Supplementary Table 1 Comparison of the relative abundance of top20 genera

Genus	Relative abundance			
	Control	OSA	HTN	Complication
Streptococcus	0.4143212007±0.14174702546	0.3964246426±0.16127655774	0.3240346322±0.09311698823	0.3988937977±0.10517081180
Neisseria	0.08995522±0.09666919635	0.1007344248±0.10987541224	0.1420568461±0.08662078742	0.0965300554±0.10580121502
Rothia	0.0501138326±0.03768348856	0.0873427844±0.06692349856	0.1017201909±0.06629898867	0.0919185577±0.06846526492
Prevotella	0.0969961056±0.07226855445	0.0570204833±0.04457849175	0.0909722965±0.06993571623	0.0753835485±0.06296925666
Actinomyces	0.0788992978±0.03642369355	0.0890082863±0.05662807492	0.0558069426±0.04658287127	0.0620509846±0.03335582696
Haemophilus	0.0406676978±0.04047247681	0.021681817±0.02068928056	0.0569539474±0.03593220977	0.0288440127±0.02819277183
Gemella	0.0256227096±0.01611470372	0.0358191633±0.02461409913	0.0353372483±0.03994551836	0.0374486869±0.02857688604
Porphyromonas	0.030147583±0.02349521451	0.0334139937±0.02461409913	0.0290799391±0.02416492297	0.0386704269±0.05857803150
Veillonella	0.0215391374±0.01754118868	0.0199111278±0.01416713604	0.0231291009±0.01620683415	0.0235916004±0.01401151193
Granulicatella	0.0154676456±0.01020172092	0.0234645896±0.01287302933	0.0150097996±0.00812322858	0.0206627154±0.01402781157
Fusobacterium	0.0165082726±0.02464224476	0.0178470378±0.01990813036	0.0207181717±0.01235823823	0.0181445119±0.01936547239
Leptotrichia	0.0071679767±0.00899310998	0.0086077033±0.01171473748	0.0093715865±0.00973087586	0.0102590138±0.02361584247
Lautropia	0.0079911752±0.03752374590	0.0010536944±0.00099921507	0.0196936448±0.04543889694	0.0049671±0.01161077164
Absconditabacteria_(SR1)_[G-1]	0.0101237674±0.04543889694	0.013377827±0.02425590095	0.0024478248±0.00278533221	0.0034356315±0.00418105546
Corynebacterium	0.0050583737±.00661114233	0.0080163007±0.01420935539	0.0036180104±0.00275804189	0.0052083988±0.00635194066
Peptostreptococcaceae_[XI][G-1]	0.0056338096±.00468853736	0.0085290619±0.01042850248	0.0028493857±0.00359940346	0.0043886208±0.00383096596
Treponema	0.0026034256±0.00422973682	0.0050886593±0.01461153556	0.0053706835±0.00936328938	0.0078494508±0.01489065747
Oribacterium	0.0052167207±0.00325652254	0.0045516485±0.00310176715	0.0043353822±0.00417630970	0.0030544838±0.00201670375
Aggregatibacter	0.0023581152±0.00335448793	0.0035719611±0.00532217133	0.00511335±0.00450703869	0.0041907996±0.00526115319
Peptostreptococcus	0.002969003±0.00250306278	0.0055778611±0.00395925535	0.0010254883±0.00154704162	0.0036311704±0.00572407768

Continued Supplementary Table 1

Genus	*P* value					
	Control vs OSA	Control vs HTN	Control vs Complication	OSA vs HTN	OSA vs Complication	HTN vs Complication
Streptococcus	0.08					
Neisseria	0.025		0.043			
Rothia	0.017	0.027	0.004	0.014		
Prevotella	0.19					
Actinomyces	0.011		0.044		0.009	0.029
Haemophilus	<0.001	0.032			<0.001	0.003
Gemella	0.375					
Porphyromonas	0.898					
Veillonella	0.642					
Granulicatella	0.026	0.013			0.012	
Fusobacterium	0.086					
Leptotrichia	0.648					
Lautropia	<0.001		<0.001		<0.001	0.01
Absconditabacteria_(SR1)_[G-1]	0.013		0.005	0.033	0.006	0.009
Corynebacterium	0.622					
Peptostreptococcaceae_[XI][G-1]	0.016				0.002	0.02
Treponema	0.148					
Oribacterium	0.047			0.016		
Aggregatibacter	0.07					
Peptostreptococcus	<0.001	0.014			<0.001	0.019

Abbreviations:

OSA: obstructive sleep apnea

HTN: hypertension

Complication: OSA comorbid HTN

Supplementary Table 2 Comparison of salivary metabolomics in each group

Group	Name	VIP	Fold change	p-value
OSA vs Control	2-Hydroxyadenine	1.137609	3.258536	0.004161
	Erucic acid	3.861169	0.623975	0.007107
	7-Methylxanthine	1.085007	3.177232	0.04235
	Pyruvaldehyde	1.264818	0.58194	0.049553
Complication vs Control	L-Phenylalanine	1.329767	0.467094	0.004614
	4-Hydroxybutanoic acid lactone	1.200538	0.361608	0.00475
	Glutaraldehyde	1.477588	0.31428	0.006203
	Tyramine	1.050239	0.51437	0.007616
	Pro-Val	1.885512	2.84563	0.009365
	DL-a-Hydroxybutyric acid	1.15014	1.727322	0.009511
	N-Acetylcadaverine	1.159623	0.254488	0.010402
	1-Stearoyl-rac-glycerol	1.133903	1.528148	0.011207
	Erucic acid	2.683396	0.538079	0.015394
	L-Arginine	1.065509	1.56692	0.026568
	3-Methylhistidine	1.122851	1.496925	0.029399
	Phe-Pro	1.077532	0.191081	0.031203
	Taurine	1.068001	1.355322	0.031389
	3-Methylindole	1.537097	0.083443	0.040283
	L-Methionine	1.153718	0.308751	0.04302
	N-Acetylneuraminic acid	1.094321	0.446246	0.043321
	Isomaltose	1.277814	0.218265	0.043385
Complication vs OSA	DL-a-Hydroxybutyric acid	1.15068	1.567957	0.017092
	L-Carnitine	2.941431	0.475409	0.017329
	Taurine	1.089218	1.28349	0.018043
	Uridine	1.001373	0.205791	0.025098
	Arg-Phe	1.164435	0.234239	0.046979
	Phosphorylcholine	6.253449	0.54013	0.048844
Complication vs HTN	L-Carnitine	6.80549	1.948888	0.038333
	Tyr-Gln	1.077126	2.824068	0.038634
	N-(omega)-Hydroxyarginine	1.586027	1.84076	0.045197
	His-Ala	2.07836	2.338729	0.047875
HTN vs Control	L-Phenylalanine	1.350863	0.439462	0.001707
	4-Hydroxybutanoic acid lactone	1.191639	0.291686	0.00298
	Phe-Tyr	1.472457	0.023188	0.004074
	Glutaraldehyde	1.499533	0.263226	0.004428
	DL-a-Hydroxybutyric acid	1.197713	1.653669	0.005876
	N-Docosanoyl-4-sphingenyl-1-O-phosphorylcholine	1.083979	0.203411	0.006292
	N-Acetylcadaverine	1.194512	0.141375	0.006581

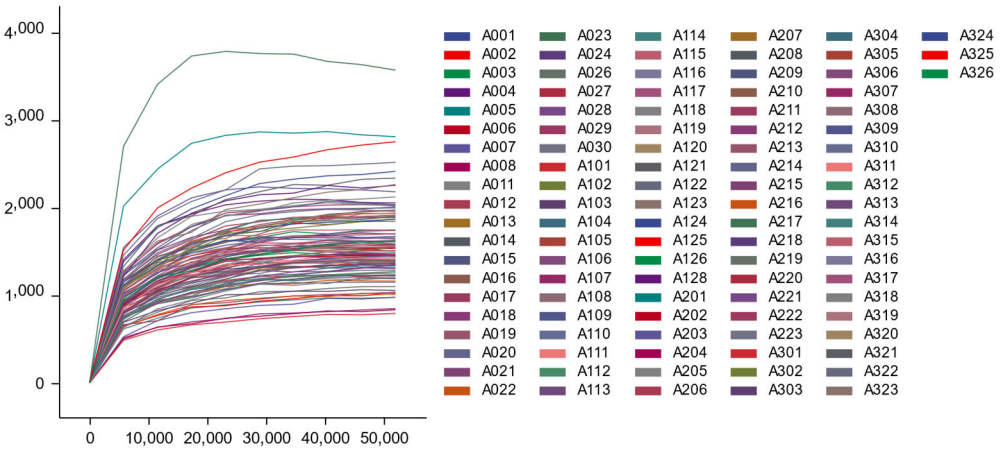
His-Val	1.016126	2.204788	0.006823
Arg-Phe	1.147679	0.131145	0.008227
Tyr-Gln	1.097486	0.160794	0.008985
1-Stearoyl-rac-glycerol	1.3282	1.779378	0.009633
N1-Methyl-2-pyridone-5-carboxamide	5.102518	0.440367	0.011055
Phe-Phe	1.978488	0.095549	0.011306
Erucic acid	1.961821	0.638302	0.013672
L-Methionine	1.487219	0.095947	0.013817
Acetylcarnitine	3.749609	0.37628	0.014437
Tyr-Ile	1.667276	0.123475	0.015654
3-Methylhistidine	1.22984	1.558859	0.016045
N-(omega)-Hydroxyarginine	1.297153	0.299651	0.017368
L-Carnitine	6.579985	0.249722	0.027145
Phe-Pro	1.153024	0.109202	0.02957
Arg-Glu	1.295633	0.20189	0.032702
Taurine	1.130959	1.338924	0.041068
Lys-Pro	1.878112	0.22952	0.042685
Sebacic acid	1.29826	0.346545	0.046038
Nicotinamide	3.359662	0.234878	0.048735

Abbreviations:

OSA: obstructive sleep apnea

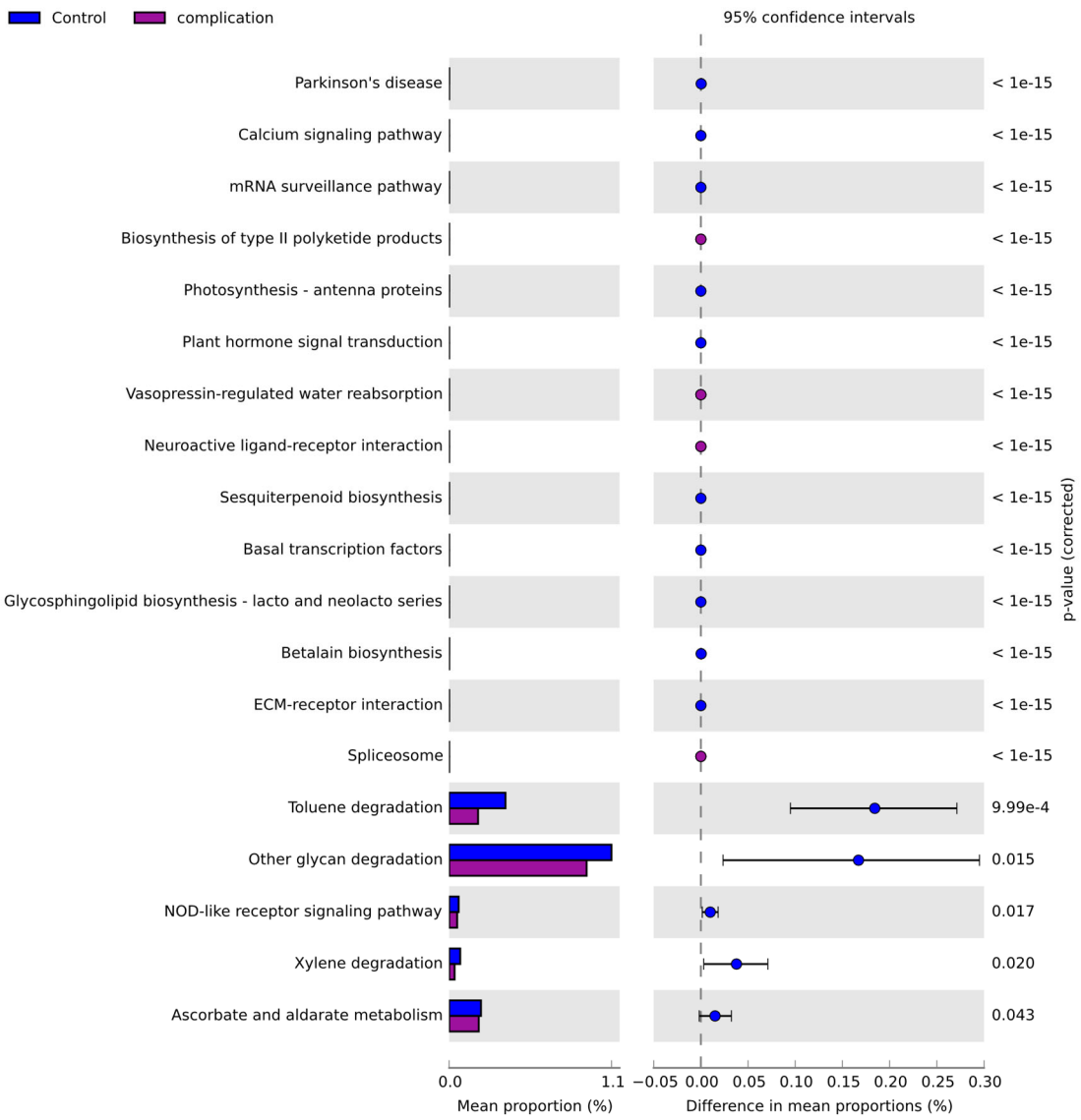
HTN: hypertension

Complication: OSA comorbid HTN



Supplementary Figure 1: Rarefaction curve

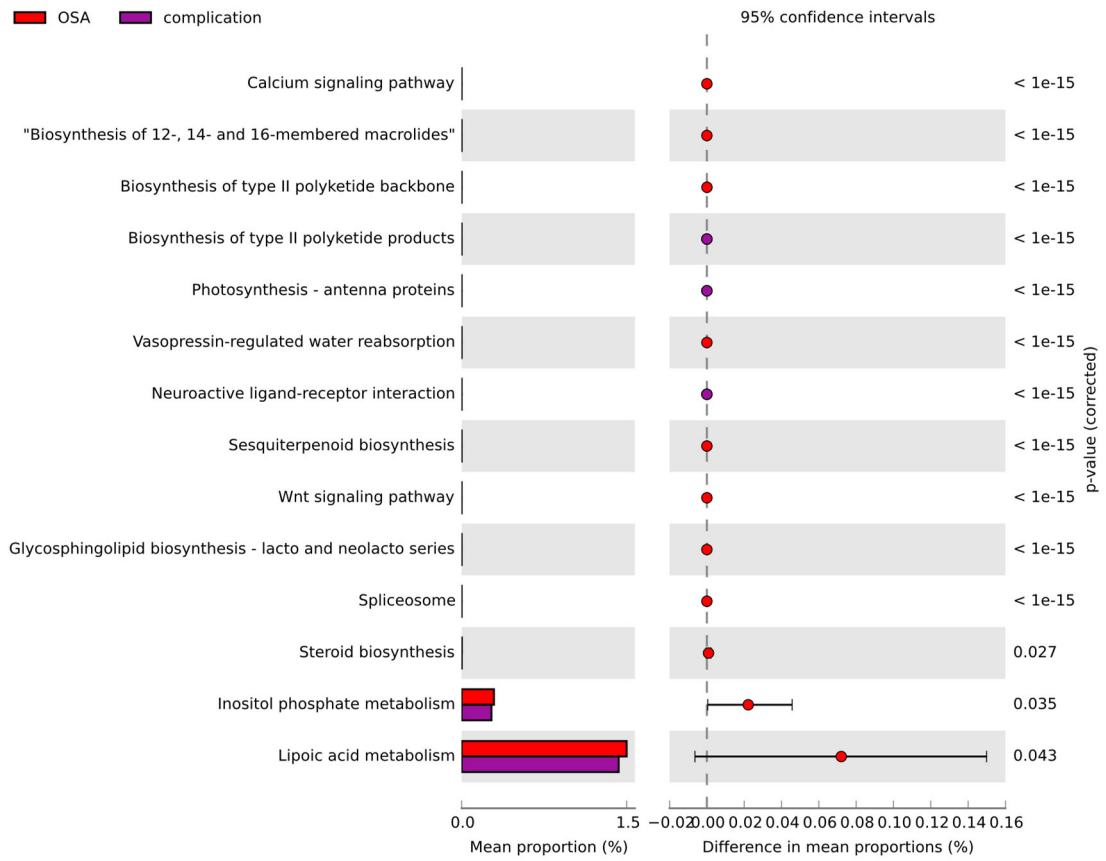
The shape of the rarefaction curve indicates that the plateauing stage has been completely reached, indicating that the sequencing depth of all samples is reasonable and the sequencing results could reflect the microbial information in the saliva samples.



Supplementary Figure 2: Analysis of functional differences between control group and complication group.

Microbial functions were predicted by PICRUSt2 upon Kyoto Encyclopedia of Genes and Genomes (KEGG) database identified by STAMP software. Compare with control group, the complication group had considerably less toluene degradation, Xylene degradation, ascorbate and aldarate metabolism than the control group.

Complication: obstructive sleep apnea comorbid hypertension

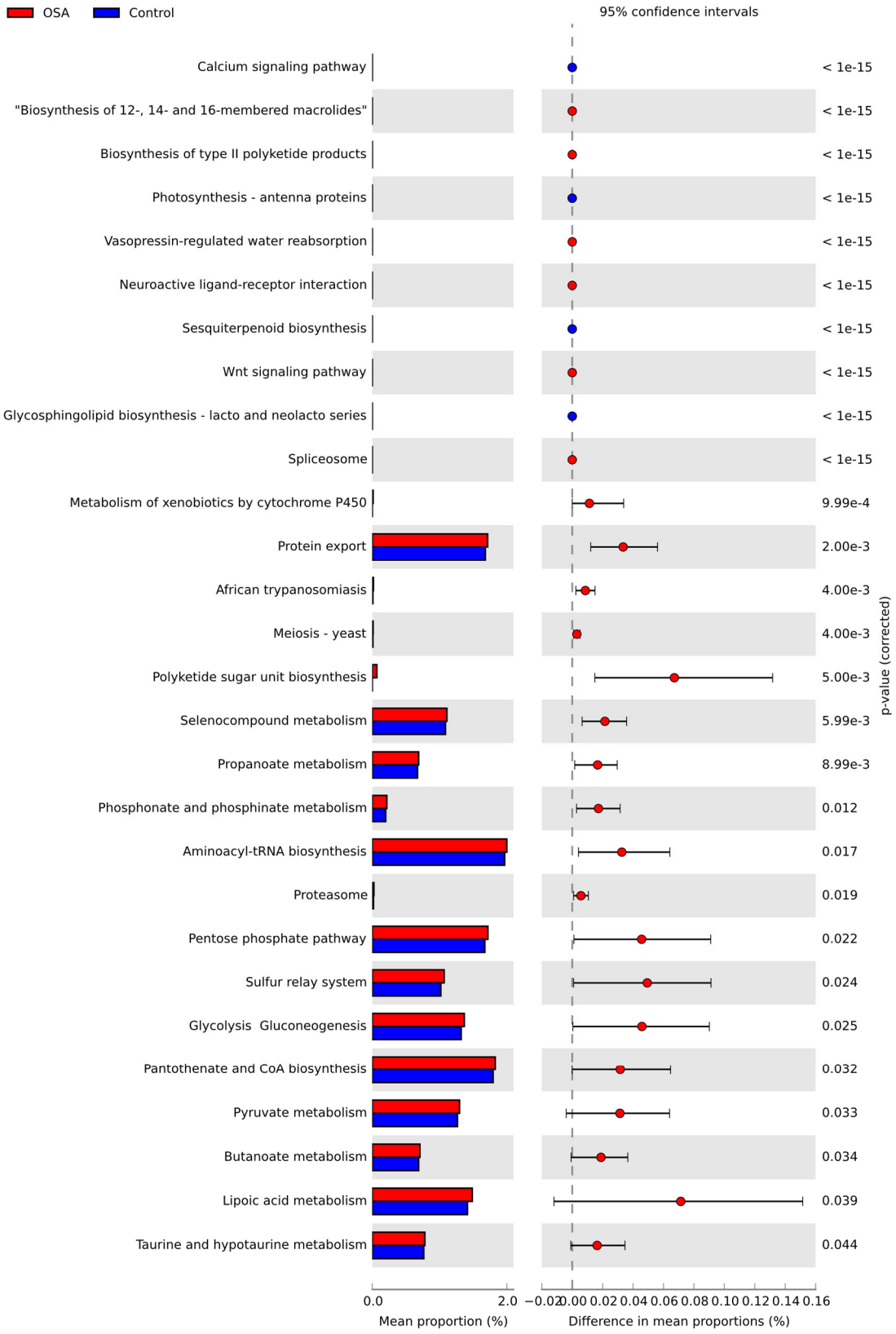


Supplementary Figure 3: Analysis of functional differences between OSA group and complication group.

Microbial functions were predicted by PICRUSt2 upon Kyoto Encyclopedia of Genes and Genomes (KEGG) database identified by STAMP software. The complication group had considerably less vasopressin-regulated water reabsorption, steroid biosynthesis, inositol phosphate metabolism, and lipoic acid metabolism than the OSA group.

OSA: obstructive sleep apnea.

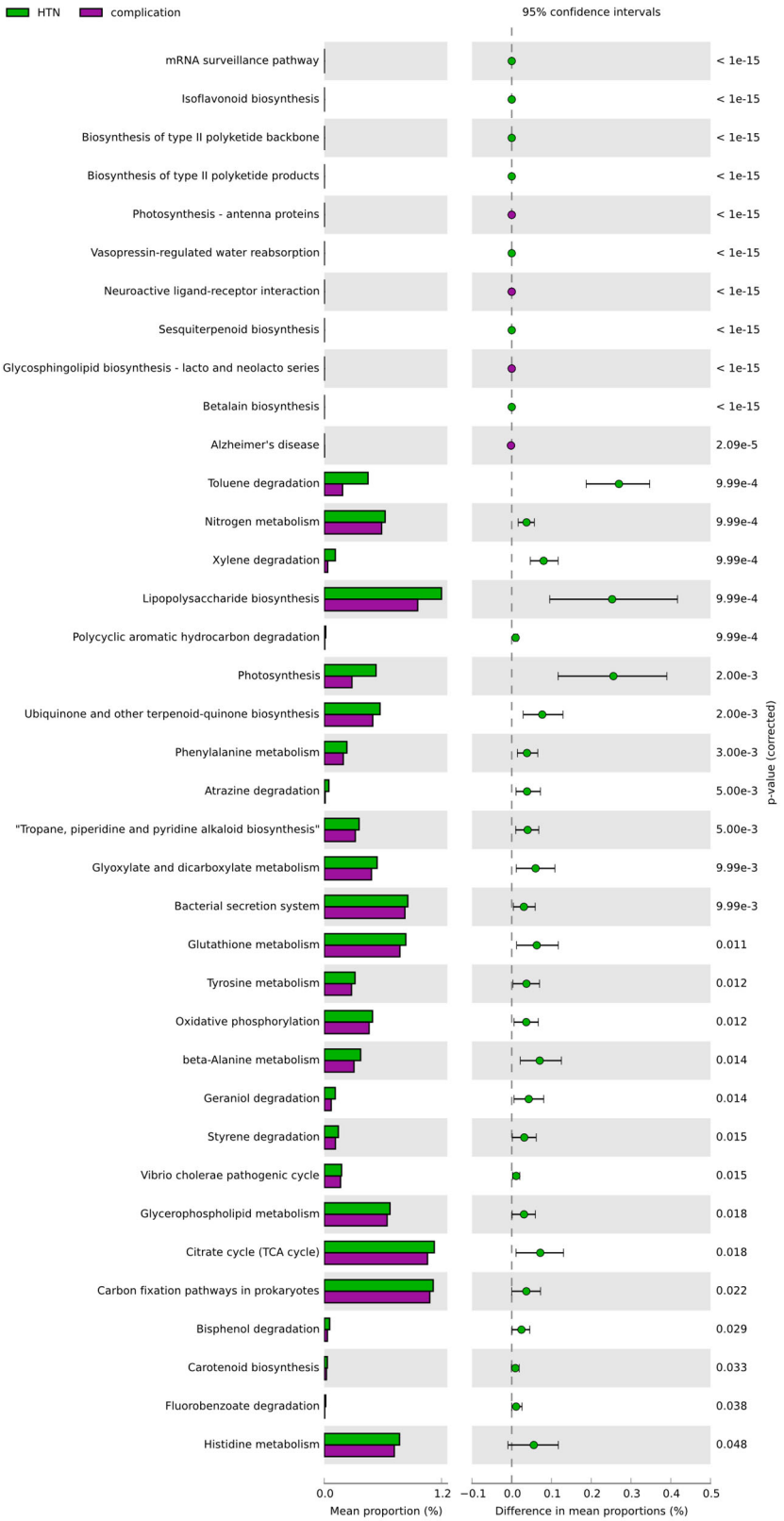
Complication: obstructive sleep apnea comorbid hypertension



Supplementary Figure 4: Analysis of functional differences between OSA group and control group.

Microbial functions were predicted by PICRUSt2 upon Kyoto Encyclopedia of Genes and Genomes (KEGG) database identified by STAMP software. Compared with control group, pathways of metabolism of xenobiotics by cytochrome P450, polyketide sugar unit biosynthesis, phosphonate and phosphinate metabolism and proteasome were significant higher in OSA group.

OSA: obstructive sleep apnea

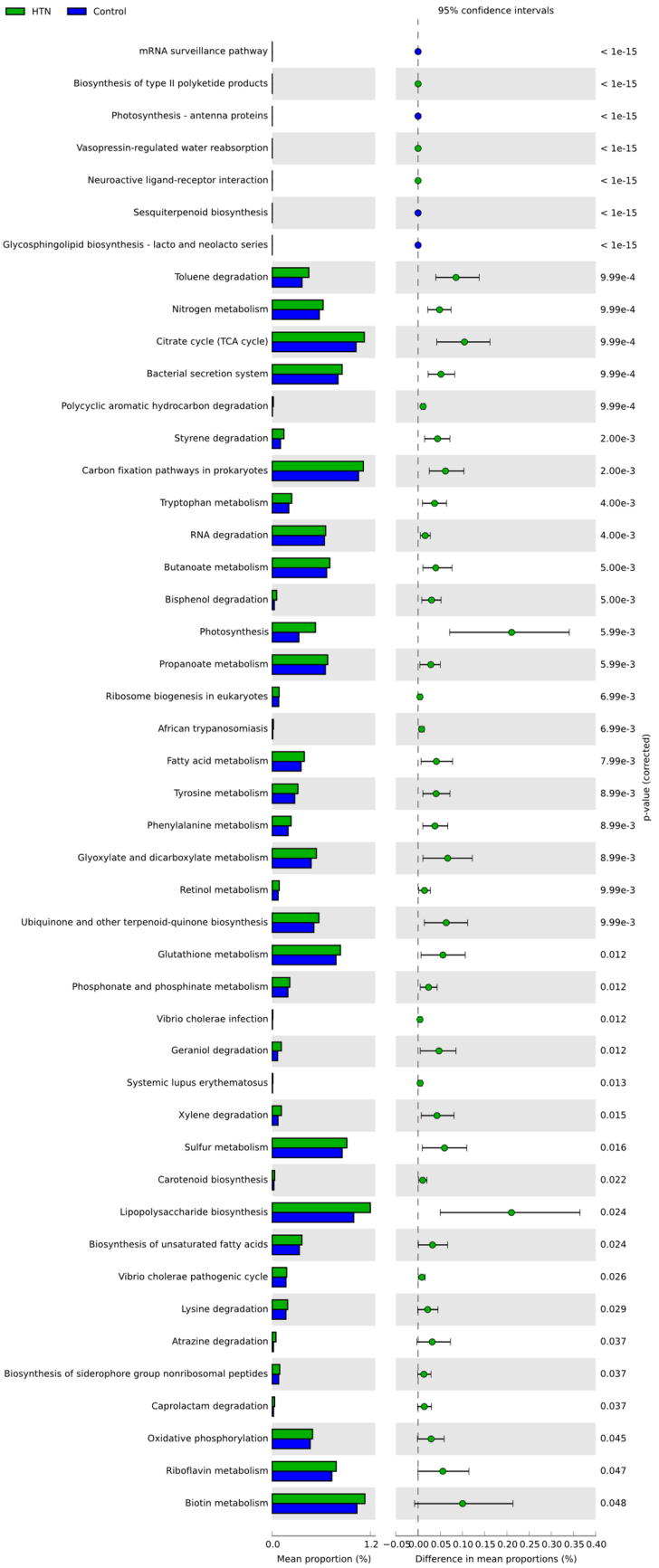


Supplementary Figure 5: Analysis of functional differences between HTN group and complication group.

Microbial functions were predicted by PICRUSt2 upon Kyoto Encyclopedia of Genes and Genomes (KEGG) database identified by STAMP software. Nitrogen metabolism, vasopressin-regulated water reabsorption, lipopolysaccharide production, and oxidative phosphorylation were significantly decreased in the complication group compared to the HTN group.

HTN: hypertension

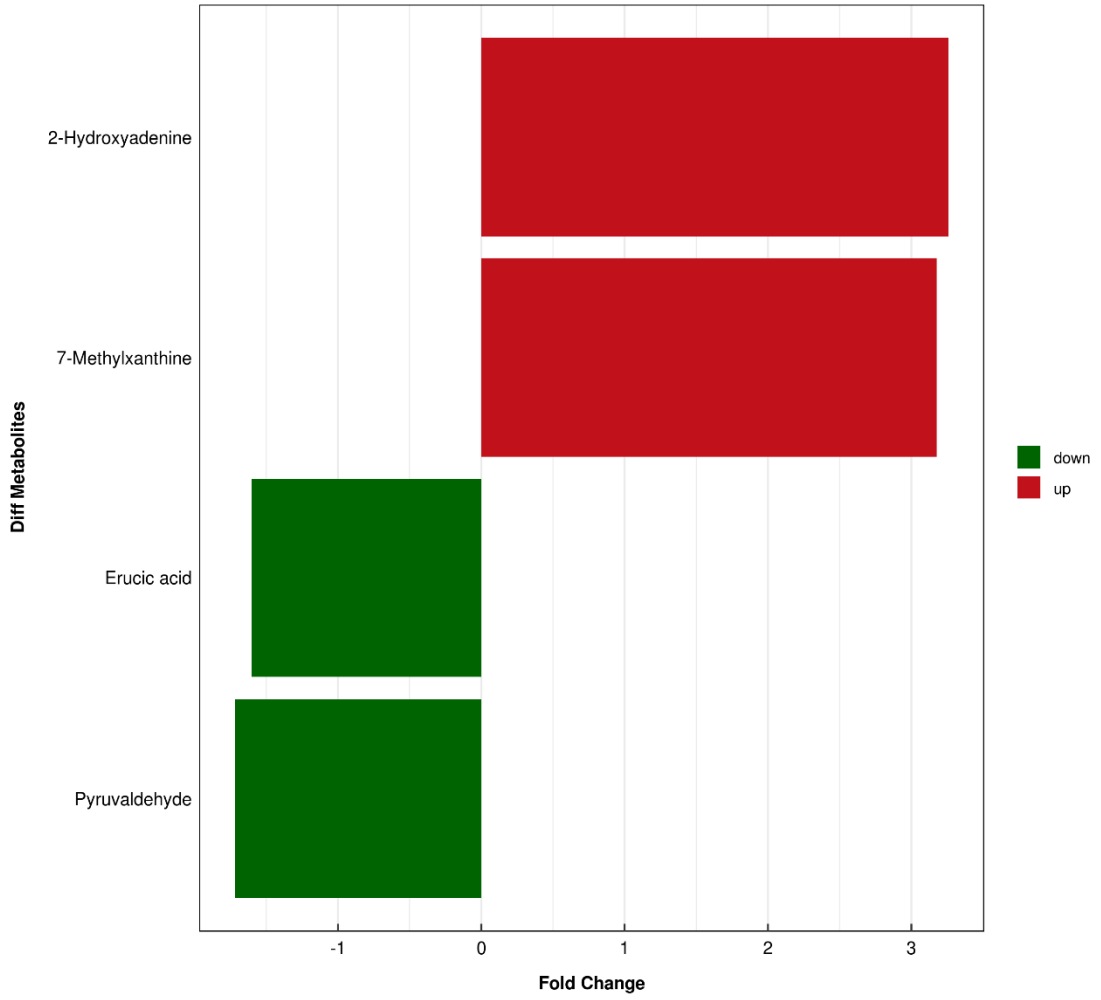
Complication: obstructive sleep apnea comorbid hypertension



Supplementary Figure 6: Analysis of functional differences between HTN group and control group.

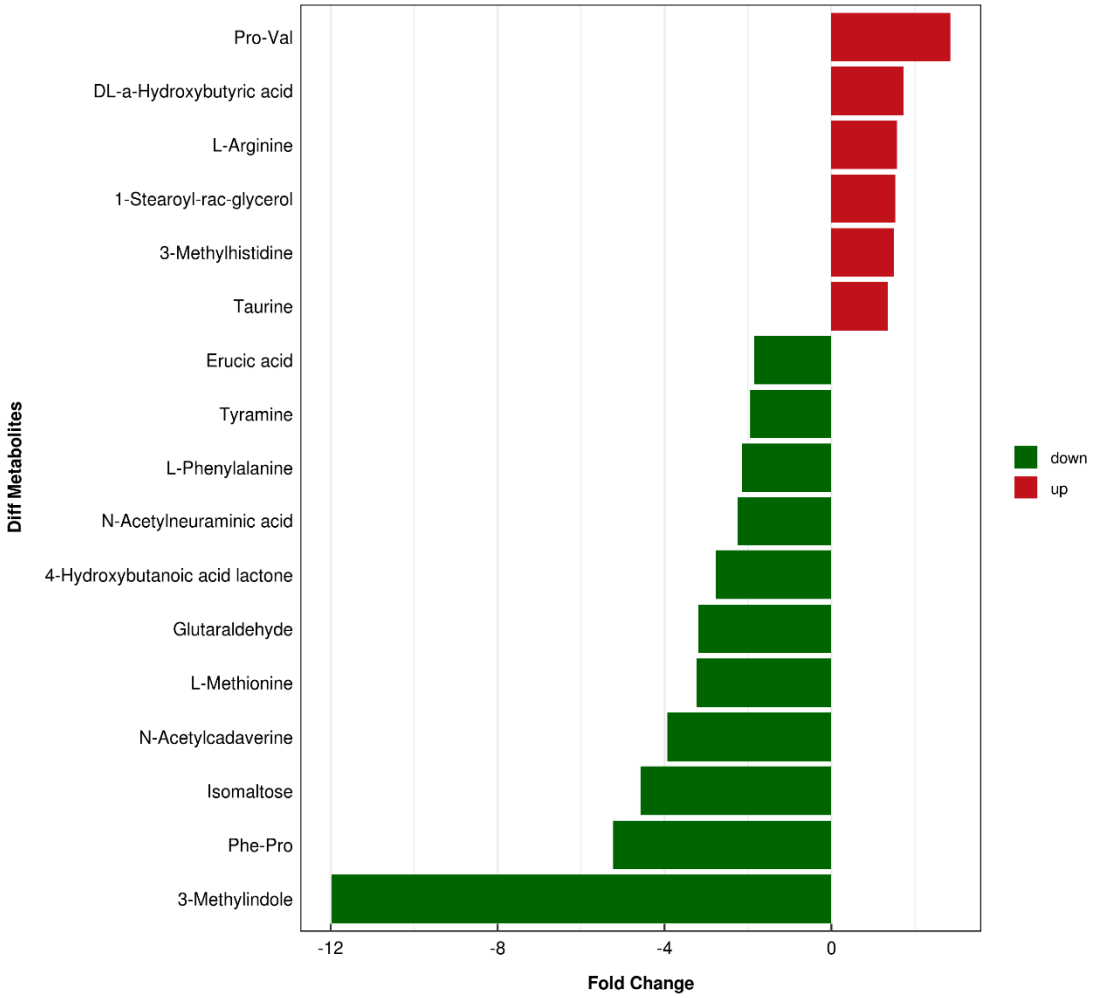
Microbial functions were predicted by PICRUSt2 upon Kyoto Encyclopedia of Genes and Genomes (KEGG) database identified by STAMP software. the result indicated that nitrogen metabolism, citrate cycle, bacterial secretion system, toluene degradation, phenylalanine metabolism, lipopolysaccharide biosynthesis, fatty acid metabolism pathways were significant higher in HTN group than the control group.

HTN: hypertension



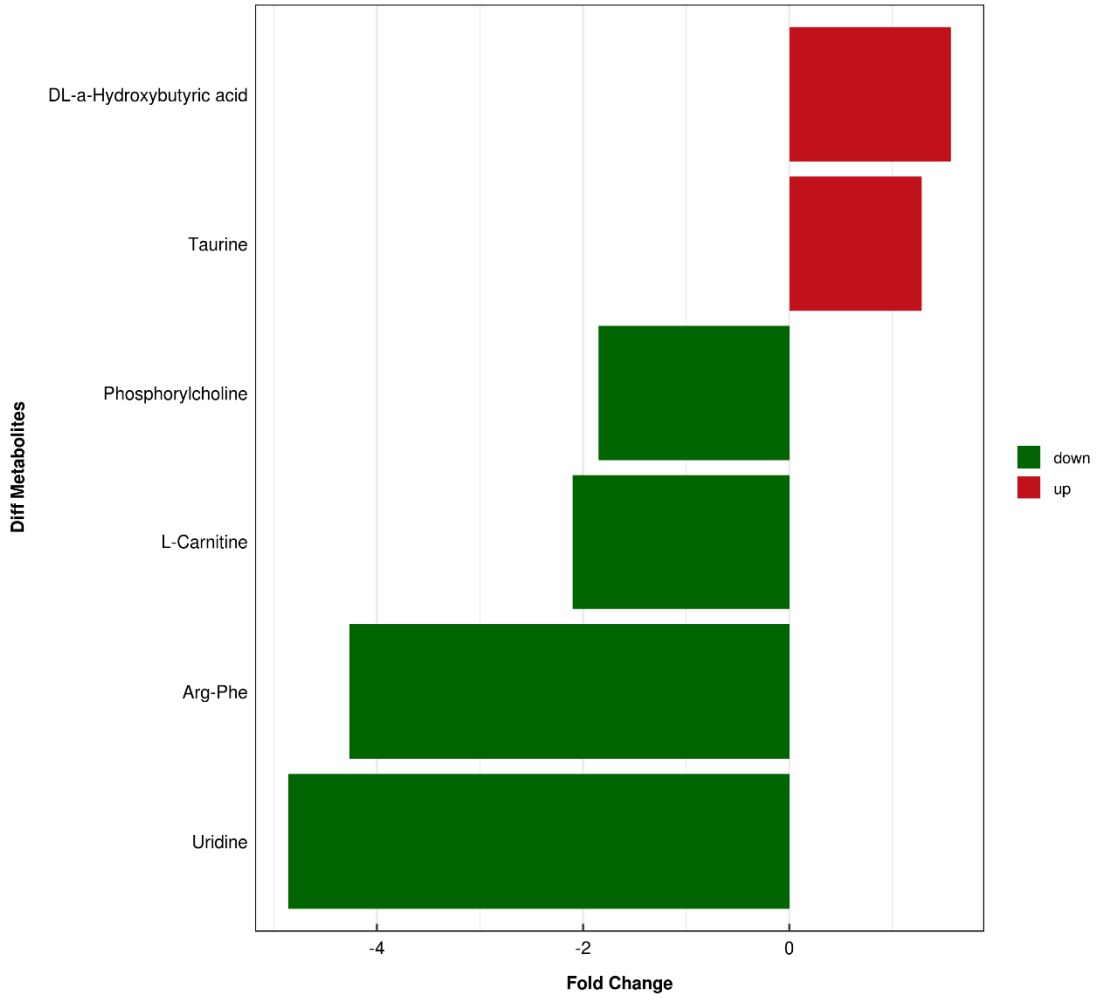
Supplementary Figure 7: Metabolomics analysis of OSA group compared with control group.

OSA: obstructive sleep apnea



Supplementary Figure 8: Metabolomics analysis of complication group compared with control group.

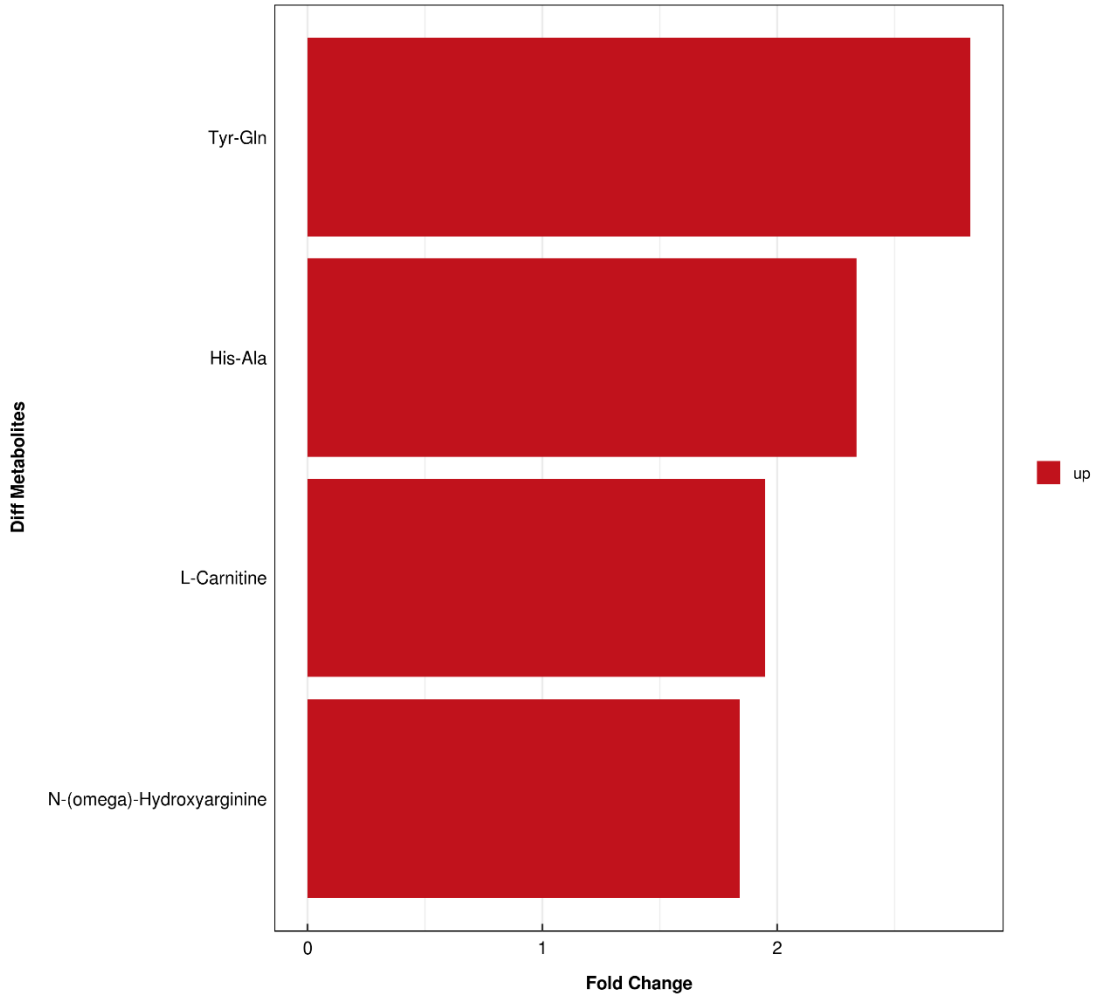
Complication: obstructive sleep apnea comorbid hypertension



Supplementary Figure 9: Metabolomics analysis of complication group compared with OSA group.

Complication: obstructive sleep apnea comorbid hypertension

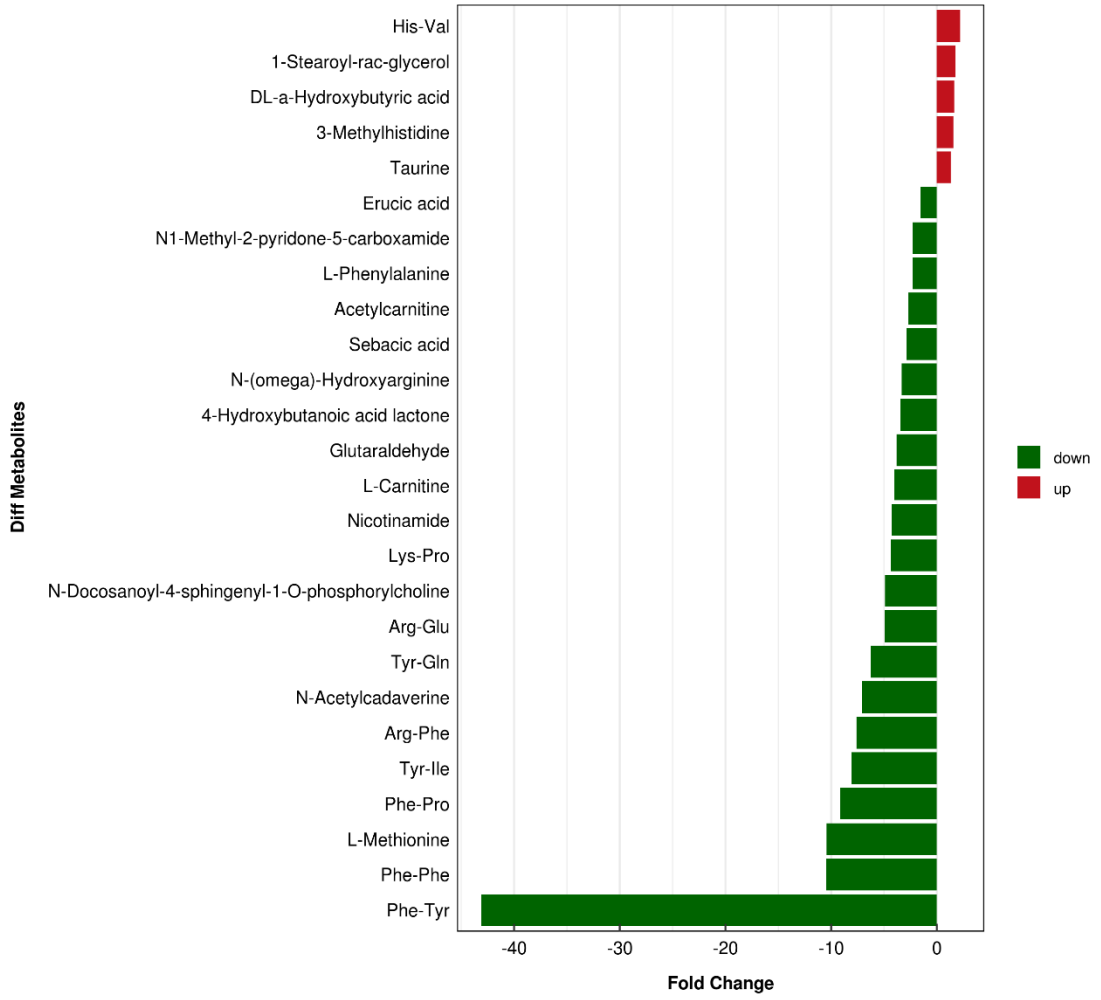
OSA: obstructive sleep apnea



Supplementary Figure 10: Metabolomics analysis of complication group compared with HTN group.

Complication: obstructive sleep apnea comorbid hypertension

HTN: hypertension



Supplementary Figure 11: Metabolomics analysis of HTN group compared with control group.

HTN: hypertension