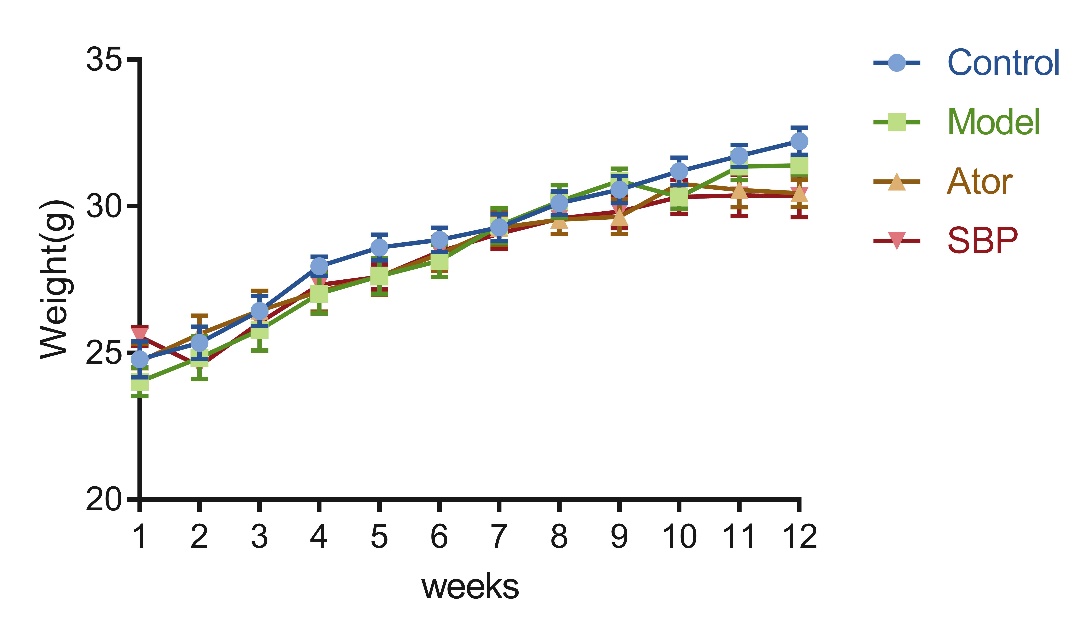
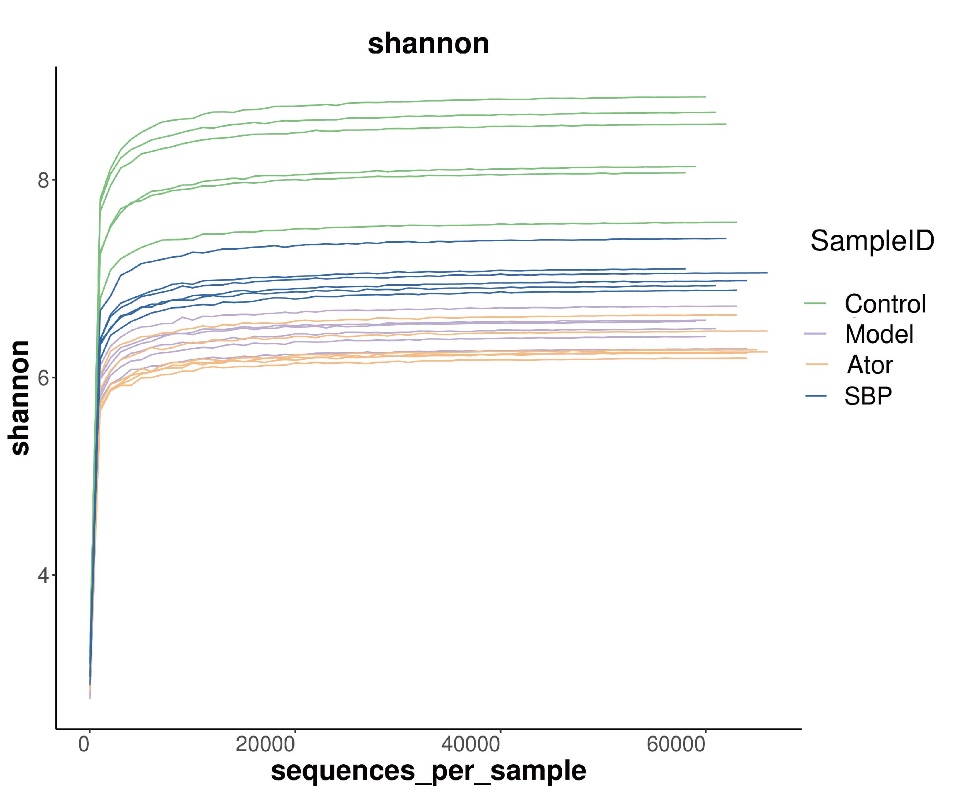
Supplementary Material

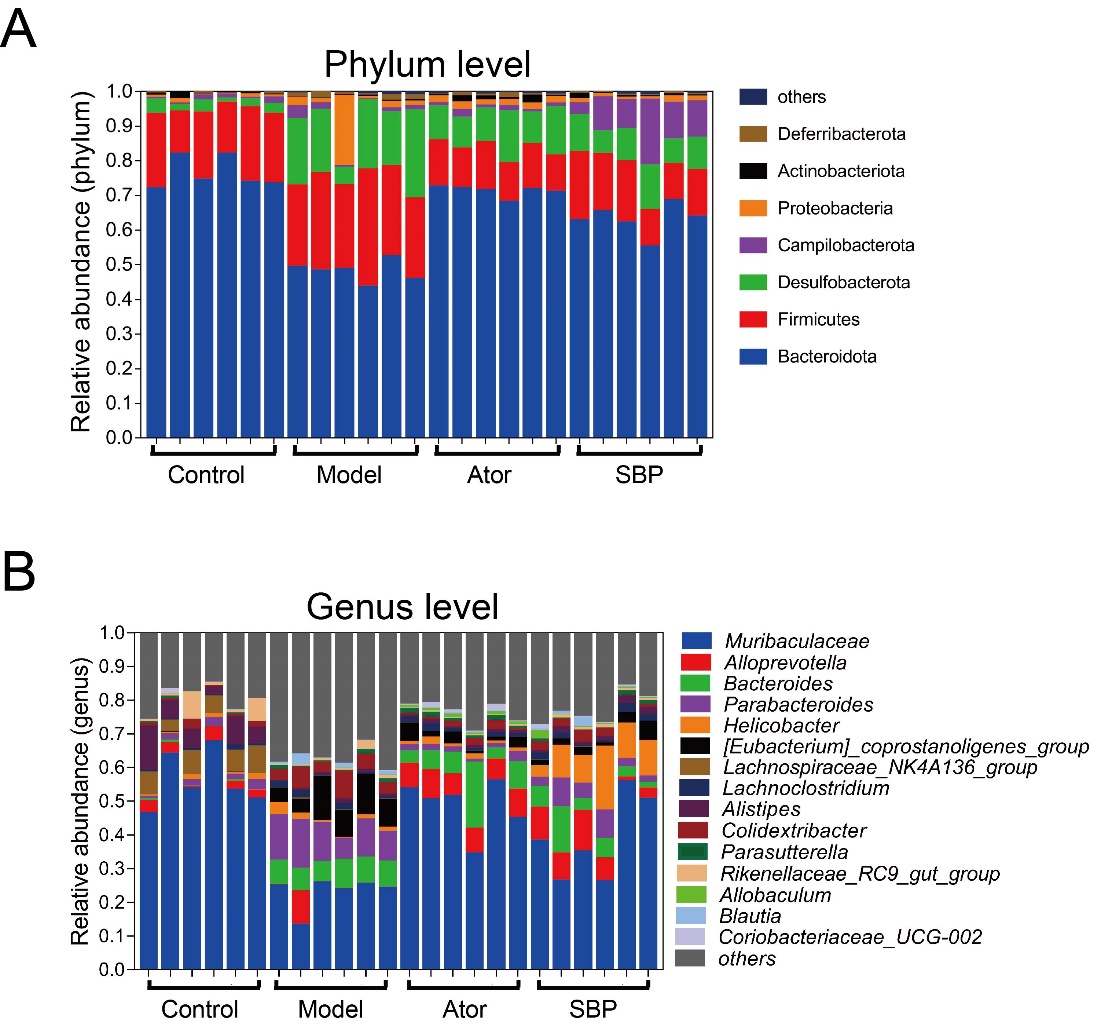
# Supplementary Figures



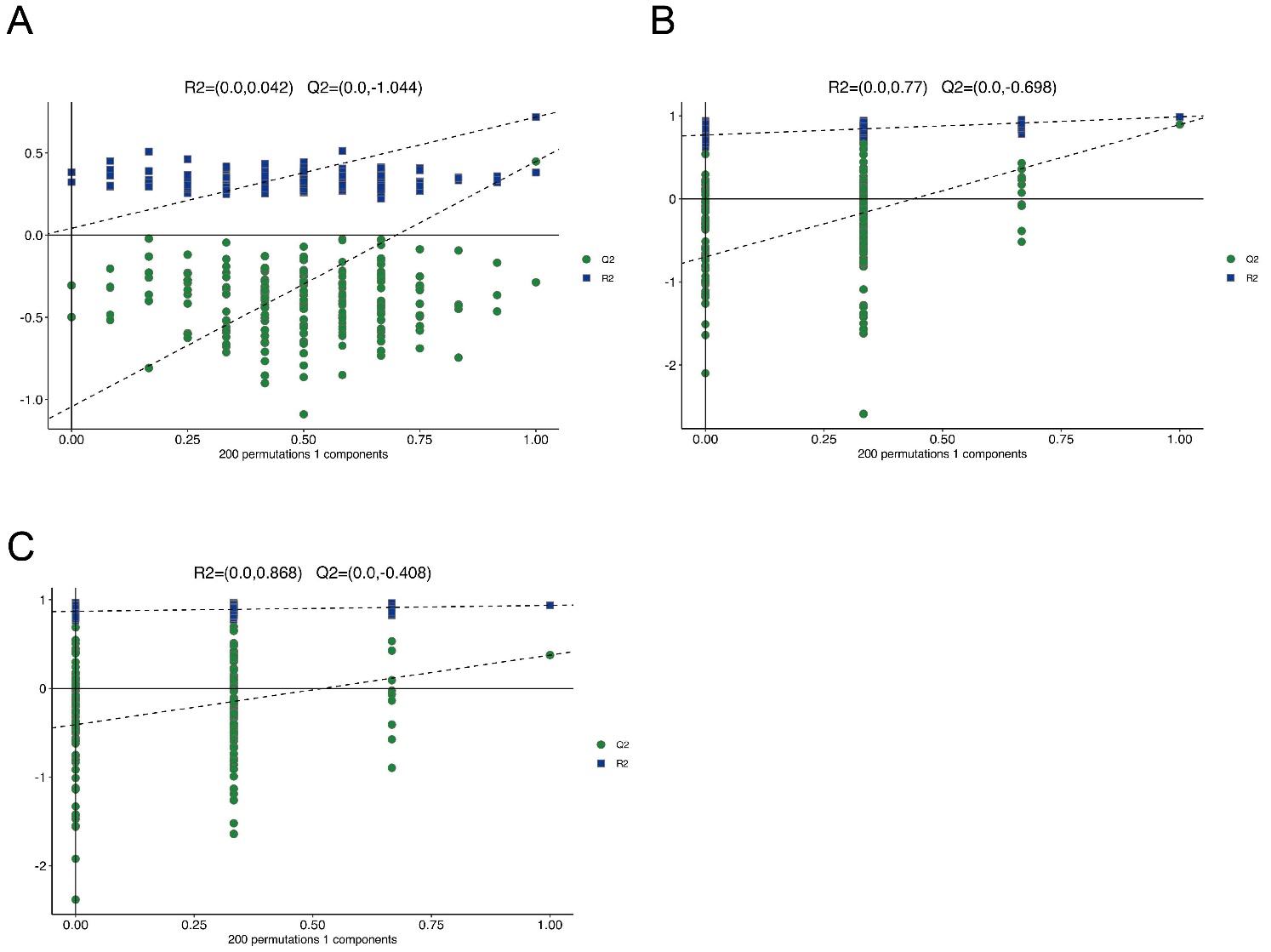
**Supplementary Figure S1.** Body weight of mice in per group.



**Supplementary Figure S2.** Shannon rarefaction curve in individual groups. The abscissa indicates the number of sequencing tags to be retrieved randomly, and ordinates reflect the estimated value of the shannon index determined when a specific number of tags are retrieved. The curve tended to flatten as the number of sequences increased, implying the amount of sequencing data in the sample was reasonable.



**Supplementary Figure S3.** The composition of gut microbiota in per sample. (**A**) The structure of gut microbiota in per sample at phylum level. (**B**) The structure of gut microbiota in per sample at genus level (Control = normal control group; Model = model group; Ator = atorvastatin group; SBP = Low dose of Shexiang Baoxin Pill group).



**Supplementary Figure S4.** Permutation test derived from the feces of mice in different group. (**A**) Permutation test from PLS-DA model among Control, Model, Ator and SBP groups. (**B**) Permutation test from OPLS-DA model between Control and Model group. (**C**) Permutation test from OPLS-DA model between SBP and Model group (Control = normal control group; Model = model group; Ator = atorvastatin group; SBP = Low dose of Shexiang Baoxin Pill group).

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# Supplementary Tables

**Table S1** Other indexes to reflect the diversity of gut microbiota

|  |  |  |  |
| --- | --- | --- | --- |
| Samples | Goods coverage | Observed species | Simpson |
| Control 1 | 0.961744662 | 2078.4 | 0.981118287 |
| Control 2 | 0.964975011 | 1796.6 | 0.972085815 |
| Control 3 | 0.96835075 | 1855.4 | 0.980980989 |
| Control 4 | 0.967655611 | 1692.1 | 0.973952096 |
| Control 5 | 0.955542935 | 2411.6 | 0.988998048 |
| Control 6 | 0.960690595 | 2216.2 | 0.990001078 |
| Model 1 | 0.975188551 | 1299.8 | 0.951237854 |
| Model 2 | 0.973421172 | 1284.1 | 0.946453787 |
| Model 3 | 0.972099046 | 1461.9 | 0.93765835 |
| Model 4 | 0.973289414 | 1403.7 | 0.94426733 |
| Model 5 | 0.97025443 | 1629.6 | 0.956922703 |
| Model 6 | 0.969618355 | 1551.8 | 0.925351103 |
| Ator 1 | 0.970940482 | 1410.8 | 0.94815045 |
| Ator 2 | 0.967419355 | 1527.8 | 0.949894022 |
| Ator 3 | 0.967655611 | 1536 | 0.949657688 |
| Ator 4 | 0.969127669 | 1416.6 | 0.93516597 |
| Ator 5 | 0.967174012 | 1603.6 | 0.956248152 |
| Ator 6 | 0.971653794 | 1349.2 | 0.943415444 |
| SBP 1 | 0.963639255 | 1758.8 | 0.958989895 |
| SBP 2 | 0.965124943 | 1781.4 | 0.972536968 |
| SBP 3 | 0.962939573 | 1737.4 | 0.953146522 |
| SBP 4 | 0.962099046 | 1810.3 | 0.940516323 |
| SBP 5 | 0.969686506 | 1508.6 | 0.96095401 |
| SBP 6 | 0.968496138 | 1625.6 | 0.963516633 |

**Table S2** The overlapped pathways between Model/Control and SBP/Model

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| NO. | | **KEGG pathway** | **Model/Control** | | **SBP/Model** | | |
| **Rich Factor** | ***p* value** |  | **Rich Factor** | ***p* value** |
| 1 | Alanine, aspartate and glutamate metabolism | | 0.1786 | 0.003646 |  | 0.1786 | 0.000352 |
| 2 | Long-term depression | | 0.2222 | 0.043759 |  | 0.3333 | 0.000867 |
| 3 | Gap junction | | 0.4545 | 0.000029 |  | 0.2727 | 0.001649 |
| 4 | Regulation of lipolysis in adipocytes | | 0.2143 | 0.014570 |  | 0.2143 | 0.003462 |
| 5 | HIF-1 signaling pathway | | 0.2000 | 0.017712 |  | 0.2000 | 0.004257 |
| 6 | beta-Alanine metabolism | | 0.1250 | 0.031956 |  | 0.1250 | 0.005532 |
| 7 | Long-term potentiation | | 0.2857 | 0.026834 |  | 0.2857 | 0.010011 |
| 8 | Spinocerebellar ataxia | | 0.2857 | 0.026834 |  | 0.2857 | 0.010011 |
| 9 | Neuroactive ligand-receptor interaction | | 0.2000 | 0.000100 |  | 0.1000 | 0.012258 |
| 10 | Porphyrin and chlorophyll metabolism | | 0.0797 | 0.015128 |  | 0.0580 | 0.012286 |
| 11 | Taurine and hypotaurine metabolism | | 0.1364 | 0.049406 |  | 0.1364 | 0.012852 |
| 12 | Glutamatergic synapse | | 0.3750 | 0.002652 |  | 0.2500 | 0.013152 |
| 13 | Cocaine addiction | | 0.5000 | 0.000126 |  | 0.2500 | 0.013152 |
| 14 | Endocrine and other factor-regulated calcium reabsorption | | 0.2500 | 0.034894 |  | 0.2500 | 0.013152 |
| 15 | Circadian entrainment | | 0.2222 | 0.043759 |  | 0.2222 | 0.016661 |
| 16 | GABAergic synapse | | 0.4444 | 0.000221 |  | 0.2222 | 0.016661 |
| 17 | Amphetamine addiction | | 0.4000 | 0.000357 |  | 0.2000 | 0.020522 |
| 18 | Alcoholism | | 0.4000 | 0.000357 |  | 0.2000 | 0.020522 |
| 19 | Adrenergic signaling in cardiomyocytes | | 0.3000 | 0.005372 |  | 0.2000 | 0.020522 |
| 20 | Dopaminergic synapse | | 0.3333 | 0.000793 |  | 0.1667 | 0.029227 |
| 21 | Central carbon metabolism in cancer | | 0.3000 | 0.000001 |  | 0.1000 | 0.029760 |
| 22 | Arginine and proline metabolism | | 0.1154 | 0.002552 |  | 0.0641 | 0.031284 |
| 23 | Tyrosine metabolism | | 0.1154 | 0.002552 |  | 0.0641 | 0.031284 |
| 24 | D-Glutamine and D-glutamate metabolism | | 0.2308 | 0.011772 |  | 0.1538 | 0.034038 |