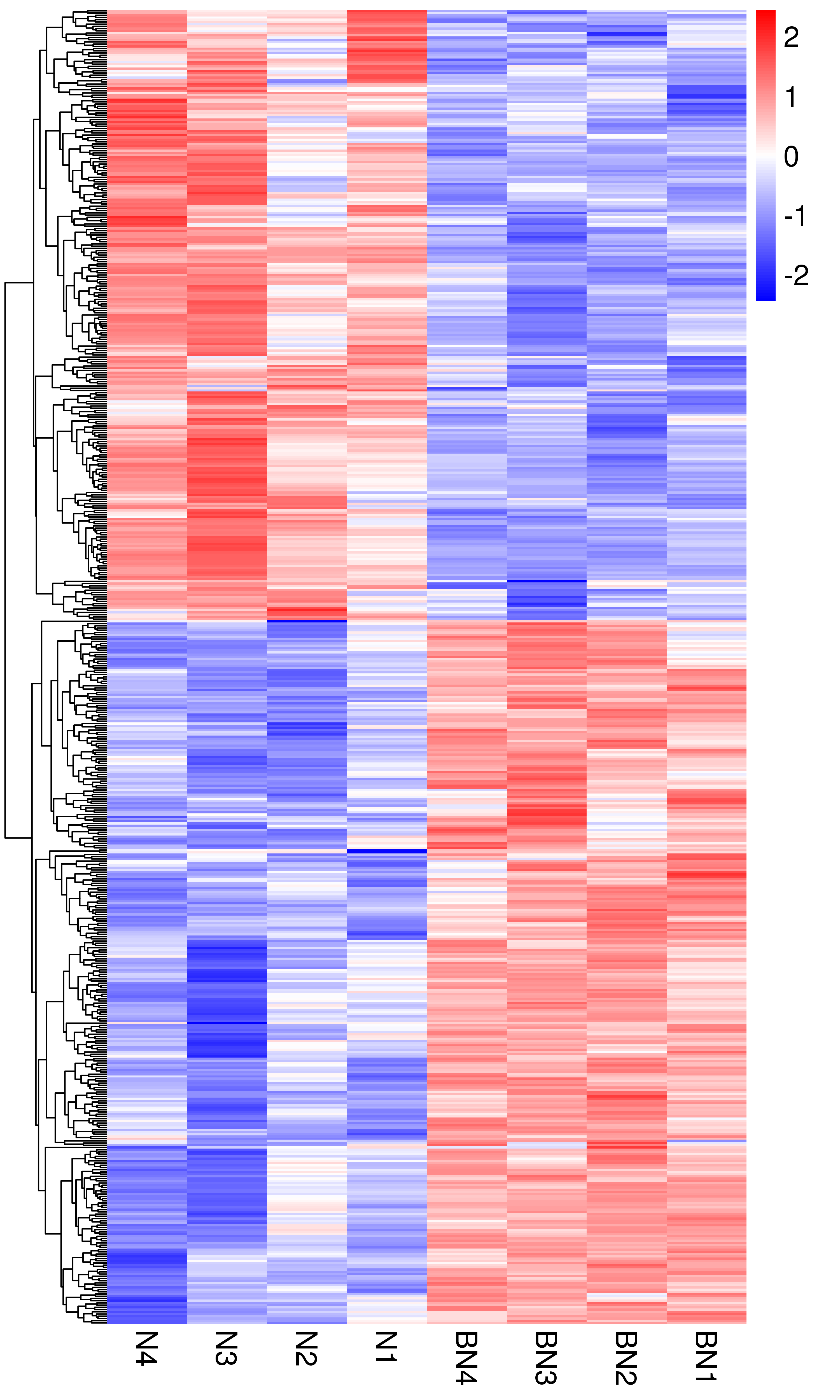
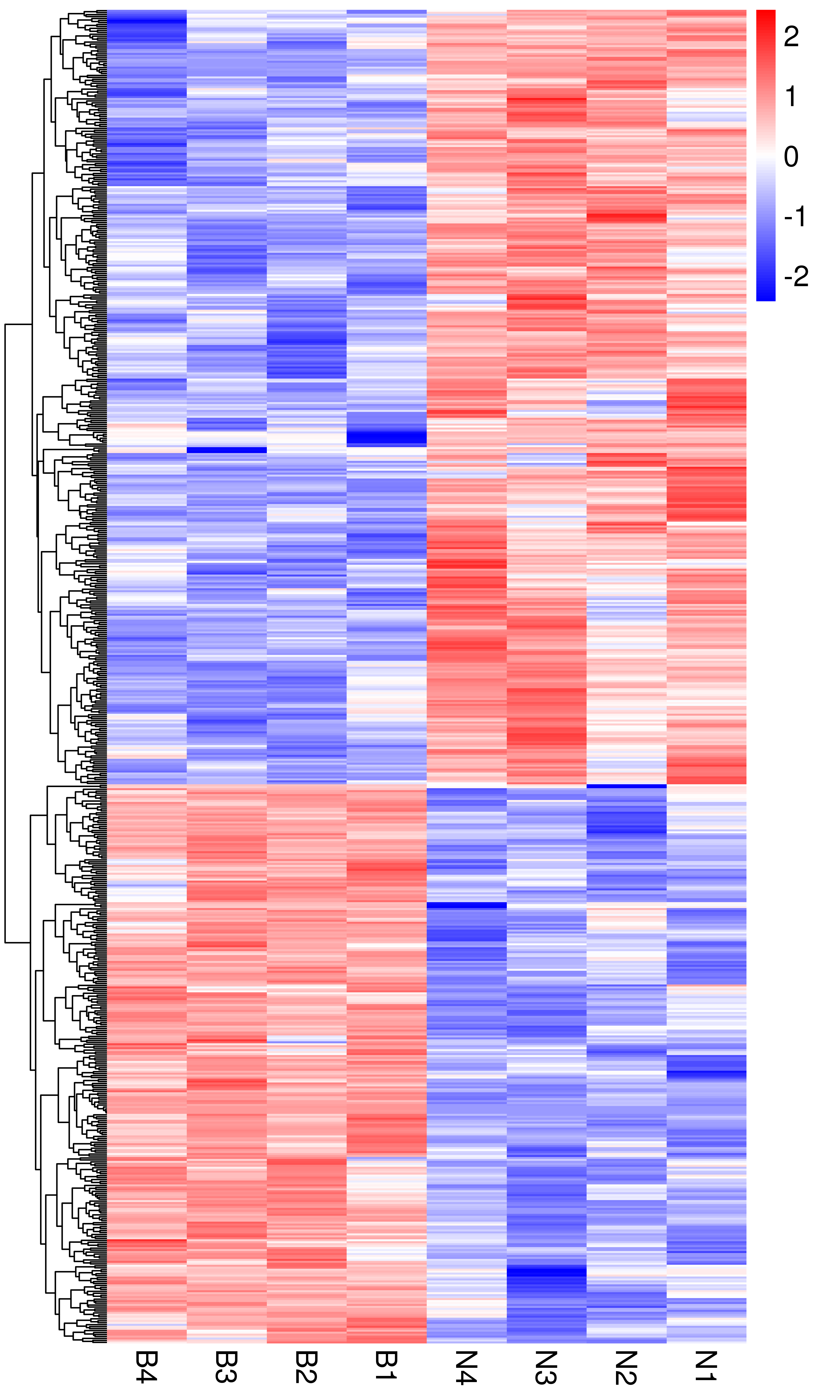
A

B

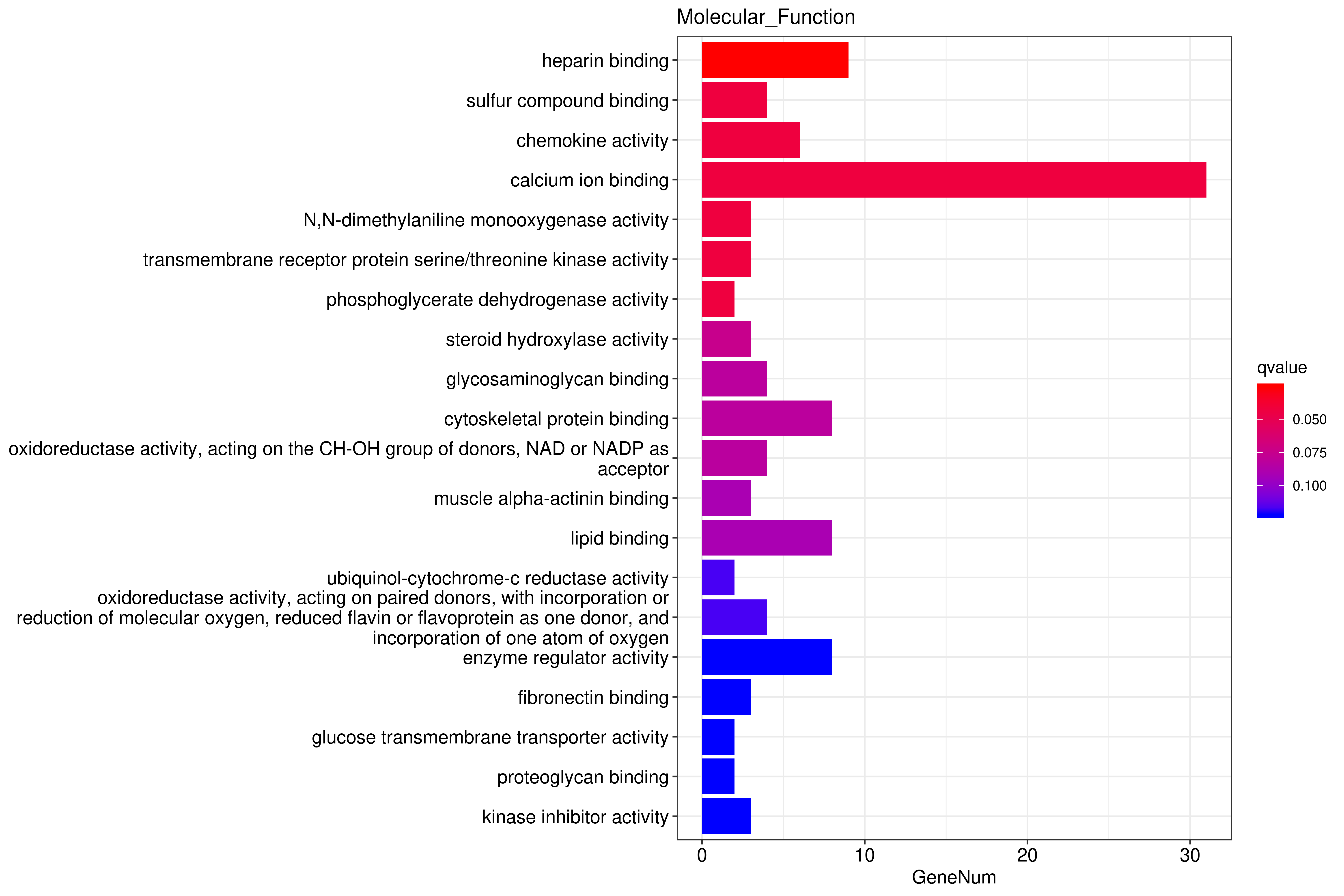
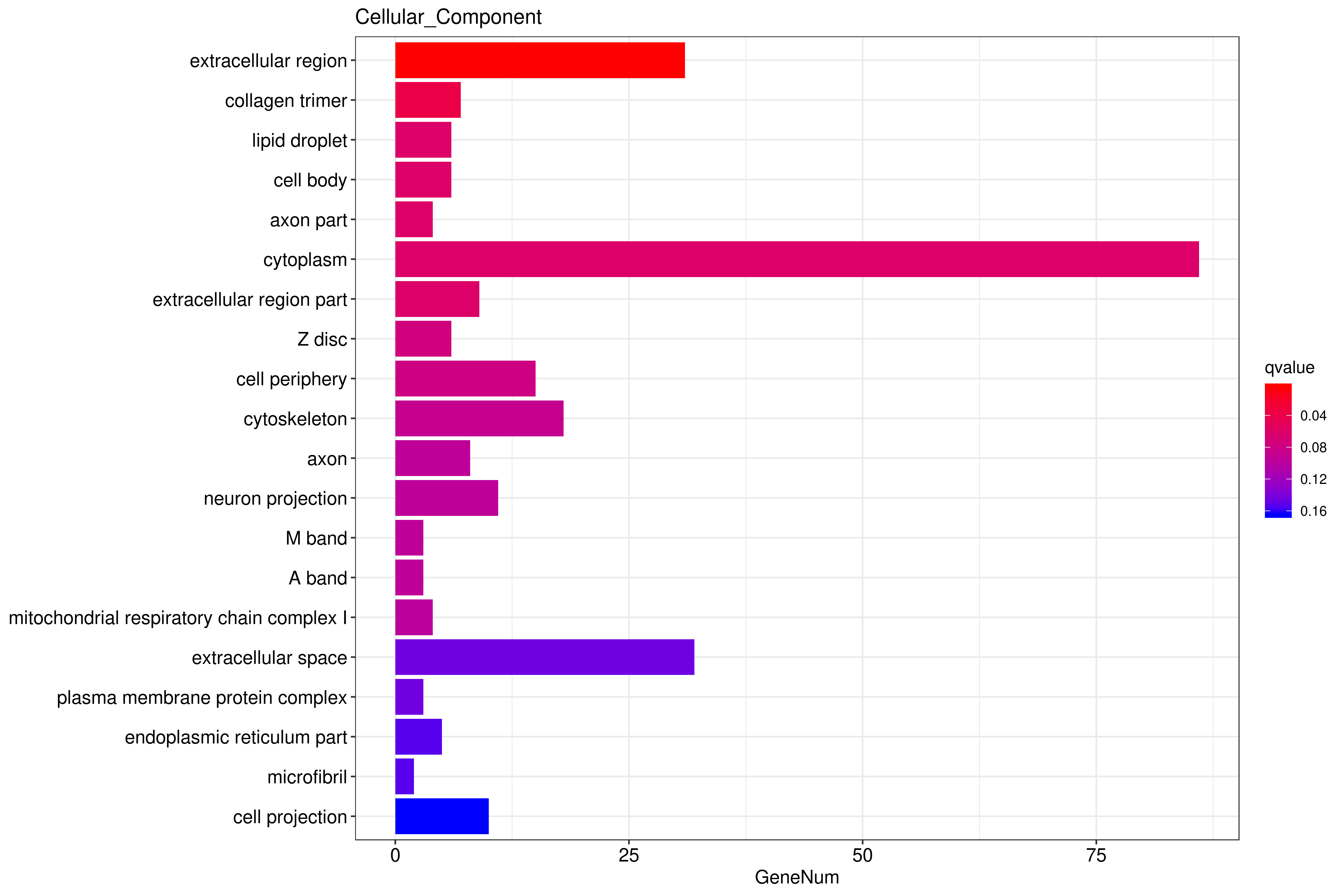
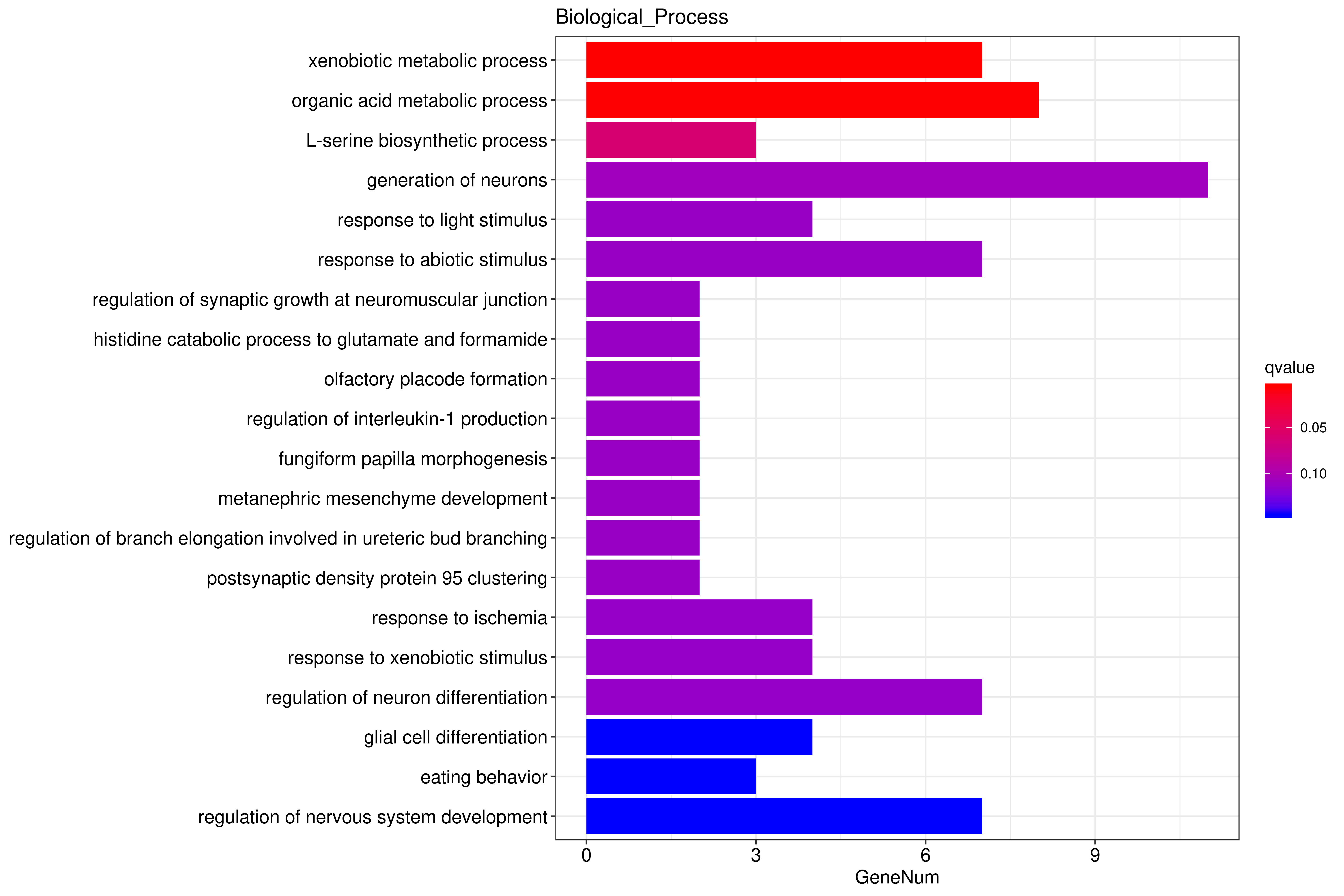
C



D



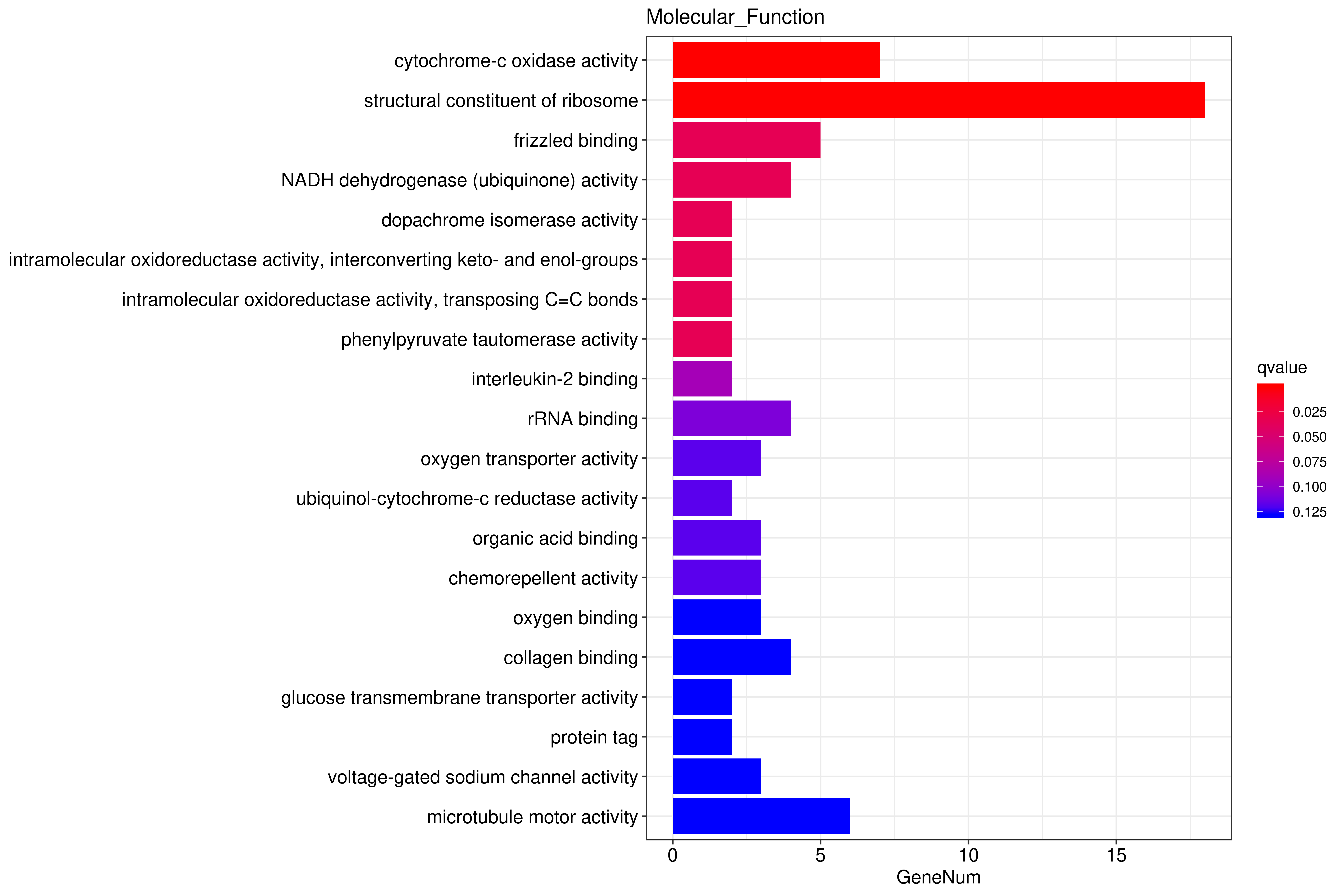
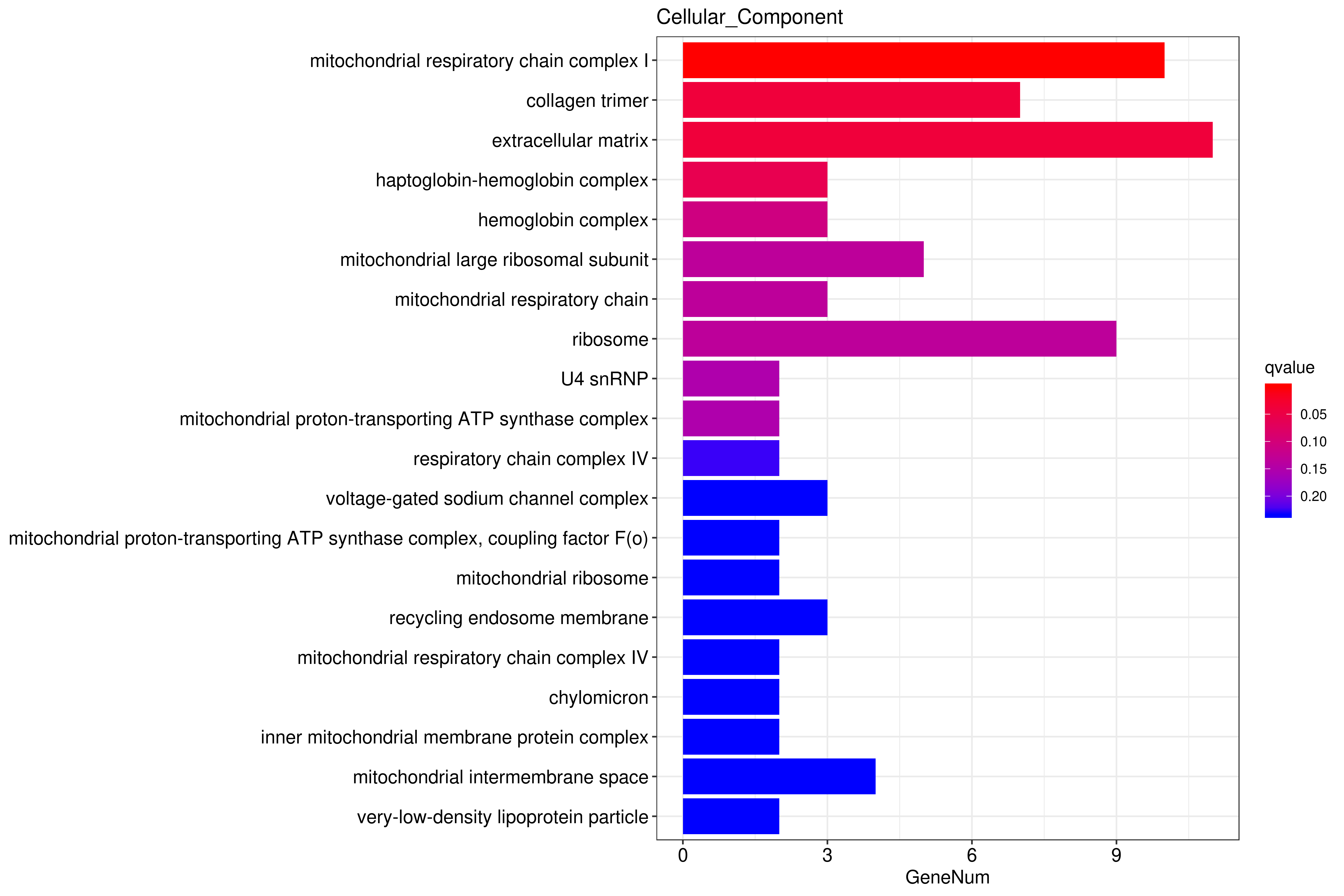
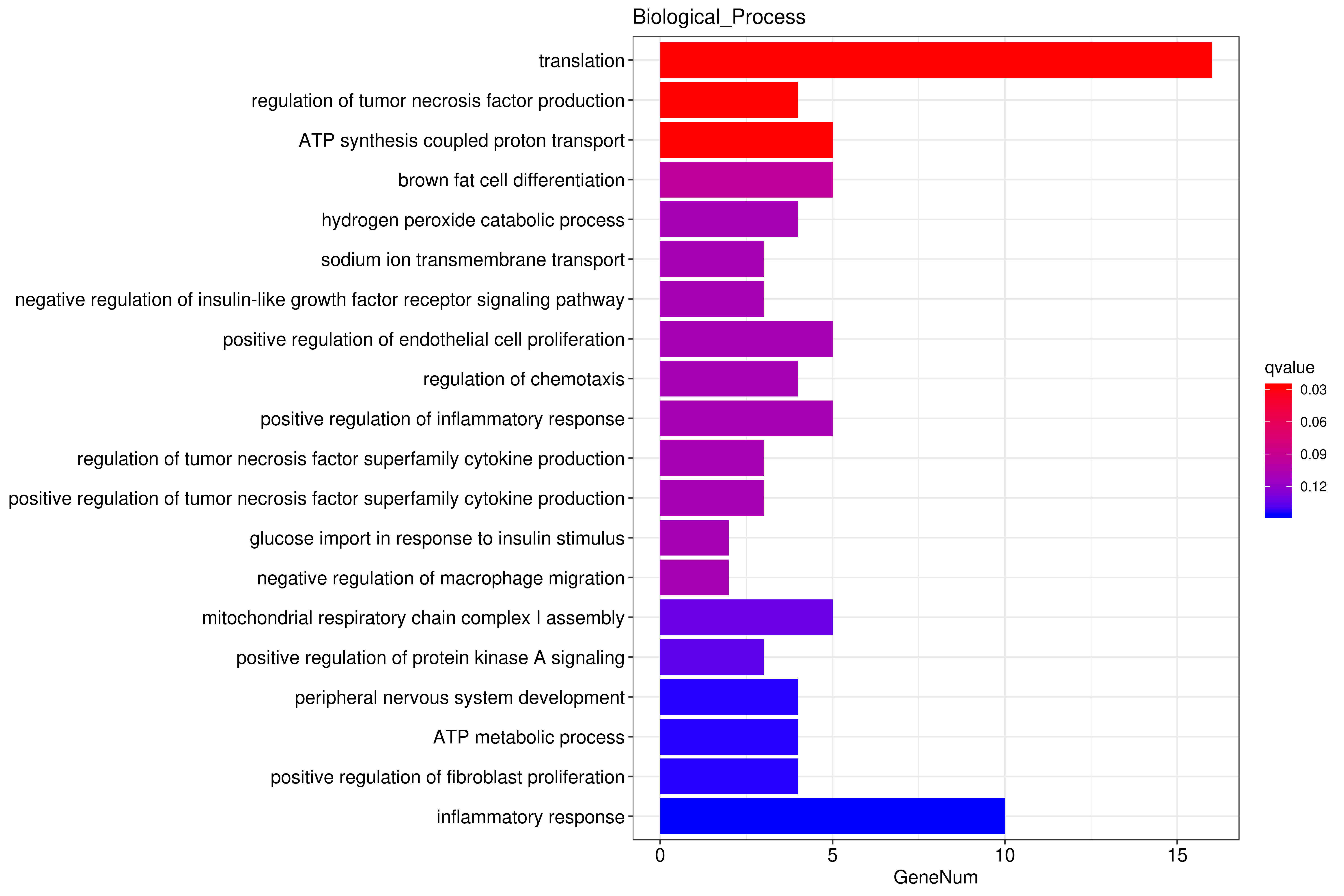
**Figure S3.** Transcriptome profiles diverse in the subcutaneous adipose tissue. (A) Transcriptome correlation analysis, B represents Berkshire pigs, N represents Ningxiang pigs, BN represents F1 pigs; (B-D) Cluster heat map of DEGs for the subcutaneous adipose tissue in the groups of Berkshire pigs vs Ningxiang pigs (B), Ningxiang pigs vs F1 pigs (C), Berkshire pigs vs F1 pigs (D), B represents Berkshire pigs, N represents Ningxiang pigs, BN represents F1 pigs.



A

B

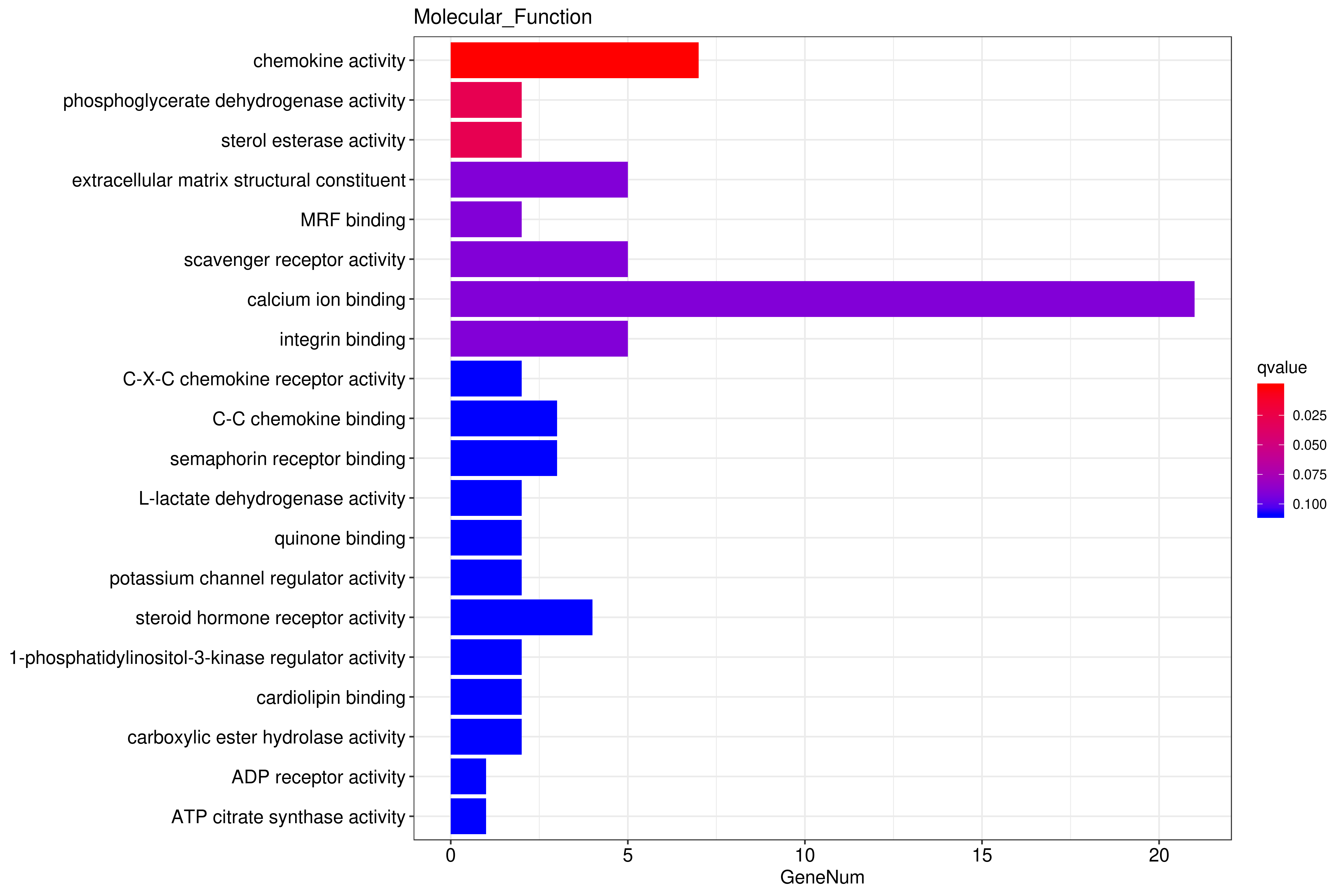
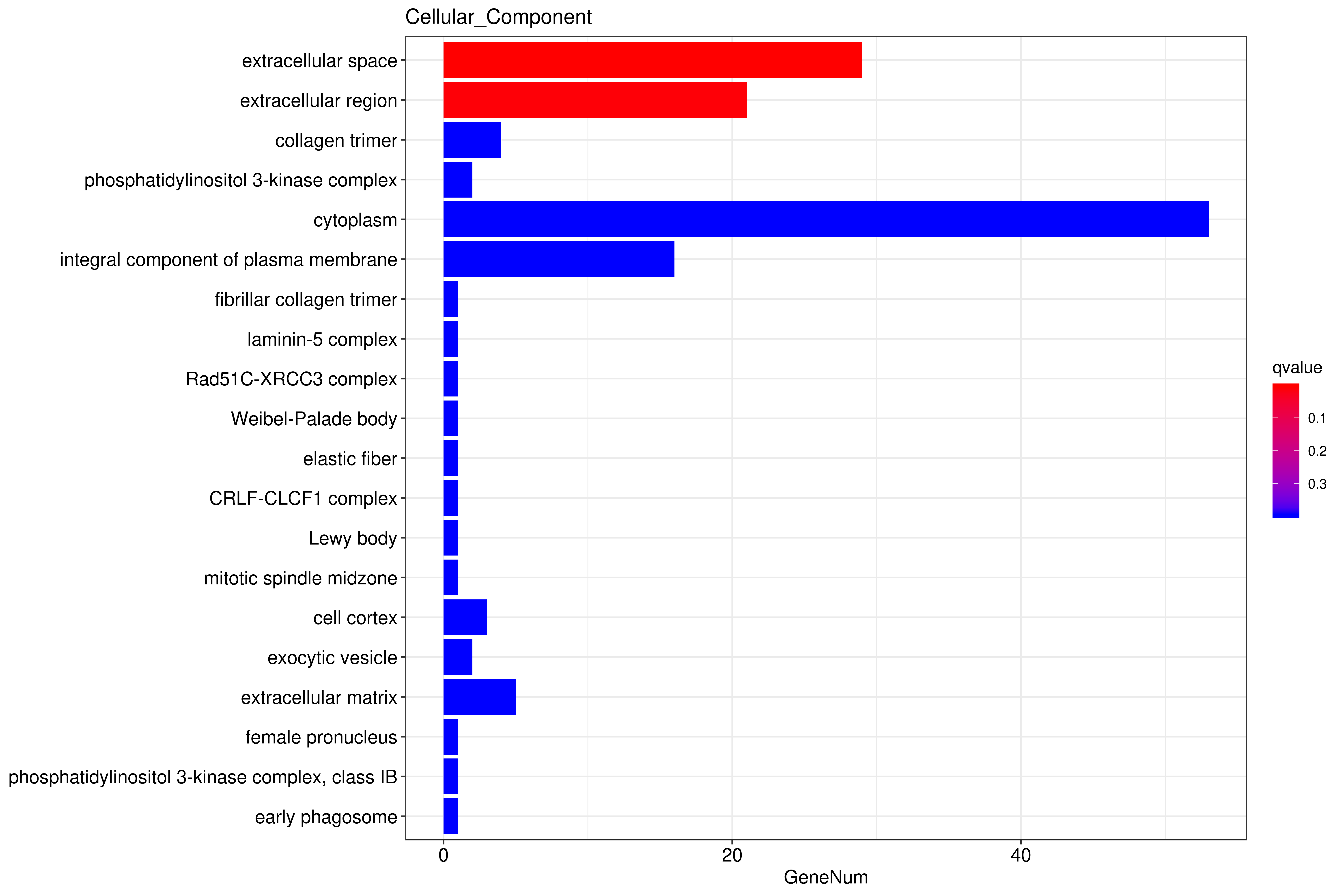
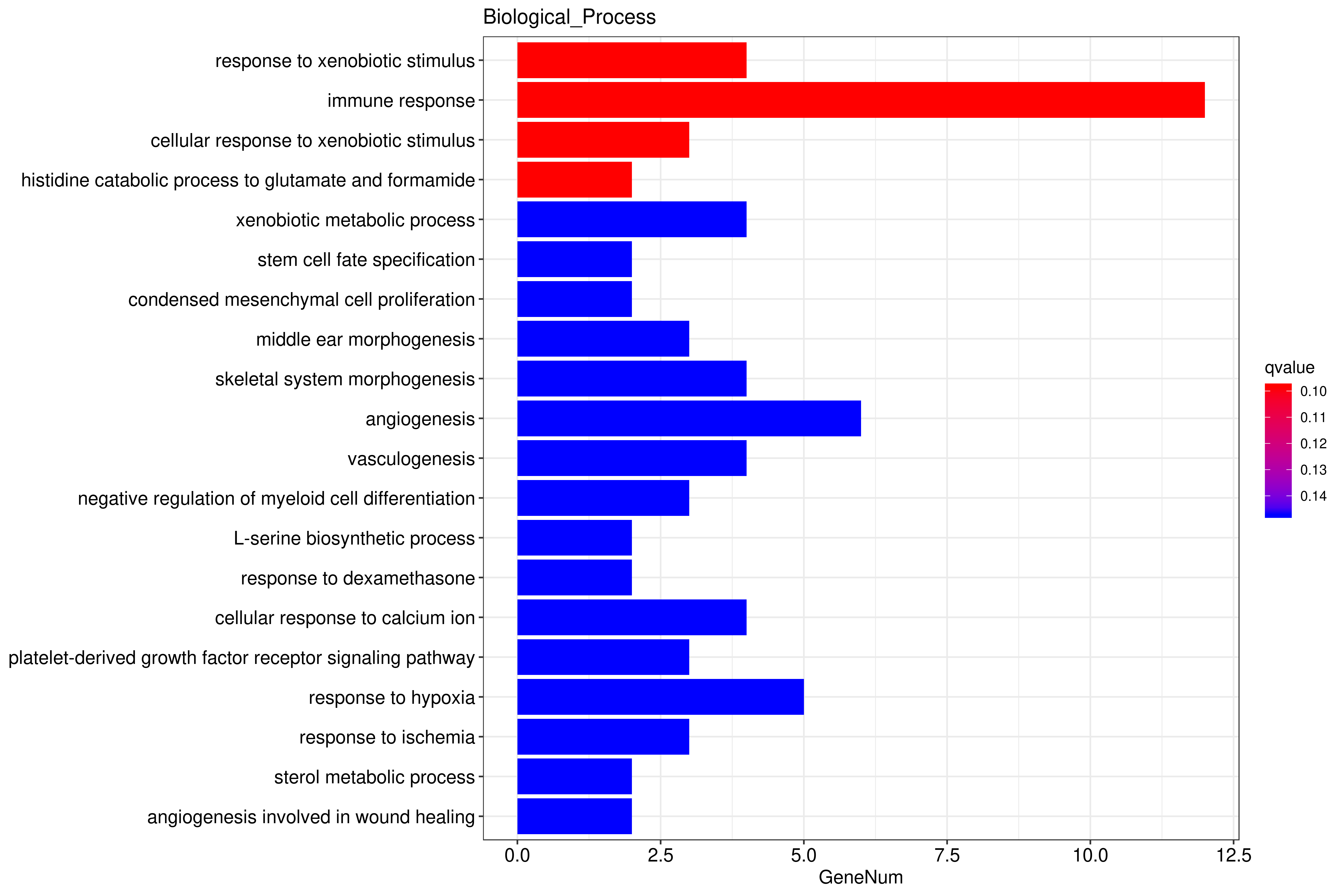
C



D

E

F



I

H

G

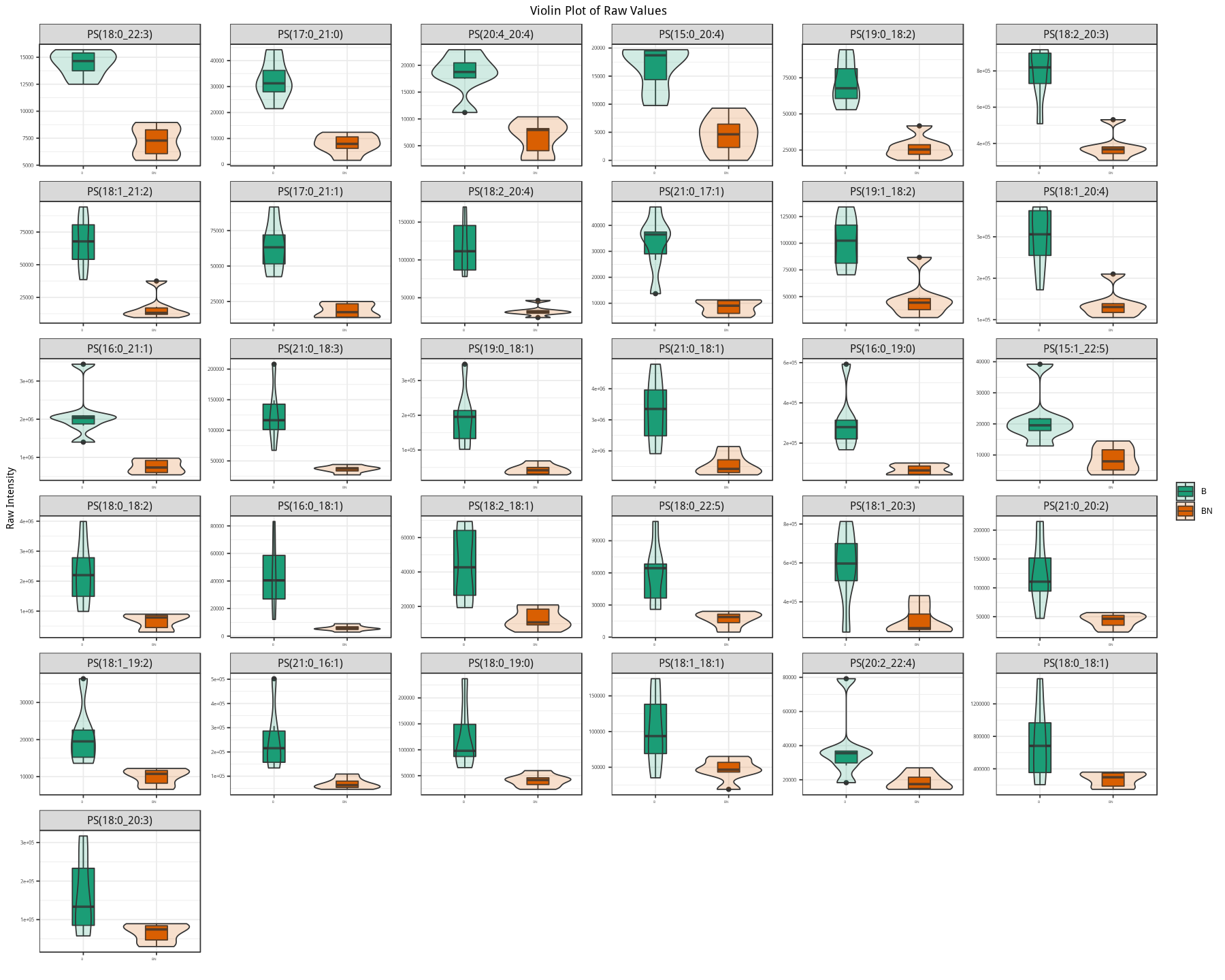
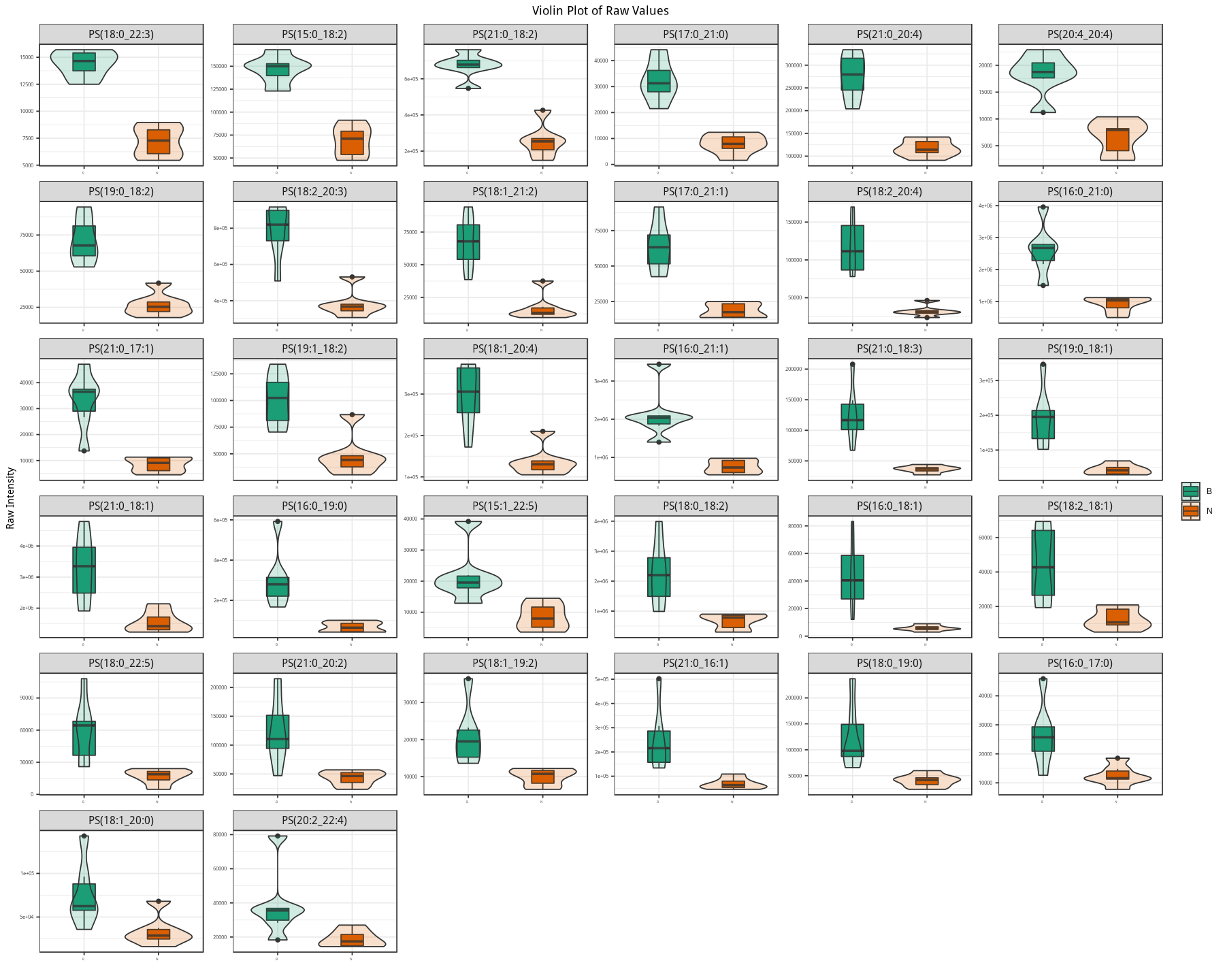
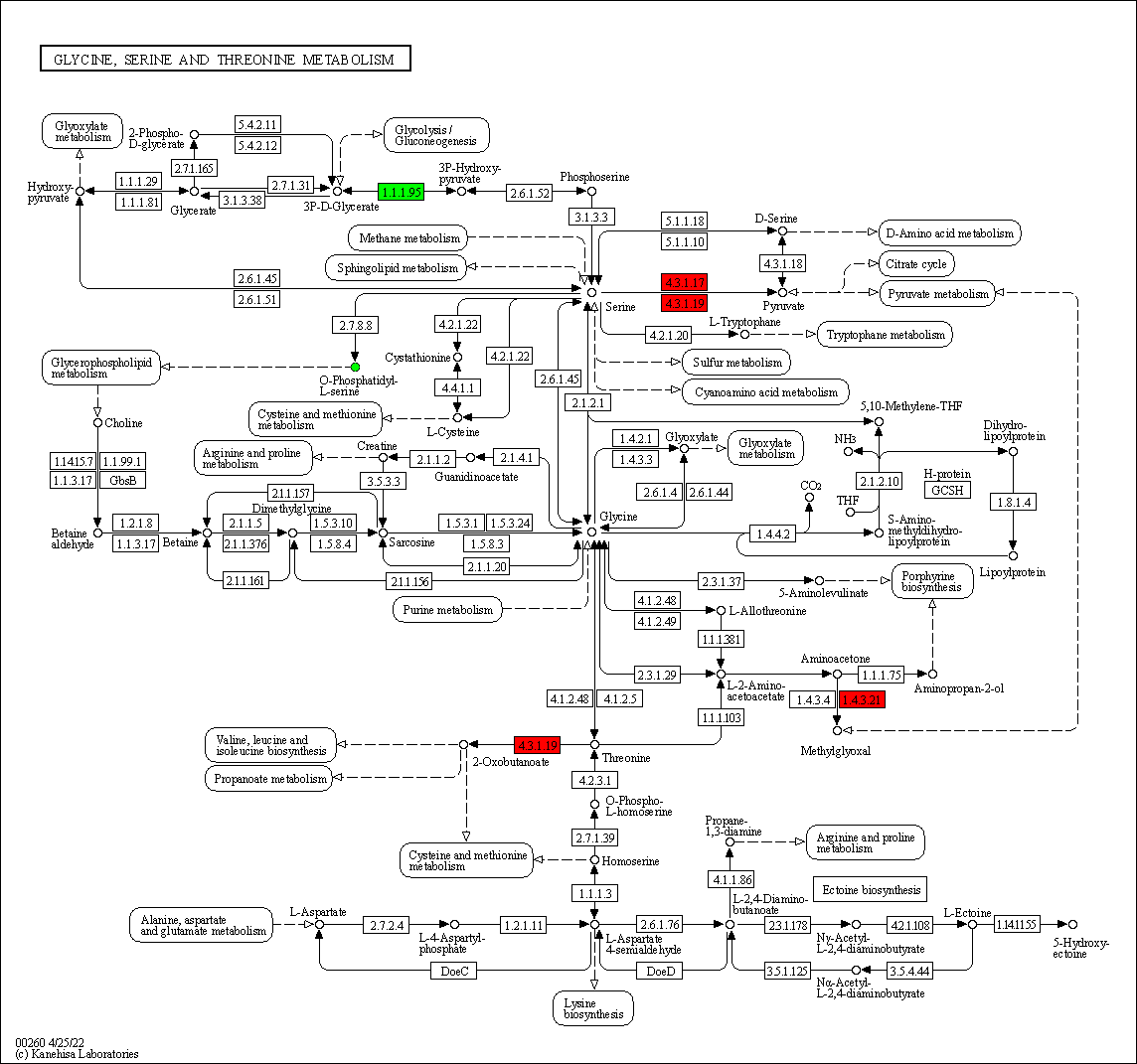
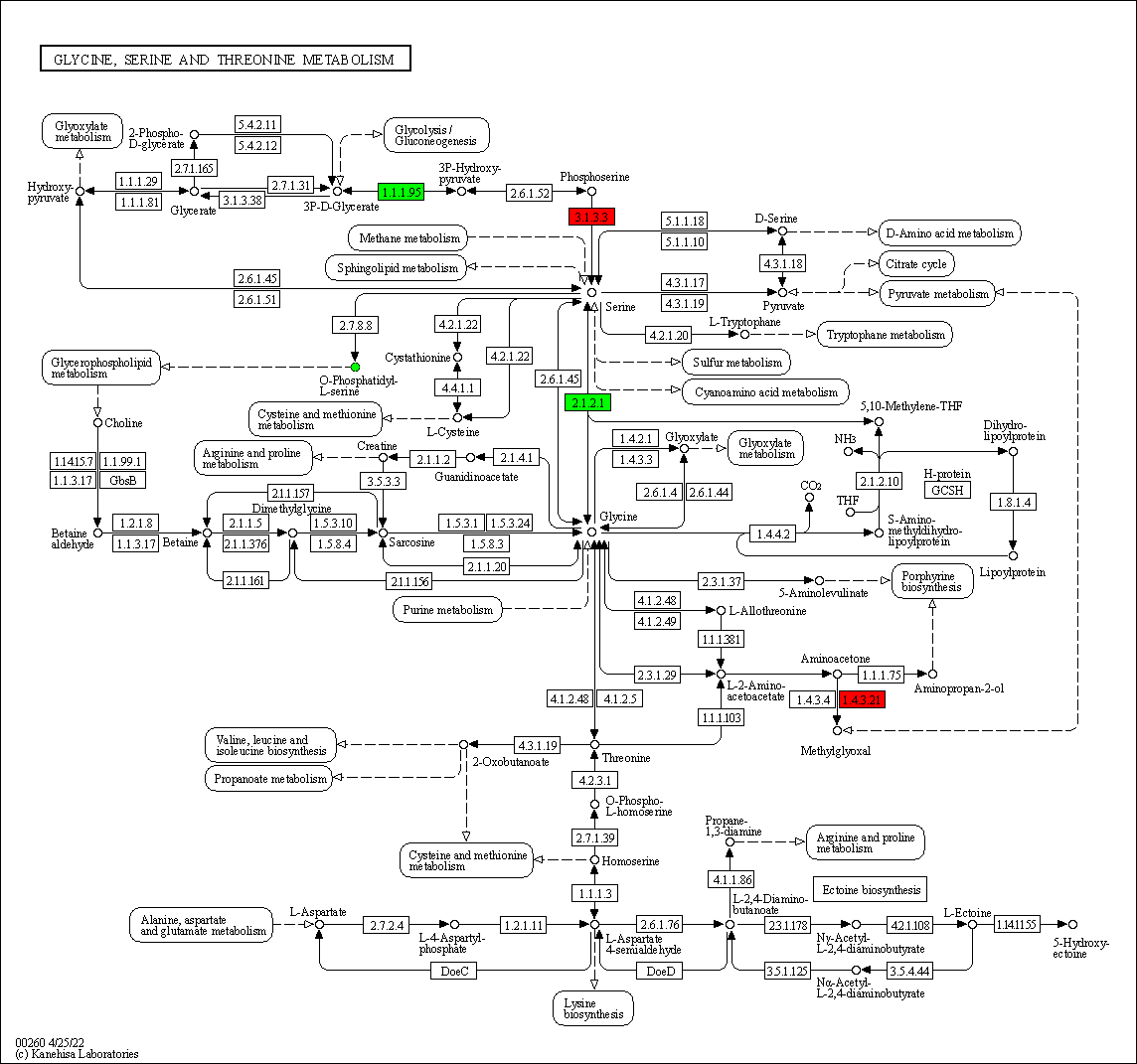
**Figure S4.** A partial list of bioinformatics analysis results using DEGs of the subcutaneous adipose tissue. (A-C) The column diagrams for the analysis of biological process (A), cellular component (B), and molecular function (C) of DEGs in Berkshire pigs vs Ningxiang pigs; (D-F) The column diagrams for the analysis of biological process (D), cellular component (E), and molecular function (F) of DEGs in Ningxiang pigs vs F1 pigs; (G-I) The column diagrams for the analysis of biological process (G), cellular component (H), and molecular function (I) of DEGs in the group of Berkshire pigs vs F1 pigs.

D

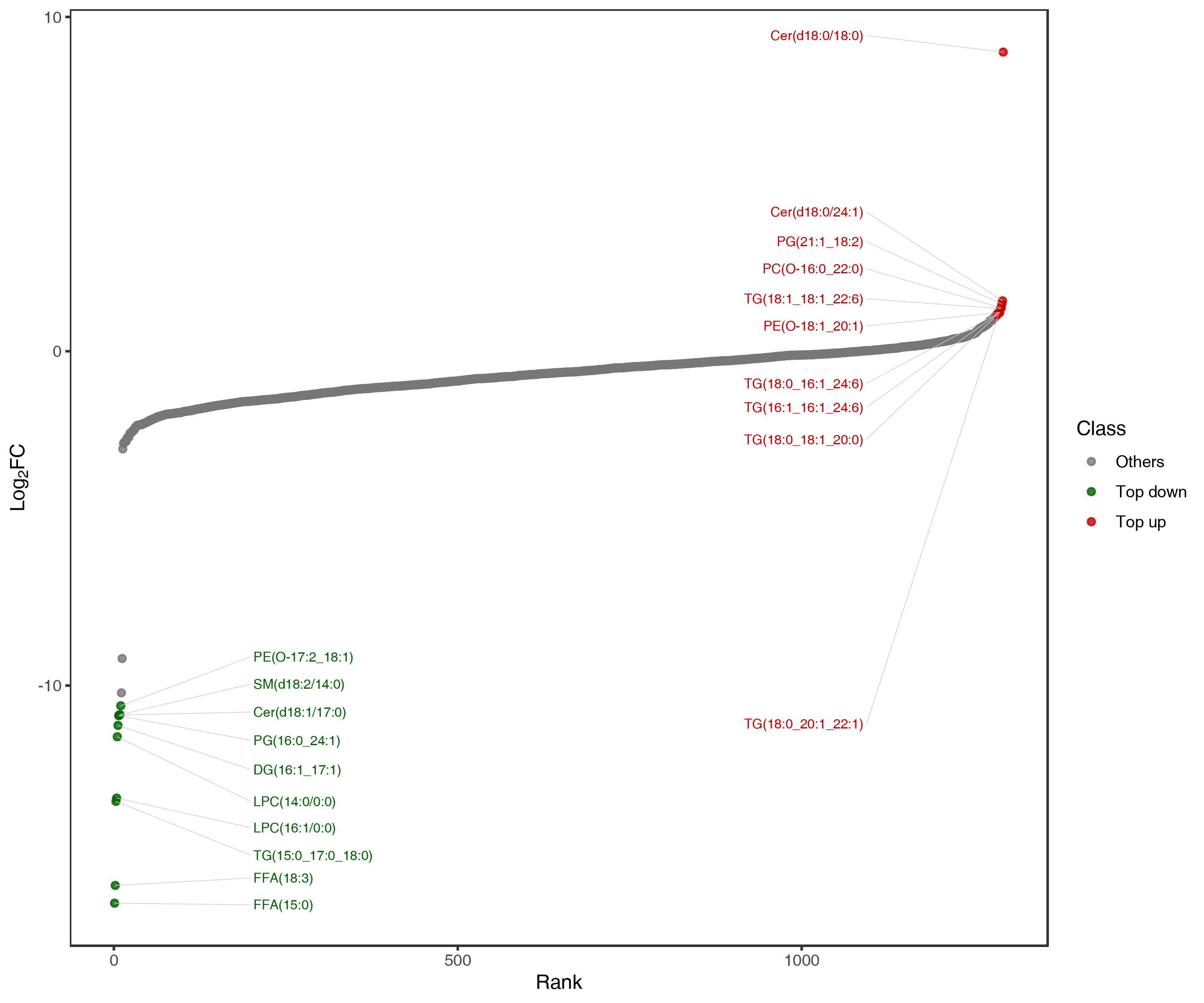
C

B

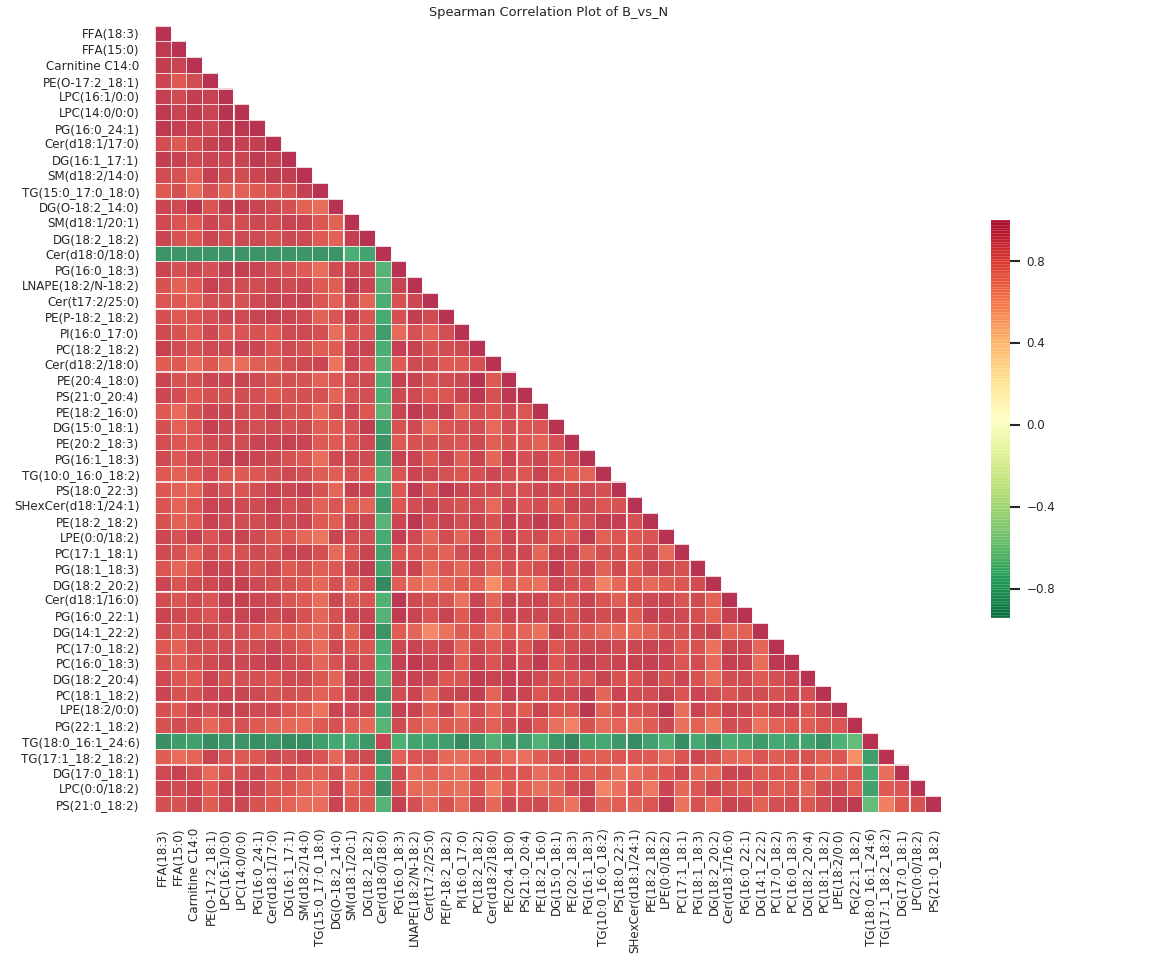
A



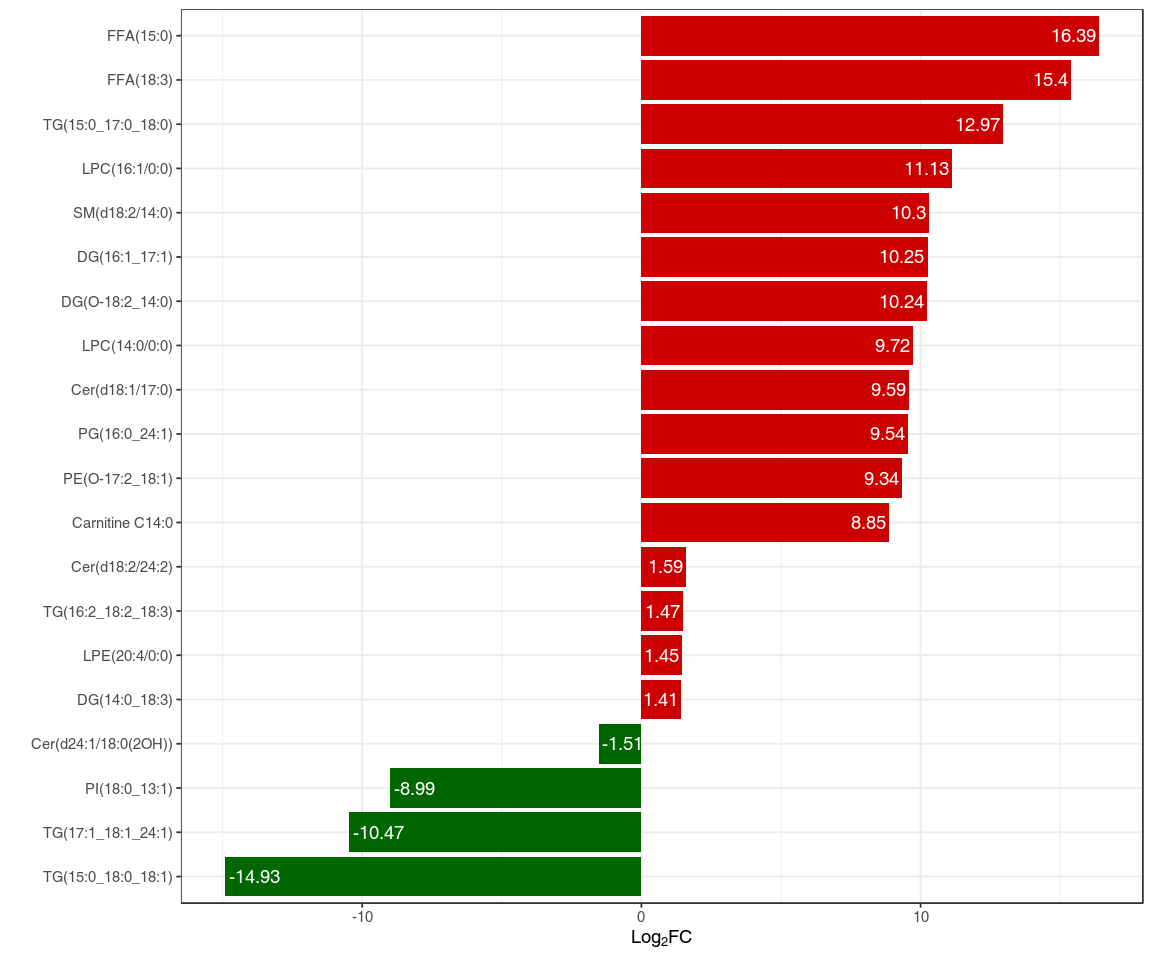
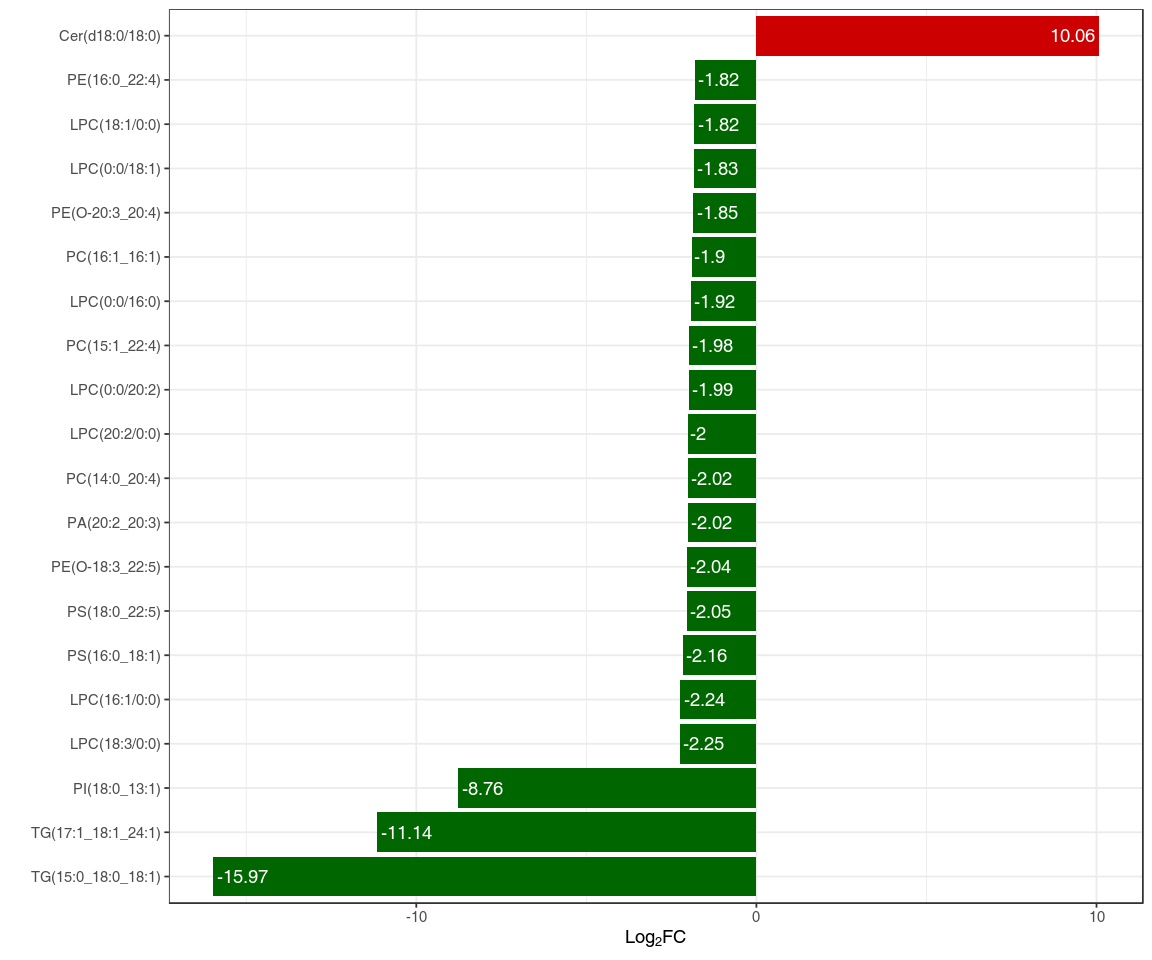
**Figure S5.** The KEGG pathway (kO00260) related DEGs and SCLs.(A, B) The KEGG pathway (kO00260) related DEGs and SCLs in the groups of Berkshire pigs vs Ningxiang pigs (A) and Berkshire pigs vs F1 pigs (B), respectively, dots and square frame represent metabolites and genes separately, red represents upregulation, green represents downregulation. (C, D) The violin chart of Phosphatidylserines in the group of Berkshire pigs vs Ningxiang pigs (C) and Berkshire pigs vs F1 pigs (D), respectively. B represents Berkshire pigs, N represents Ningxiang pigs, BN represents F1 pigs.



**Figure S6.** Dynamic distribution map of lipid content differences in the subcutaneous adipose tissue from the group of Berkshire pigs vs Ningxiang pigs. The horizontal ordinate represents the difference multiples of substances, the Y-axis represents the log2FC. Each point represents a substance, green dots represents the substances in the top 10 of the downward ranking and red dots represents the substances in the top 10 of the upward ranking.



**Figure S7.** The correlation heat map for significantly different lipids with the top VIP value in the subcutaneous adipose tissue from the group of Berkshire pigs vs Ningxiang pigs. Red represents positive correlation, green represents negative correlation.



A

B

**Figure S8.** Bar chart of difference lipids in the subcutaneous adipose tissue from the groups of Berkshire pigs vs F1 Ningxiang pigs (A) and Ningxiang pigs vs F1 pigs (B). The horizontal ordinate represents the log2FC of difference 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 the groups of Berkshire pigs 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 |
| *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** | | | | | | |
| *ATP1A* | 83.22 | 34.41 | 2.93E-7 | -1.17 | down | sodium/potassium-transporting ATPase subunit alpha |
| *HK* | 4,41 | 9.39 | 6.21E-3 | 1.24 | up | hexokinase |
| *SLC2A5* | 12.86 | 32.20 | 5.91E-3 | 1.44 | up | Solute carrier family 2 member 5 |
| *PLCB* | 4.49 | 2.06 | 1.14E-6 | -1.01 | down | phosphatidylinositol phospholipase C |
| **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 |