Electronic Supplementary Material (ESI) for Food & Function.
This journal is © The Royal Society of Chemistry 2024

supplementary method

Experimental procedures of Metagenomic sequencing

1. Sample testing

There are mainly two methods in QC for DNA samples:

(1) DNA degradation degree and potential contamination was monitored on 1% agarose gels.

(2) DNA concentration was measured using Qubit® dsDNA Assay Kit in Qubit® 2.0 Fluorometer (Life Technologies, CA, USA). OD value is between 1.8~2.0, and DNA contents above 1ug are used to construct library.

2. Library construction

A total amount of 1μg DNA per sample was used as input material for the DNA sample preparations. Sequencing libraries were generated using NEBNext® Ultra™ DNA Library Prep Kit for Illumina (NEB, USA) following manufacturer's recommendations and index codes were added to attribute sequences to each sample. Briefly, the DNA sample was fragmented by sonication to a size of 350 bp, then DNA fragments were end-polished, A-tailed, and ligated with the full-length adaptor for Illumina sequencing with further PCR amplification. At last, PCR products were purified (AMPure XP system) and libraries were analyzed for size distribution by Agilent2100 Bioanalyzer and quantified using real-time PCR.

3. Sequencing

The clustering of the index-coded samples was performed on a cBot Cluster Generation System according to the manufacturer's instructions. After cluster generation, the library preparations were sequenced on an Illumina NovaSeq platform and paired-end reads were generated.

4.

Gut bacterial Metabolomics Analysis

1 Sample preparation and extraction

(1) Solid samples

The sample stored at -80 °C refrigerator was thawed on ice. A 400 μL solution (Methanol : Water =7:3, V/V) containing internal standard was added into 20 mg

sample, and vortexed for 3 min. The sample was sonicated in an ice bath for 10 min and vortexed for 1 min and then placed at -20 ℃ for 30 min. The sample was then centrifuged at 12000 rpm for 10 min (4 ℃). And the sediment was removed, then centrifuged the supernatant at 12000 rpm for 3 min (4 ℃). A 200 μL aliquots of supernatant were transferred for LC-MS analysis.

(2) HPLC Conditions (T3)

All samples were acquired by the LC-MS system followed machine orders. The analytical conditions were as follows, UPLC: column, Waters ACQUITY UPLC HSS T3 C18 (1.8 μm, 2.1 mm*100 mm); column temperature, 40℃; flow rate, 0.4 mL/min; injection volume, 2 μL; solvent system, water (0.1% formic acid): acetonitrile (0.1% formic acid); gradient program, 95:5 V/V at 0 min, 10:90 V/V at 11.0 min, 10:90 V/V at 12.0 min, 95:5 V/V at 12.1 min, 95:5 V/V at 14.0 min.

2. Analysis

The original data file acquired by LC-MS was converted into mzML format by ProteoWizard software. Peak extraction, peak alignment and retention time correction were respectively performed by the XCMS program. The “SVR” method was used to correct the peak area. The peaks with detetion rate lower than 50 % in each group of samples were discarded. After that, metabolic identification information was obtained by searching the laboratory’s self-built database, integrated public database, AI database and metDNA.

(1) PCA

Unsupervised PCA (principal component analysis) was performed by statistics function prcomp within R (www.r-project.org). The data was unit variance scaled before unsupervised PCA.

(2) Hierarchical Cluster Analysis and Pearson Correlation Coefficients

The HCA (hierarchical cluster analysis) results of samples and metabolites were presented as heatmaps with dendrograms, while Pearson correlation coefficients (PCC) between samples were calculated by the cor functioning R and presented as only heatmaps. Both HCA and PCC were carried out by R package ComplexHeatmap. For HCA, normalized signal intensities of metabolites (unit

variance scaling) are visualized as a color spectrum.

(3) Differential metabolites selected

For two-group analysis, differential metabolites were determined by VIP (VIP ≥ 1), P-value (P-value < 0.05, Student's t-test), and absolute Log2FC (|Log2FC| ≥ 1.0). VIP values were extracted from the OPLS-DA result, which also contains score plots and permutation plots, and was generated using the R package MetaboAnalystR. The data was log transform (log2) and mean centering before OPLS-DA. In order to avoid overfitting, a permutation test (200 permutations) was performed.

(4) KEGG annotation and enrichment analysis Identified metabolites were annotated using the KEGG Compound database (http://www.kegg.jp/kegg/ compound/), annotated metabolites were then mapped to the KEGG Pathway database (http://www.kegg.jp/kegg/ pathway.html). Significantly enriched pathways are identified with a hypergeometric test's P-value for a given list of metabolites.

RNA Sequencing

1. Sample collection and preparation

(1) RNA quantification and qualification

RNA degradation and contamination were monitored on 1% agarose gels. RNA purity was checked using the NanoPhotometer® spectrophotometer (IMPLEN, CA, USA). RNA concentration was measured using Qubit® RNA Assay Kit in Qubit®2.0 Fluorometer (Life Technologies, CA, USA). RNA integrity was assessed using the RNA Nano 6000 Assay Kit of the Bioanalyzer 2100 system (Agilent Technologies, CA, USA).

(2) Library preparation for Transcriptome sequencing

A total amount of 1 μg RNA per sample was used as input material for the RNA sample preparations. Sequencing libraries were generated using NEBNext®UltraTM RNA Library Prep Kit for Illumina® (NEB, USA) following the manufacturer's recommendations and index codes were added to attribute sequences to each sample. Briefly, mRNA was purified from total RNA using poly-T oligo-attached magnetic beads. Fragmentation was carried out using divalent cations under elevated temperature in NEBNext First Strand Synthesis Reaction Buffer(5X). First-strand cDNA was

synthesized using random hexamer primer and M-MuLV Reverse Transcriptase (RNase H-). Second-strand cDNA synthesis was subsequently performed using DNA Polymerase I and RNase H. Remaining overhangs was converted into blunt ends via exonuclease/polymerase activities. After adenylation of 3' ends of DNA fragments, NEBNext Adaptor with hairpin loop structure was ligated to prepare for hybridization. In order to select cDNA fragments of preferentially 250~300 bp in length, the library fragments were purified with the AMPure XP system (Beckman Coulter, Beverly, USA). Then 3 μl USER Enzyme (NEB, USA) was used with size-selected, adaptor-ligated cDNA at 37°C for 15 min followed by 5 min at 95 °C before PCR. Then PCR was performed with Phusion High-Fidelity DNA polymerase, Universal PCR primers and Index (X) Primer. At last, PCR products were purified (AMPure XP system) and library quality was assessed on the Agilent Bioanalyzer 2100 system.

(3) Clustering and sequencing

The clustering of the index-coded samples was performed on a cBot Cluster Generation System using TruSeq PE Cluster Kit v3-cBot-HS (Illumia) according to the manufacturer's instructions. After cluster generation, the library preparations were sequenced on an Illumina platform and 150 bp paired-end reads were generated.

2. Data Analysis

(1) Data quality control

Use fastp v 0.19.3 to filter the original data, mainly to remove reads with adapters; when the N content in any sequencing reads exceeds 10% of the base number of the reads, remove the paired reads; when any sequencing reads When the number of low-quality (Q<=20) bases contained in reads exceeds 50% of the bases of the reads, these paired reads will be removed. All subsequent analyses are based on clean reads.

(2) Reads mapping to the reference genome

Download the reference genome and its annotation files from the designated website, use HISAT v2.1.0 to construct the index, and compare clean reads to the reference genome.

(3) New transcript prediction

Use StringTie v1.3.4d for new gene prediction. StringTie applies network streaming

algorithms and optional de novo to splice transcripts. Compared with Cufflinks and other software, StringTie can splice a more complete and accurate transcript, and the splicing speed is faster.

(4) Quantification of gene expression levels

Use featureCounts v1.6.2 /StringTie v1.3.4d to calculate the gene alignment and FPKM . FPKM is currently the most commonly used method to estimate gene expression levels.

(5) Difference analysis

DESeq2 v1.22.1 /edgeR v3.24.3 was used to analyze the differential expression between the two groups, and the P value was corrected using the Benjamini & Hochberg method. The corrected P value and |log2foldchange| are used as the threshold for significant difference expression.

(6) Differential gene enrichment analysis

The enrichment analysis is performed based on the hypergeometric test. For KEGG, the hypergeometric distribution test is performed with the unit of pathway; for GO, it is performed based on the GO term.

(7) Differential AS analysis

Use rMATS v3.1.0 to analyze variable splicing events, including five alternative splicing events: SE, RI, MXE, A5SS, and A3SS.

(8) SNP analysis

Use GATK v4.1.9.0 to analyze the variant sites, and use annovar to annotate the variant sites.

(9) Differential gene protein interaction analysis

The protein interaction analysis of differentially expressed genes is based on the STRING database of known and predicted protein-protein interactions. For the species existing in the database, we construct the network by extracting the target gene list from the database; otherwise, use diamond v0.9.24.125 to compare the target gene sequence with the selected reference protein sequence, and then according to the selected reference species Know the interaction to build a network.

(10) GSEA

Use gsea-3.0.jar for gene set enrichment analysis.

(11) WGCNA

Use WGCNA v1.69 for weighted gene co-expression network analysis.

Supplementary figures

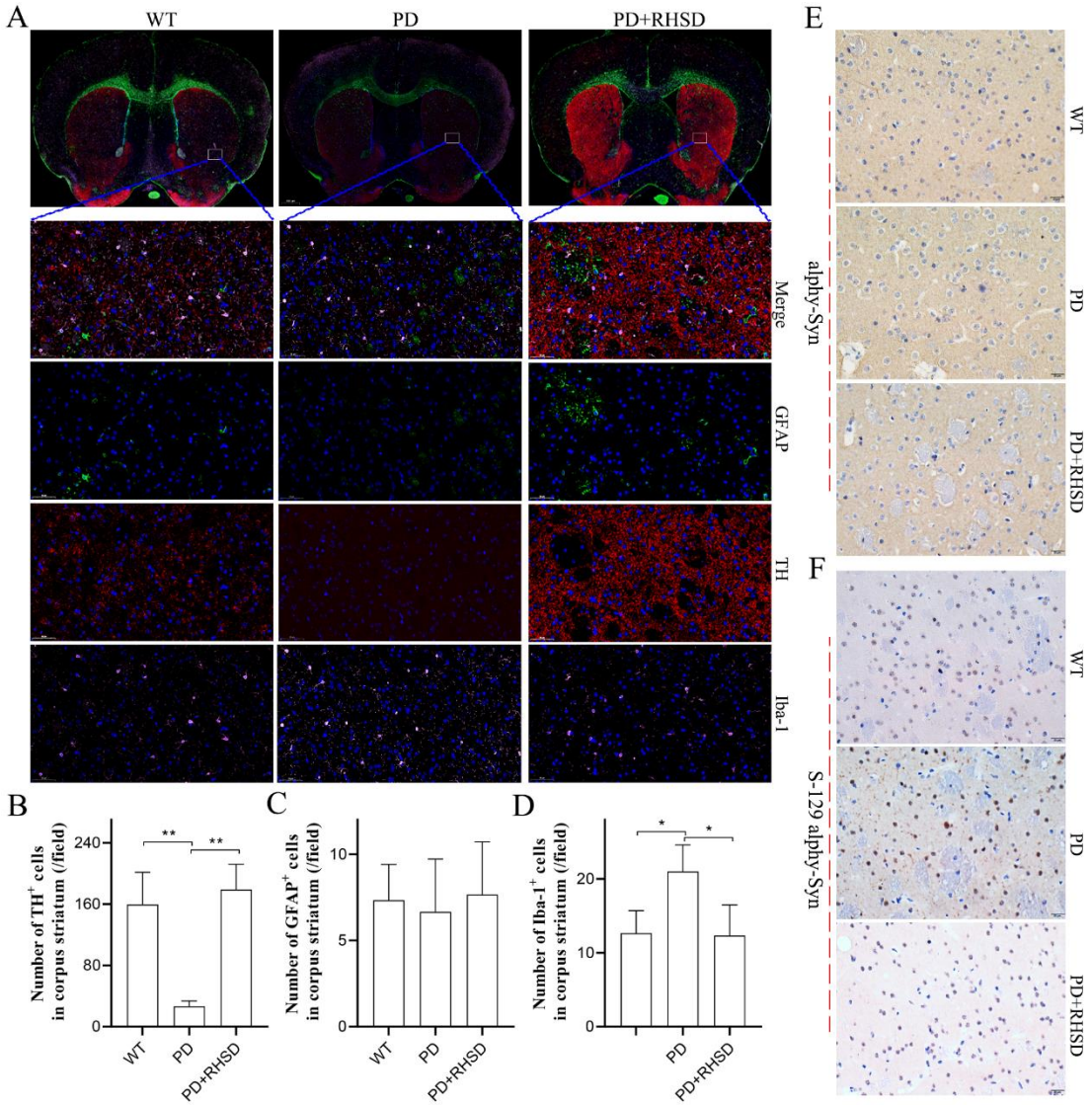

Fig. S1 RHSD administration attenuates PD-associated histological features in the striatum of the A53T transgenic mice. **A** Representative capture of immunofluorescence in the striatum of nuclei (DAPI, blue), astrocytes (GFAP, green), total dopaminergic neurons (TH, red), and microglial cells (Iba-1, pink). **B** Numbers of TH^+ cells in the striatum. **C** Numbers of $GFAP^+$ cells (activated astrocytes) in the striatum. **D** Numbers of Iba-1^+ cells (activated microglial cells) in the striatum. **E** Representative captures of α-Syn in the striatum, scale bar, 20 μm. **F** Representative captures of S-129 α-Syn in the striatum, scale bar, 20 μm. For **B-D**, n = 4 for each

group. Data are presented as mean ± SD. *$p < 0.05$; **$p < 0.01$.

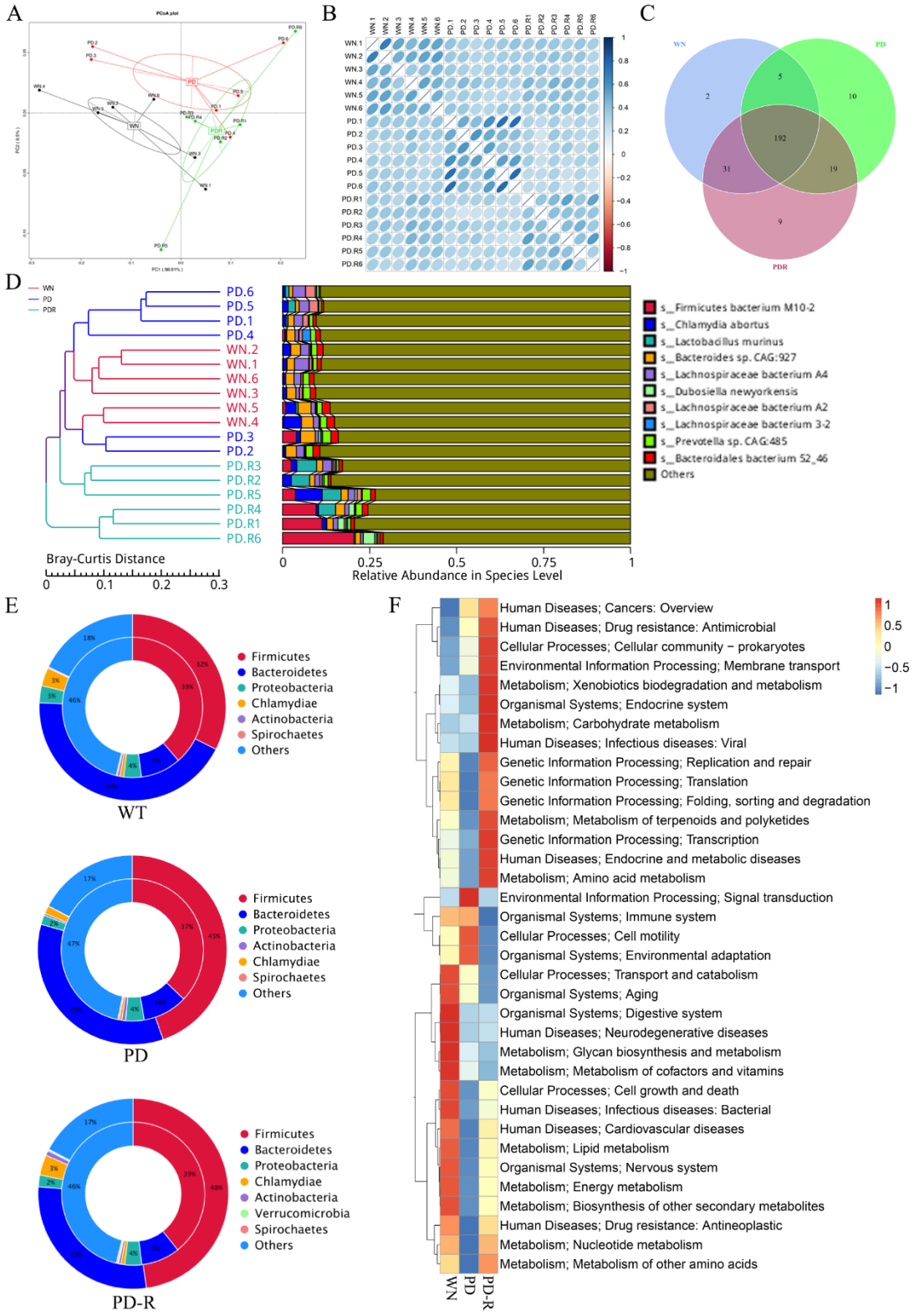

Fig. S2 RHSD reverses gut dysbiosis in A53T transgenic mice. RHSD reverses gut dysbiosis in A53T transgenic mice. **A** Bray-Curtis PcoA showed clear separation

among groups. **B** the correlation heatmap. **C** The Venn diagram of metagenomics data at the species level. **D** Cluster Tree of the phylum level by using Metastats and LEfSe analysis. **E** The twocircle plot of taxonomy at the phylum level. **F** The top 35 species were shown in the heatmap through cluster analysis of species abundance between groups.

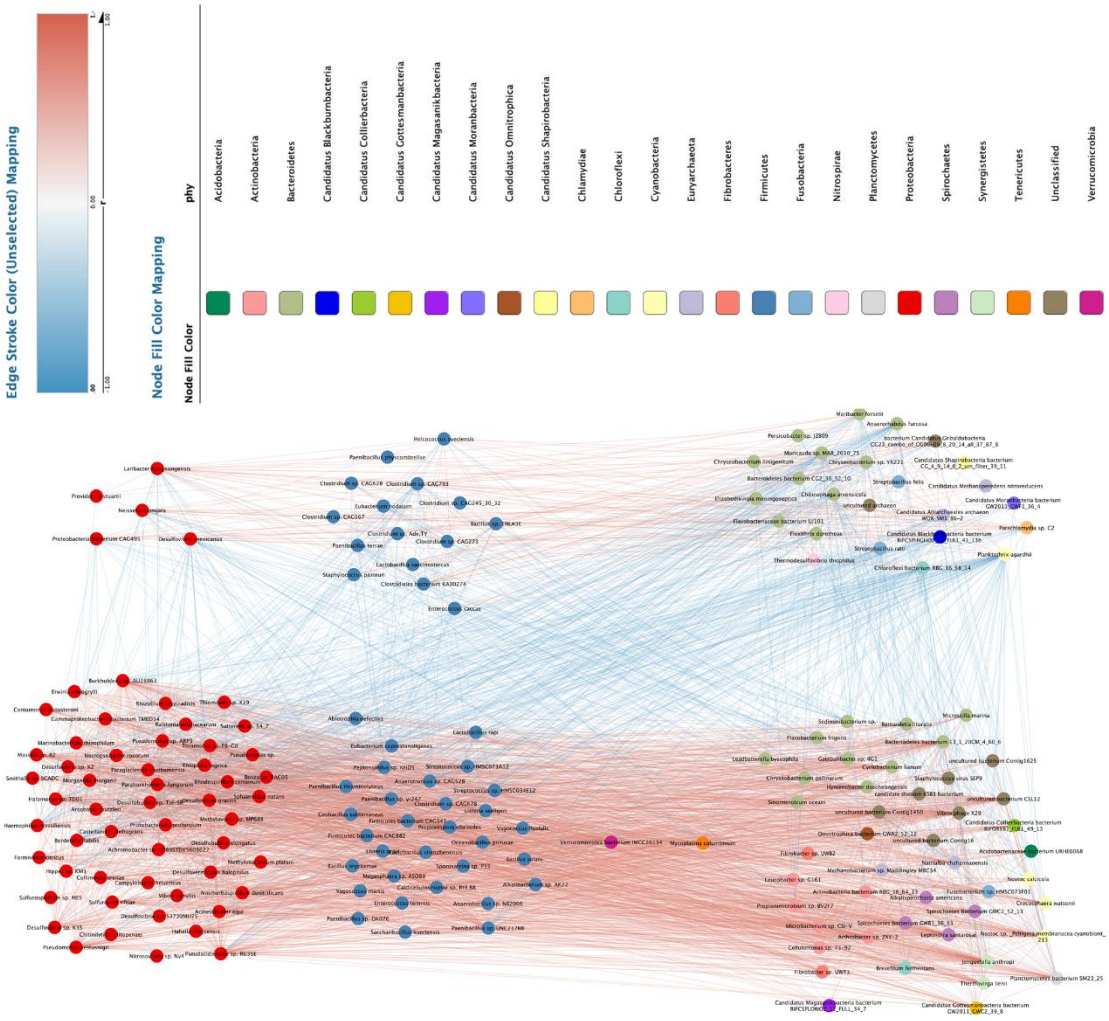

Fig. S3 The Spearman correlation network. The top half is up-regulated bacteria, and the bottom half is down-regulated bacteria.

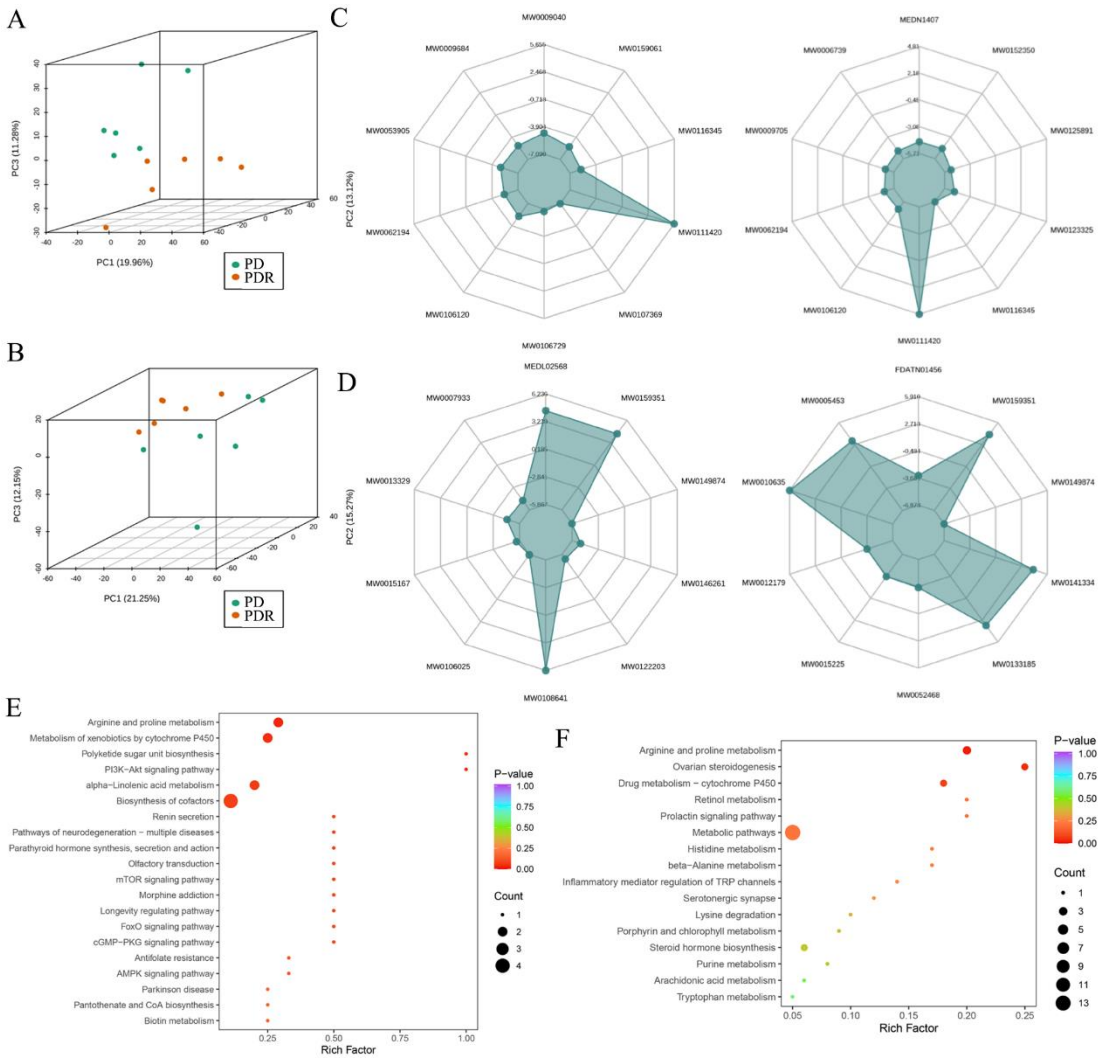

Fig. S4 RHSD reverses metabolomic changes in A53T transgenic mice. The unsupervised PCA in both positive (**A**) and negative modes (**B**). The radar maps of differential metabolite in both positive (**C**) and negative modes (**D**). KEGG Enrichment between the A53TR and A53T groups (**E**) and between the WT and A53T groups (**F**).

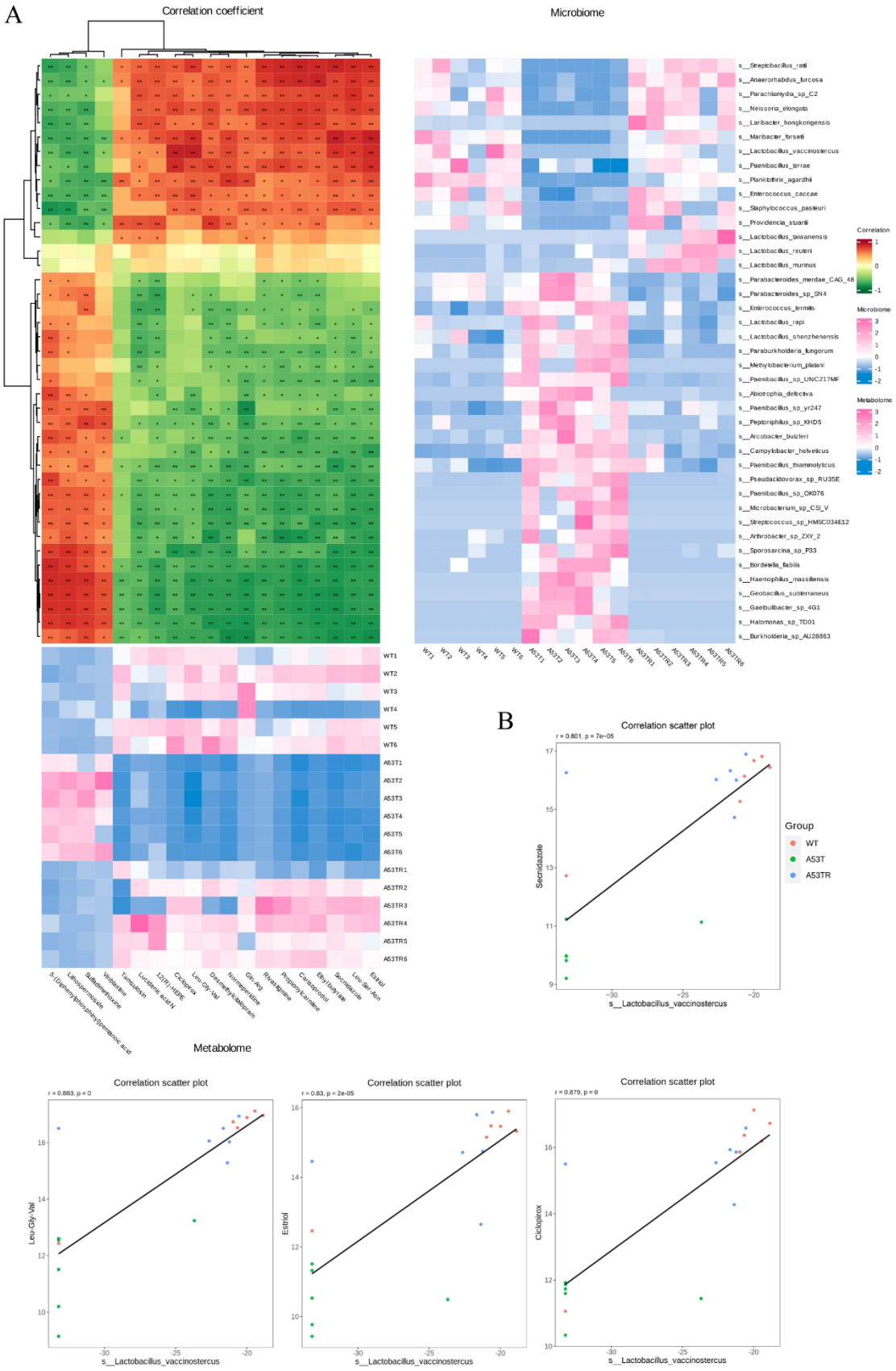

Fig. S5 RES Modulates Gut Microbiome Metabolites in A53T Transgenic Mice. **A** Spearman's correlation analysis was performed between the significant difference

bacterial species and the 19 metabolites with fold difference which was reversed by RHSD administration. **B** Scatter plots illustrating the statistical association between the relative abundance of *Lactobacillus_vaccinostercus* and the LC-MS spectrum intensities of some significant difference which include Secnidazole, Leu-Gly-Val, Ciclopirox, and Estriol.

Table S1 Relative abundance of microbiota at species taxon levels

Species	Relative abundance			WT vs. PD		PDR vs. PD	
	WT	PD	PDR	P value	Fold change	P value	Fold change
g__Cellulomonas;s__Cellulomonas sp. 73-92	4.45E-08	3.17E-07	4.96E-09	0.007226	0.140590648	0.002827	0.015668
g__Microbacterium;s__Microbacterium sp. CSI-V	0	5.87E-07	0	0.004604	0	0.004862	0
g__Arthrobacter;s__Arthrobacter sp. ZXY-2	0	3.85E-07	0	0.004087	0	0.002212	0
g__Bernardetia;s__Bernardetia litoralis	1.98E-06	7.04E-06	3.28E-07	0.000403	0.28186683	2.29E-05	0.04659
g__Gaetbulibacter;s__Gaetbulibacter sp. 4G1	0	4.4E-07	0	0.000928	0	0.000901	0
g__Nostoc;s__Nostoc sp. _Peltigera membranacea cyanobiont_ 213	2.92E-08	7.87E-07	1.17E-08	0.000904	0.037078918	0.000737	0.014853
g__Geobacillus;s__Geobacillus subterraneus	0	4.57E-07	0	0.00552	0	0.00595	0
g__Paenibacillus;s__Paenibacillus sp. OK076	0	2.85E-07	0	0.001089	0	0.001066	0
g__Paenibacillus;s__Paenibacillus sp. UNC217MF	1.09E-06	4.42E-06	2.15E-07	0.009301	0.247812	0.000149	0.048607
g__Sporosarcina;s__Sporosarcina sp. P33	1.15E-08	3.04E-07	1.34E-08	0.004011	0.037661	0.004324	0.044214
g__Abiotrophia;s__Abiotrophia defectiva	4.93E-08	6.77E-07	1.1E-08	0.007523	0.072914	0.00492	0.016266
g__Streptococcus;s__Streptococcus sp. HMSC034E12	0	6.93E-07	0	0.008414	0	0.009158	0
g__Peptoniphilus;s__Peptoniphilus sp. KHD5	4.5E-08	4.99E-07	2.42E-08	0.003569	0.090213	0.002124	0.048611
g__Methylobacterium;s__Methylobacterium platani	3.81E-08	6.56E-07	0	0.009301	0.0581	0.006552	0
g__Achromobacter;s__Achromobacter sp. 2789STDY5608622	2.13E-08	1.05E-06	2.02E-08	0.000227	0.020386	0.00021	0.019256
g__Bordetella;s__Bordetella flabilis	2.08E-08	3.64E-07	0	0.001633	0.057169	0.000913	0
g__Burkholderia;s__Burkholderia sp. AU28863	0	8.98E-07	1.87E-08	0.004139	0	0.004999	0.020848
g__Paraburkholderia;s__Paraburkholderia fungorum	1.79E-07	1.05E-06	2.74E-08	0.00055	0.16933	9.38E-05	0.026037
g__Pseudacidovorax;s__Pseudacidovorax sp. RU35E	9.6E-09	7.61E-07	3.17E-09	0.000405	0.012611	0.000351	0.004163
g__Halomonas;s__Halomonas sp. TD01	0	4.21E-07	0	0.000801	0	0.000768	0
g__Haemophilus;s__Haemophilus massiliensis	0	2.53E-07	0	0.003184	0	0.00326	0
g__Acinetobacter;s__Acinetobacter equi	7.47E-09	1.04E-06	2.94E-08	0.005413	0.007213	0.006639	0.028413
g__Pseudomonas;s__Pseudomonas sp. ARP3	2.88E-08	5.18E-07	9.97E-09	0.000218	0.055585	0.0001	0.019249

g__Leptospira;s__Leptospira santarosai	1.85E-06	1.04E-05	1.06E-06	0.002265	0.178327	0.00126	0.101936
g__Jonquetella;s__Jonquetella anthropi	6.43E-07	6.37E-06	2.77E-07	0.001837	0.100998	0.001157	0.043439
g__Mycoplasma;s__Mycoplasma columbinum	0	3.83E-07	0	0.004764	0	0.005041	0
g__Unclassified;s__Vibrio phage X29	3.61E-08	5.86E-07	2.68E-08	0.002683	0.061573	0.002376	0.045718
g__Candidatus Methanoperedens;s__Candidatus Methanoperedens nitroreducens	4.61E-06	1.18E-06	3.12E-06	0.001798	3.924127	0.001698	2.653285
g__Anaerorhabdus;s__Anaerorhabdus furcosa	9.46E-05	2.14E-05	0.000193	0.000778	4.424661	2.36E-05	9.016789
g__Chitinophaga;s__Chitinophaga arvensicola	1.15E-06	1.2E-07	6.22E-07	0.000887	9.53933	0.002251	5.168084
g__Flexithrix;s__Flexithrix dorotheae	5.64E-06	1.79E-07	3.86E-06	0.000785	31.50786	0.00529	21.52901
g__Persicobacter;s__Persicobacter sp. JZB09	9.35E-07	4.58E-07	1.11E-06	0.000661	2.042868	0.007169	2.417404
g__Chryseobacterium;s__Chryseobacterium limigenitum	5.23E-07	2.11E-07	9.42E-07	0.006581	2.480594	0.0016	4.464858
g__Chryseobacterium;s__Chryseobacterium sp. YR221	1.65E-05	3.55E-08	3.22E-06	0.001449	464.4997	0.006857	90.82123
g__Elizabethkingia;s__Elizabethkingia meningoseptica	1.58E-06	7.53E-07	2.26E-06	0.000901	2.104774	0.00454	3.005723
g__Maribacter;s__Maribacter forsetii	3.43E-07	1.41E-08	2.77E-07	0.000741	24.39698	0.000372	19.66921
g__Muricauda;s__Muricauda sp. MAR_2010_75	4.47E-07	1.37E-08	7.14E-07	0.004921	32.56341	8.39E-05	52.05598
g__Parachlamydia;s__Parachlamydia sp. C2	1.93E-06	3.87E-07	2.26E-06	0.006848	4.997787	0.001065	5.856718
g__Planktothrix;s__Planktothrix agardhii	1.68E-06	1.34E-08	7.42E-07	5.36E-06	125.7588	0.000154	55.61511
g__Bacillus;s__Bacillus sp. 1NLA3E	3.26E-06	6.84E-07	7.76E-06	0.002573	4.76372	0.006904	11.34002
g__Paenibacillus;s__Paenibacillus physcomitrellae	3.2E-06	4.9E-07	4.34E-06	0.000929	6.527138	0.002056	8.852054
g__Paenibacillus;s__Paenibacillus terrae	4.86E-06	1.83E-06	3.82E-06	0.009523	2.66046	0.006947	2.0875
g__Staphylococcus;s__Staphylococcus pasteuri	7.97E-07	2.29E-08	1.06E-06	0.004639	34.74265	0.007313	46.38033
g__Enterococcus;s__Enterococcus caccae	1.39E-06	3.25E-07	1.3E-06	0.003829	4.265646	0.007866	4.002035
g__Lactobacillus;s__Lactobacillus vaccinostercus	9.24E-07	1.23E-08	3.14E-07	0.007478	75.29088	0.00511	25.55019
g__Clostridium;s__Clostridium sp. Ade.TY	1.72E-06	5.49E-07	3.1E-06	0.008404	3.130985	0.007547	5.656207
g__Clostridium;s__Clostridium sp. CAG245_30_32	0.000116	4.66E-05	0.000191	0.004871	2.494422	0.002329	4.094184
g__Clostridium;s__Clostridium sp. CAG273	0.000307	8.33E-05	0.000506	0.005111	3.68353	0.002229	6.077385

g__Clostridium;s__Clostridium sp. CAG567	0.000277	8.24E-05	0.000525	0.00704	3.355838	0.005206	6.365544
g__Clostridium;s__Clostridium sp. CAG628	0.000193	4.2E-05	0.000332	0.005407	4.588797	0.002517	7.909699
g__Clostridium;s__Clostridium sp. CAG793	0.000252	3E-05	0.00068	0.005834	8.401206	0.002838	22.64079
g__Helcococcus;s__Helcococcus sueciensis	1.28E-06	4.59E-07	1.74E-06	0.003196	2.782968	0.005055	3.788337
g__Streptobacillus;s__Streptobacillus felis	1.05E-06	2.69E-07	9.88E-07	0.005655	3.895555	0.004634	3.669271
g__Streptobacillus;s__Streptobacillus ratti	2.79E-07	5.47E-09	4.16E-07	0.004827	50.92442	6.07E-06	76.02373
g__Thermodesulfovibrio;s__Thermodesulfovibrio thiophilus	6.53E-07	2.19E-07	7.89E-07	0.000779	2.978457	0.008932	3.595864
g__Laribacter;s__Laribacter hongkongensis	3.14E-07	1.76E-08	3.01E-06	0.000152	17.88051	0.005387	171.5726
g__Neisseria;s__Neisseria elongata	9.15E-07	2.67E-08	1.27E-06	0.0007	34.28029	0.000435	47.45381
g__Desulfovibrio;s__Desulfovibrio mexicanus	9.75E-06	3.13E-06	1.01E-05	0.000596	3.111948	0.000409	3.23308
g__Providencia;s__Providencia stuartii	9.75E-06	3.13E-06	1.01E-05	0.000596	3.111948	0.000409	3.23308

Table S2 A list of screened differential metabolites

Index	Compounds	Class II	WT_vs_A53T	A53TR_vs_A53T
MW0106120	Carisoprodol	Esters	down	down
MW0125891	Normeperidine	Heterocyclic compounds	down	down
MW0111420	Lithospermoside	Hydrocarbon derivatives	up	up
MW0006739	Desmethylcitalopram	Benzene and substituted derivatives	down	down
MEDN1407	Estriol	Hormones and hormone-related compounds	down	down
MW0116345	Secnidazole	Heterocyclic compounds	down	down
MW0123325	Ciclopirox	Medicine	down	down
MW0062194	Propionylcarnitine	CAR	down	down
MW0009684	Rivastigmine	Benzene and substituted derivatives	down	down
MW0009837	Tamsulosin	Benzene and substituted derivatives	down	down
MEDP0778	Ethyl butyrate	Esters	down	down
MW0152480	Leu-Ser-Asn	Small Peptide	down	down
MW0152350	Leu-Gly-Val	Small Peptide	down	down
MW0149874	Gln-Arg	Small Peptide	down	down
MW0054437	Lucidenic acid N	Organic acid And Its derivatives	down	down
MW0012179	12(R)-HEPE	Oxidized lipids	down	down

MW0005453	5-(Diphenylphosphinyl) pentanoic acid	Benzene and substituted derivatives	up	up
MW0159351	Vinblastine	Esters	up	up
MW0009787	Sulfadimethoxine	Benzene and substituted derivatives	up	up

Table S3 A list of metabolites belonging to the hormones and hormone-related compounds

Index	Formula	Compounds	WT_vs_A53T	A53TR_vs_A53T
MW0052658	C23H32O3	Estradiol valerate	FALSE	up
MW0012746	C19H24O3	19-Aldoandrostenedione	FALSE	up
MW0006724	C21H30O3	Desoxycortone	FALSE	up
MW0006998	C18H22O2	Estrone	down	down
MW0013232	C27H46O2	20-Hydroxycholesterol	FALSE	up
MW0152679	C28H44O	Lichesterol	down	down
MEDN1407	C18H24O3	Estriol	down	down
MW0012109	C20H32O4	11-Deoxyprostaglandin E2	FALSE	up
MW0062147	C26H40O3	Prasterone enanthate	FALSE	up
MW0013323	C27H46O2	25-Hydroxycholesterol	FALSE	up
MW0012392	C21H34O5	15(R)-15-Methylprostaglandin D2	FALSE	up
MW0155048	C21H38O4	PGF2 Alcohol methyl ether	FALSE	up
MW0015246	C27H46O3	7alpha,24(S)-Dihydroxycholesterol	FALSE	down
MW0012654	C23H30O5	17-Phenyltrinorprostaglandin D2	FALSE	down
MW0010939	C27H46O3	(20R,22R)-20,22-Dihydroxycholesterol	FALSE	down
MEDN0798	C20H32O5	PGK1	FALSE	down
MW0015442	C21H34O4	9-deoxy-9-methylene-PGE2	FALSE	FALSE
MW0141430	C21H34O5	15-cyclohexyl pentanor PGF2	FALSE	up
MW0012480	C21H34O5	15-methyl-15R-PGE2	FALSE	up
MW0141408	C20H32O6	15(R),19(R)-hydroxy Prostaglandin E2	FALSE	up
MW0012105	C22H36O4	11-deoxy-16,16-dimethyl-PGE2	FALSE	down
MW0157453	C16H22O6	tetranor-PGAM	up	up
MW0049029	C21H30O4	Corticosterone	FALSE	up

MW0012521	C22H36O5	16,16-dimethyl-PGE2	FALSE	down
MW0061345	C22H37NO5	PGE2-EA	FALSE	up
MW0156120	C20H26D4O4	Prostaglandin A2-d4	FALSE	up
MW0155706	C21H34O5S	Pregnanolone Sulphate	FALSE	up
MW0062140	C33H54O11	Ponasteroside A	FALSE	down
MW0012578	C22H30O5	16-Phenyltetranorprostaglandin E1	FALSE	up
MW0012287	C20H30O4	13,14-Dihydro-15-ketoprostaglandin J2	FALSE	up

Table S4 A list of 46 metabolites that were subjected to correlation analysis with gut microbial biomarker

Index	Formula	Compounds	Class II	WT_vs_A53T	A53TR_vs_A53T
MEDP1001	C6H10O2	Delta-Hexalactone	Esters	up	up
MW0106120	C12H24N2O4	Carisoprodol	Esters	down	down
MEDN0243	C8H11NO3	Pyridoxine	Heterocyclic compounds	FALSE	up
MW0111420	C14H19NO8	Lithospermoside	Hydrocarbon derivatives	up	up
MEDP1675	C14H27N3O4	Leu-Leu-Gly	Small Peptide	down	down
MEDP0519	C6H13NO2	L-Norleucine	Amino acids	down	down
MW0012859	C21H38O4	1-Monolinoleoyl-rac-glycerol	MG	down	down
MEDL00392	C26H52NO7P	1-Oleoyl-sn-glycero-3-phosphocholine	LPC	down	down
MW0158838	C33H42N4O6	Urobilin	Organic acid And Its derivatives	up	up
MW0062194	C10H19NO4	Propionylcarnitine	CAR	down	down
MW0104004	C6H10N2O5	Carglumic Acid	Organic acid And Its derivatives	down	down
MEDP0778	C6H12O2	Ethyl butyrate	Esters	down	down
MW0158415	C24H34N4O10	Tyr-Asp-Leu-Glu	Small Peptide	up	up
MW0157839	C33H46N6O11	Thr-Tyr-Glu-Lys-Tyr	Small Peptide	up	up
MW0157732	C25H46N6O9S	Thr-Lys-Met-Val-Glu	Small Peptide	up	up
MW0109911	C13H26N4O5	Thr-Ala-Lys	Small Peptide	up	up
MEDL00370	C17H25N3O4	Phe-Ile-Gly	Small Peptide	down	down
MW0154728	C28H50N4O3S	Oleic Acid-biotin	Others	down	down
MW0153141	C13H26N4O5	Lys-Thr-Ala	Small Peptide	up	up
MW0152522	C21H30N4O5	Leu-Thr-Trp	Small Peptide	up	up
MW0152480	C13H24N4O6	Leu-Ser-Asn	Small Peptide	down	down
MW0152405	C29H45N5O8	Leu-Leu-Ser-Pro-Tyr	Small Peptide	down	down
MW0150821	C21H38N8O5	His-Ala-Lys-Lys	Small Peptide	down	down

MW0150406	C14H27N3O4	Gly-Leu-Leu	Small Peptide	down	down
MW0149905	C28H44N8O8	Glu-Ala-Phe-Arg-Val	Small Peptide	up	up
MW0146084	C24H40N6O12	Asp-Gln-Leu-Thr-Glu	Small Peptide	down	down
MW0105648	C12H26N8O3	Arg-Arg	Small Peptide	up	up
MW0113020	C4H9NO	4-Aminobutanal	Aldehydes	up	up
MW0107895	C6H13NO2	L-Isoleucine	Amino acids	FALSE	down
MW0107960	C4H9NO3	L-Threonine	Amino acids	FALSE	down
MW0010027	C5H11NO2	L-Valine	Amino acids	FALSE	up
MW0111715	C10H18O9	1,4-D-Xylobiose	Sugars	FALSE	up
MW0103512	C9H13N3O5	Cytidine	Nucleotide and Its metabolites	FALSE	down
MW0102908	C12H20O4	trans-Traumatic acid	FFA	up	up
MW0168852	C10H16N2O3S	biotin	CoEnzyme and vitamins	up	up
MW0105914	C4H7NO4	L-Aspartic Acid	Amino acids	FALSE	down
MW0015225	C12H20O3	7-Oxo-11-dodecenoic acid	Oxidized lipids	down	down
MEDN0213	C6H14O6	D-Sorbitol	Sugar alcohols	FALSE	up
MEDP0752	C6H13NO2	DL-Leucine	Amino acids	FALSE	up
MW0110250	C14H18N2O6	Tyr-Glu	Small Peptide	up	up
MW0103659	C14H23N6O3S	S-Adenosylmethioninamine	Nucleotide and Its metabolites	down	down
MW0009765	C18H28O2	Stearidonic acid	FFA	up	up
MW0012179	C20H30O3	12(R)-HEPE	Oxidized lipids	down	down
MW0155447	C15H18N4O3	Phe-His-OH	Small Peptide	up	up
MW0054437	C27H40O6	Lucidenic acid N	Organic acid And Its derivatives	down	down
MW0149874	C11H22N6O4	Gln-Arg	Small Peptide	down	down