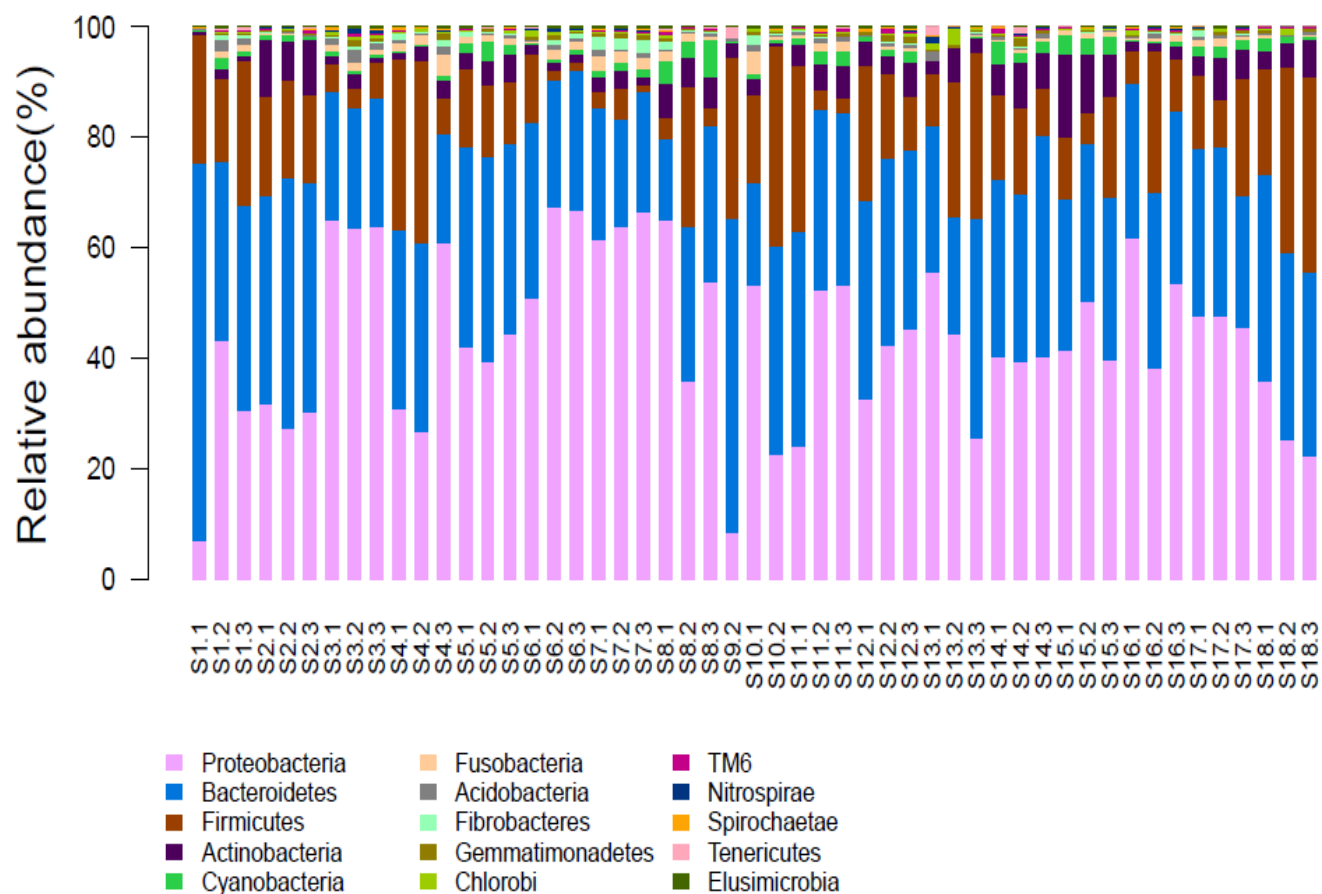
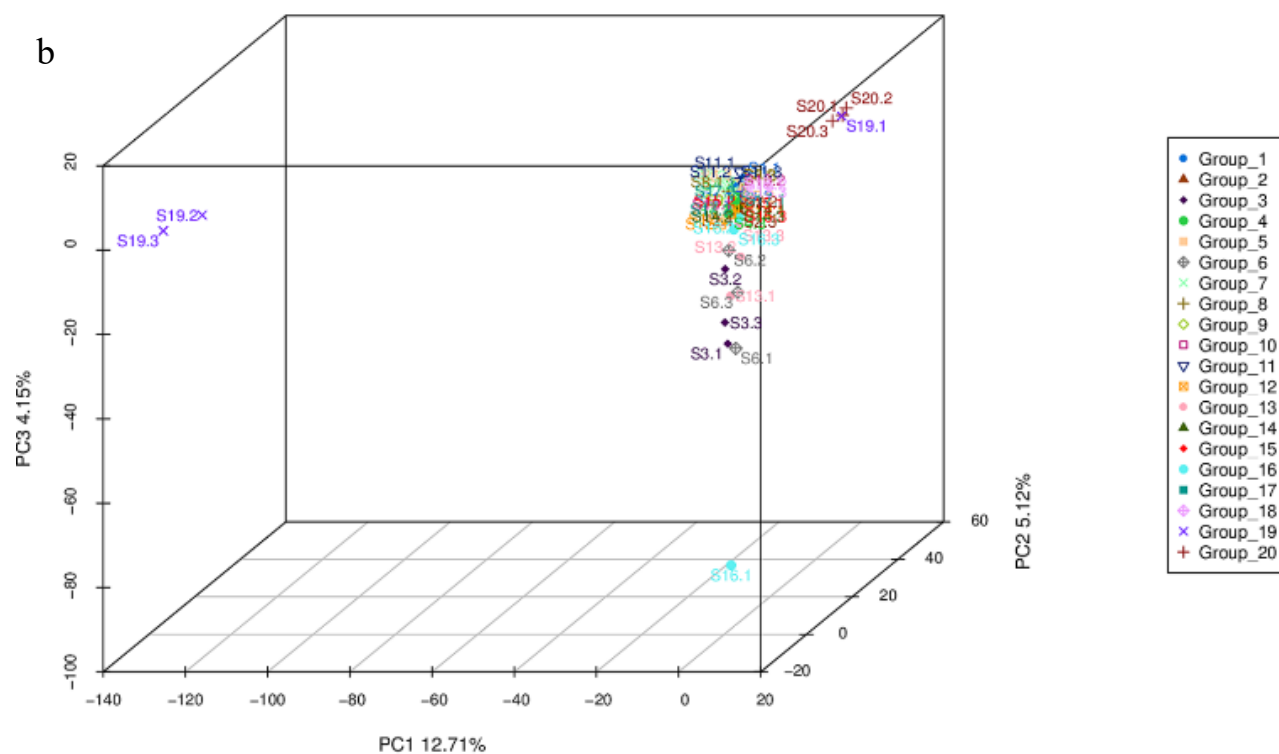


a



b



(d continued)

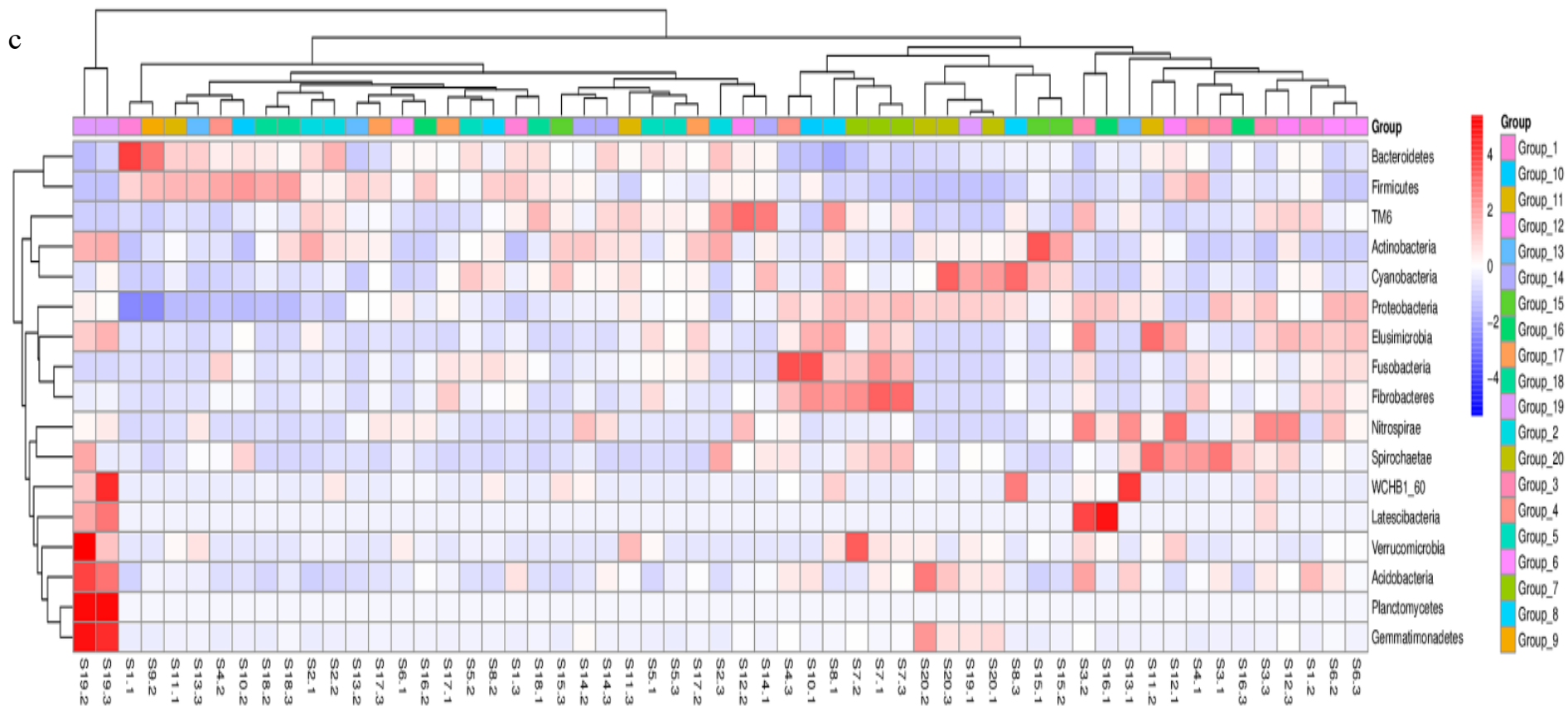


Figure S1. The most top 15 phylum (b), PCA analysis (c) and heatmap of phylum via ANOVA (d) among different samples. b, The horizontal and vertical axes represent two characteristic values that can best reflect the variance. c, Horizontal refers to sample information; vertical is species annotation information. Red indicates that the relative abundance of species is high, and blue indicates that the relative abundance of species is low.

Table S1 Sequencing of the overall situation and α -diversity ($n=3$).

| Sample_ID | Clean tags | Functional tags | Avg len(bp) | OTUs | Chao1 | Shannon | Simpson |
|-----------------------------|------------|-----------------|-------------|----------|----------------|-----------|-------------|
| Group1 (0d-CK-water) | 34373±2143 | 33627±2515 | 412±1 | 2490±280 | 4916.05±183.31 | 7.94±1.20 | 0.968±0.046 |
| Group2 (0d-HcT1-water) | 33767±807 | 33428±841 | 417±4 | 2663±134 | 5263.33±645.97 | 8.22±0.11 | 0.990±0.002 |
| Group3 (0d-HcT1-root) | 33946±305 | 33389±368 | 412±0 | 3027±291 | 4747.96±774.18 | 9.25±0.35 | 0.995±0.004 |
| Group4 (0d-HcT1-sediment) | 29476±799 | 29068±588 | 413±2 | 2446±807 | 4918.28±589.44 | 8.58±0.66 | 0.993±0.002 |
| Group5 (0d-HcT2-water) | 35062±1391 | 34457±1100 | 416±4 | 2696±78 | 4944.35±400.47 | 8.72±0.11 | 0.994±0.001 |
| Group6 (0d-HcT2-root) | 35000±453 | 34009±381 | 411±4 | 3356±441 | 5994.33±690.42 | 9.23±0.39 | 0.996±0.001 |
| Group7 (0d-HcT2-sediment) | 35528±893 | 35038±888 | 411±6 | 2969±99 | 5433.42±381.88 | 9.07±0.05 | 0.996±0.000 |
| Group8 (0d-Jr-water) | 34767±1011 | 34093±1420 | 415±4 | 2934±445 | 5314.11±400.06 | 8.83±0.31 | 0.993±0.002 |
| Group9 (0d-Jr-root) | 35701±421 | 35246±561 | 406±1 | 1606±123 | 4297.99±403.27 | 7.35±1.28 | 0.967±0.044 |
| Group10 (0d-Jr-sediment) | 34848±1524 | 34450±1484 | 413±0 | 2093±202 | 4348.53±153.18 | 8.24±0.34 | 0.987±0.006 |
| Group11 (30d-CK-water) | 34541±1867 | 33546±2289 | 419±4 | 2440±65 | 5069.37±600.49 | 8.35±0.80 | 0.991±0.004 |
| Group12 (30d-HcT1-water) | 35496±1338 | 35404±1368 | 404±9 | 2553±489 | 4943.62±523.49 | 8.46±0.44 | 0.993±0.002 |
| Group13 (30d-HcT1-root) | 35274±1824 | 34535±1223 | 405±9 | 2651±294 | 5183.91±735.64 | 7.94±0.23 | 0.990±0.002 |
| Group14 (30d-HcT1-sediment) | 35584±1094 | 35554±1086 | 408±3 | 2331±180 | 4949.85±156.21 | 8.16±0.27 | 0.990±0.002 |
| Group15 (30d-HcT2-water) | 35744±1134 | 35347±1002 | 406±7 | 2525±223 | 5388.72±966.63 | 8.92±0.37 | 0.994±0.003 |
| Group16 (30d-HcT2-root) | 35792±1078 | 34599±2255 | 409±5 | 3077±515 | 4839.40±964.27 | 8.20±0.41 | 0.992±0.003 |
| Group17 (30d-HcT2-sediment) | 34033±1025 | 33973±1062 | 412±0 | 2351±284 | 4336.52±484.77 | 7.38±0.37 | 0.986±0.003 |
| Group18 (30d-Jr-water) | 35516±1032 | 35300±932 | 409±3 | 1928±153 | 4555.76±124.32 | 6.73±0.28 | 0.983±0.003 |
| Group19 (30d-Jr-root) | 26534±1024 | 21249±412 | 357±9 | 1103±106 | 4363.14±316.34 | 8.41±0.81 | 0.993±0.004 |
| Group20 (30d-Jr-sediment) | 25279±1206 | 21388±377 | 386±4 | 694±3 | 4866.03±121.40 | 7.28±0.16 | 0.986±0.002 |

Note: clean tags means the filtered ones from the original tags with high quality, and "Avg len (average length)" stands for average length of the OTUs. The Chao index is an estimate of the actual number of OTUs in the community. It is obtained by calculating the number of OTUs detected only once and twice in the community. The value is equal to the estimated number of OTUs. Shannon Wiener index is the Shannon index. The larger the value, the higher the sample diversity and the more uniform the individual distribution. Simpson index refers to the probability that two individuals randomly selected belong to different species. The higher the Simpson index, the higher the community diversity.

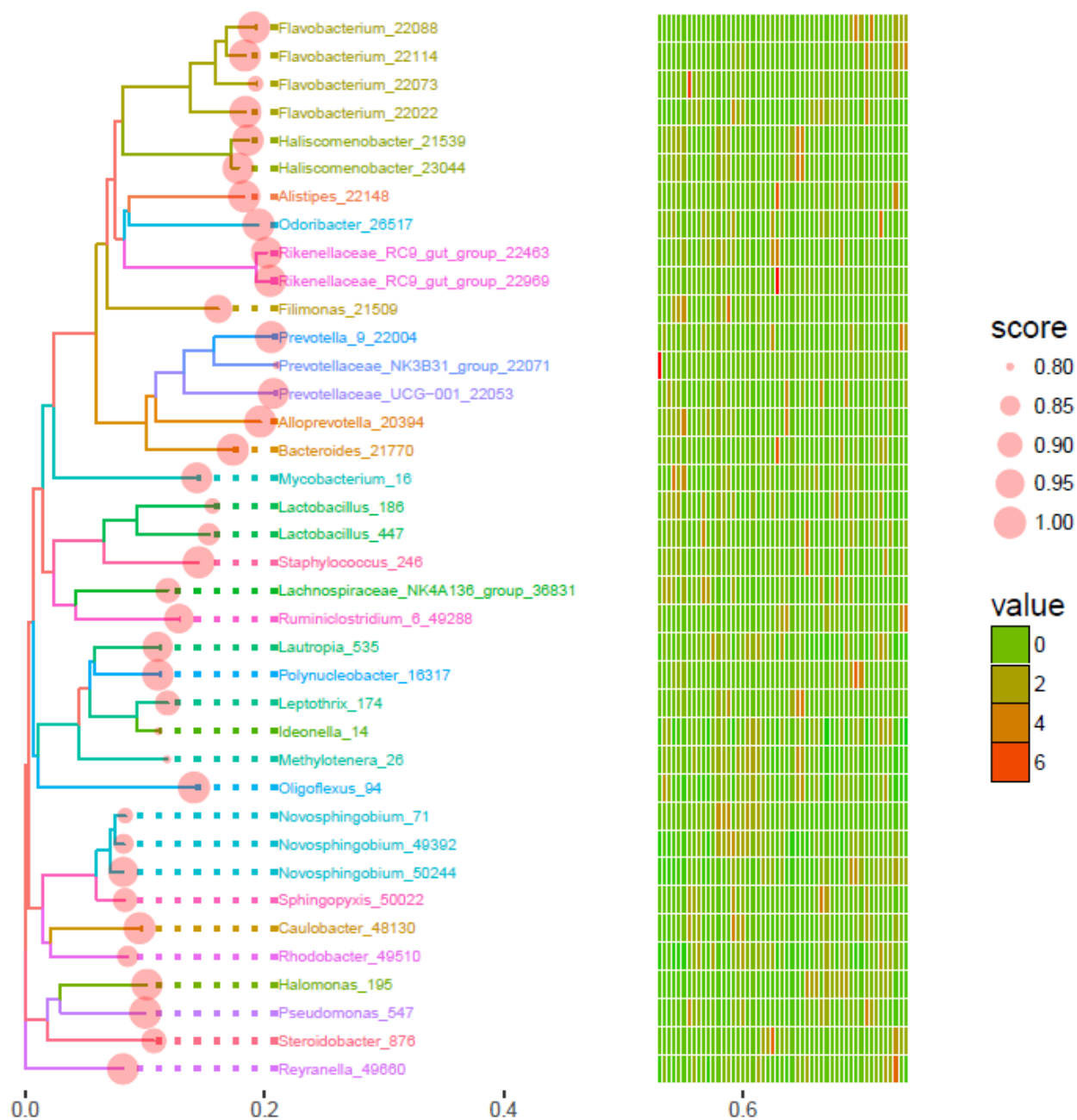
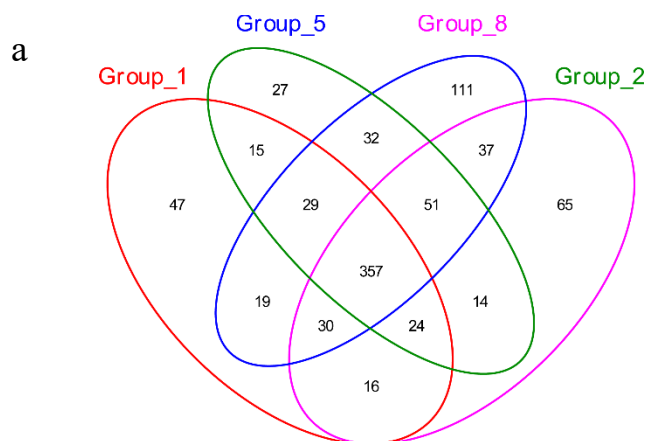
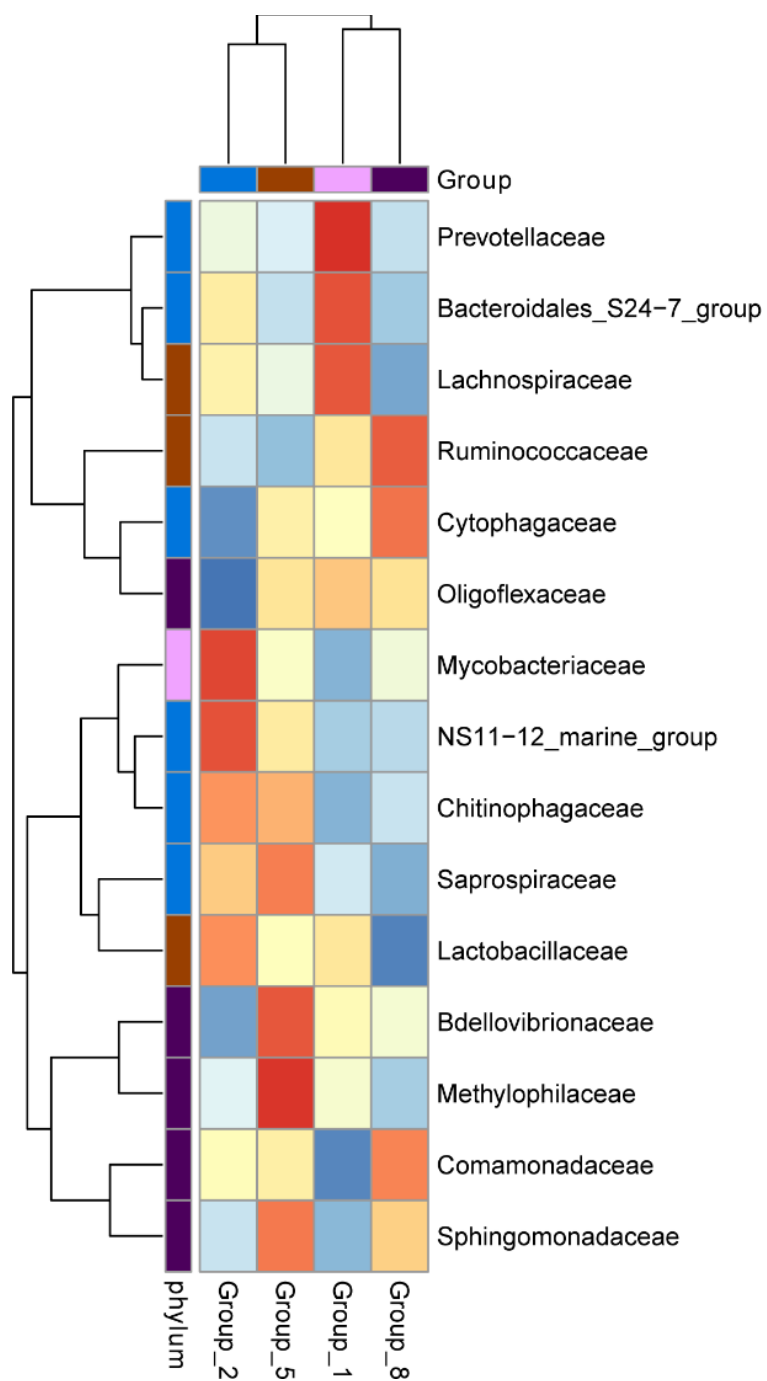


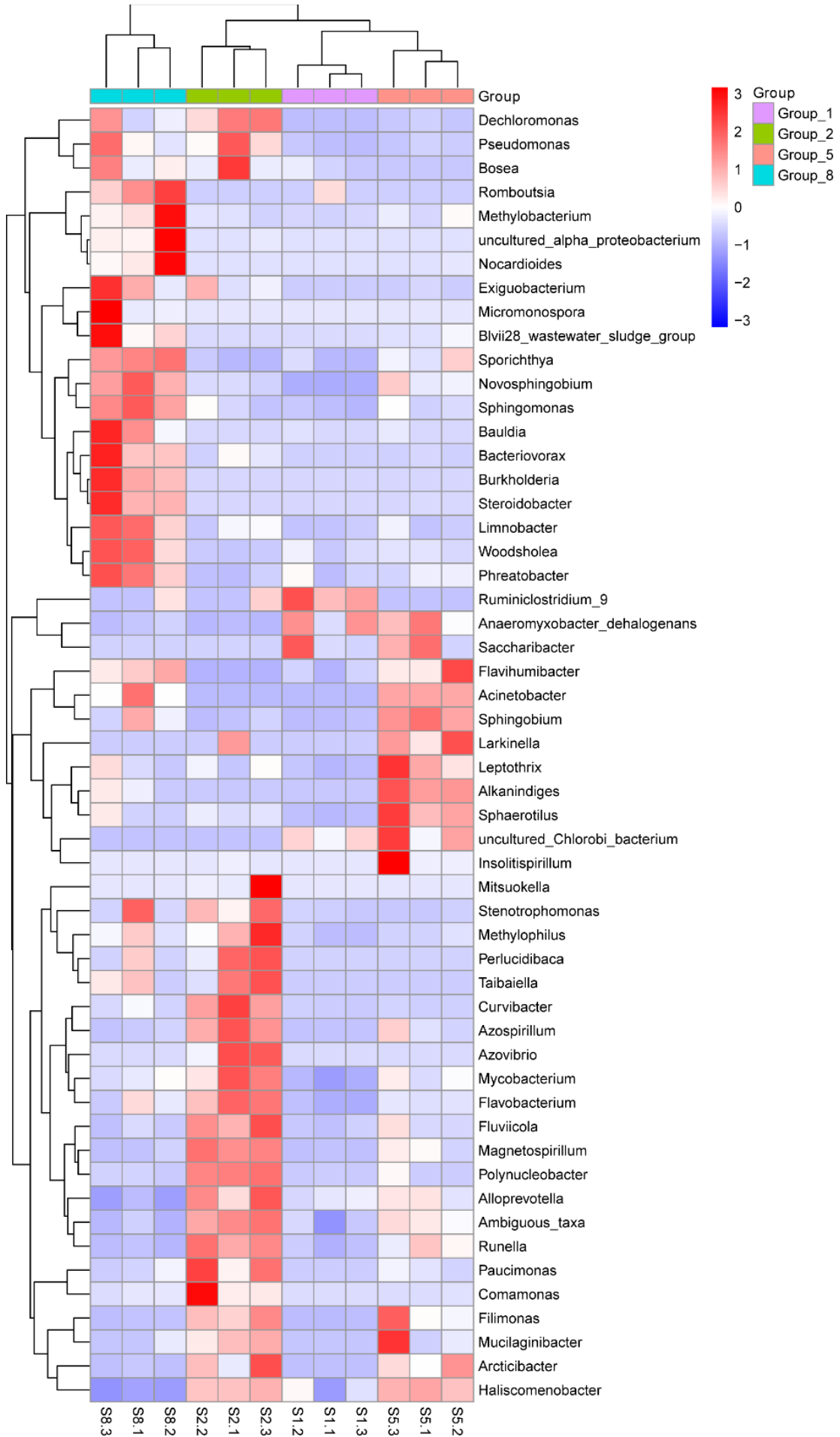
Figure S2 The species evolution tree and OTU abundance map of top 50 OTUs among different samples.



b



c



d

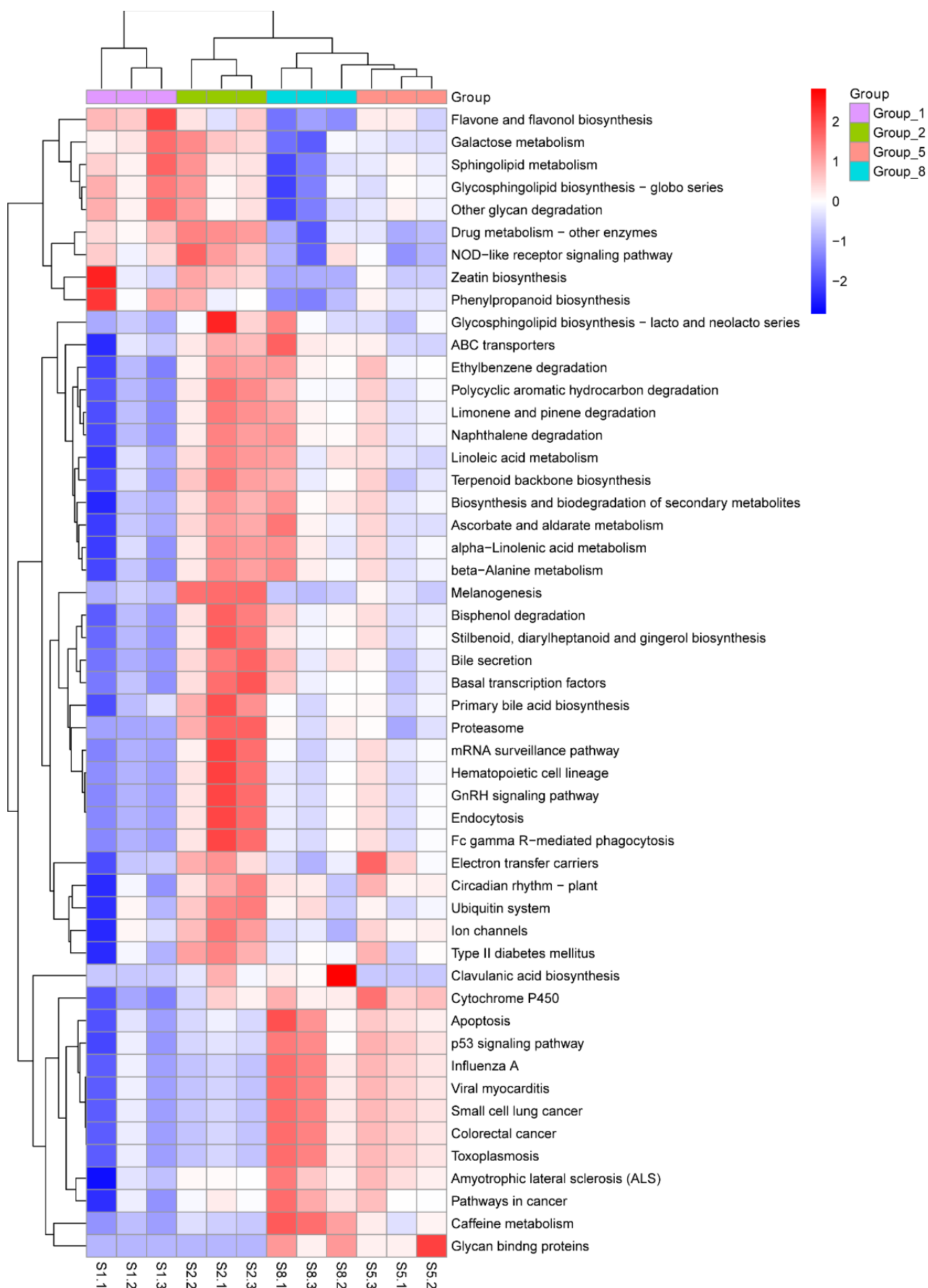


Figure S3. The venn chart (a), heatmap of phylum (b) via ANOVA (c) between 0 and 30 d water samples. Orange represents species with high relative abundance, and blue represents species with low relative abundance from b to d.

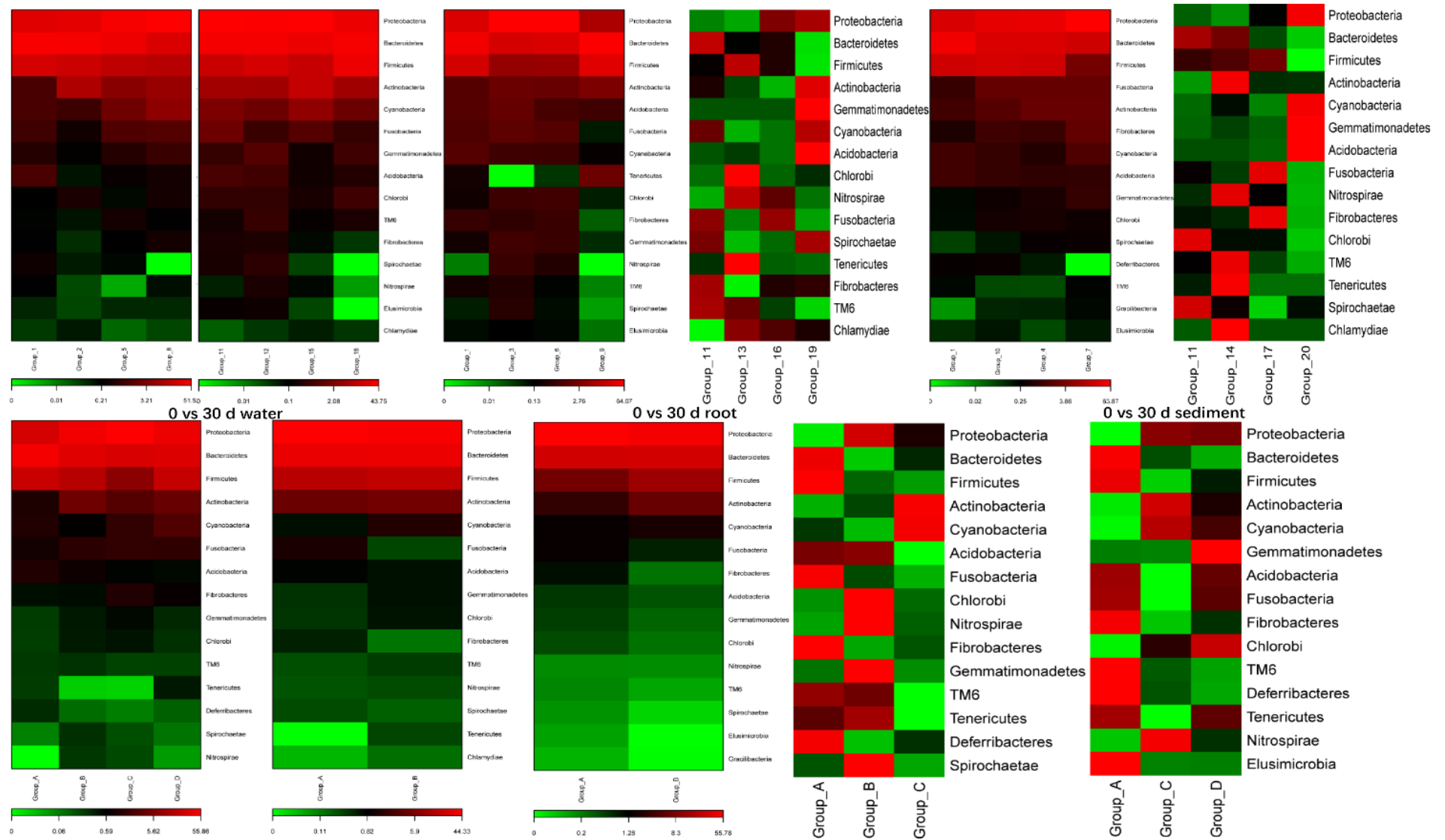


Figure S4. The top 15 phylum among different comparisons. The above figure shows the abundance changes of species in different groups. Bright green indicates low relative abundance of species, while red indicates high relative abundance of species. Group A, B, C, D stand for control, 60% (HcT1), 30% (HcT2) and 30% (Jr), respectively.

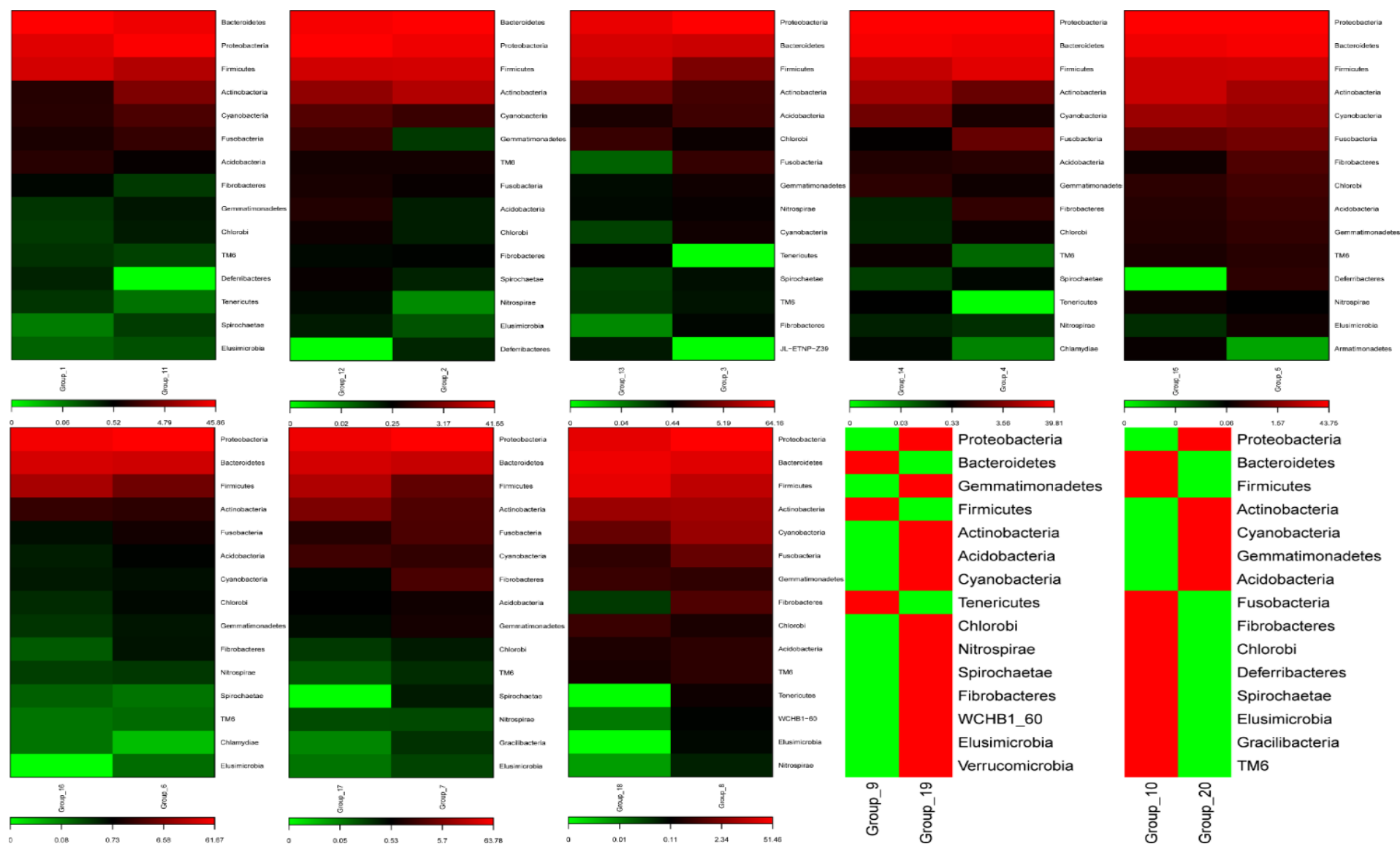


Figure S5 The top 50 OTUs found in the water, root and sediment among different comparisons.

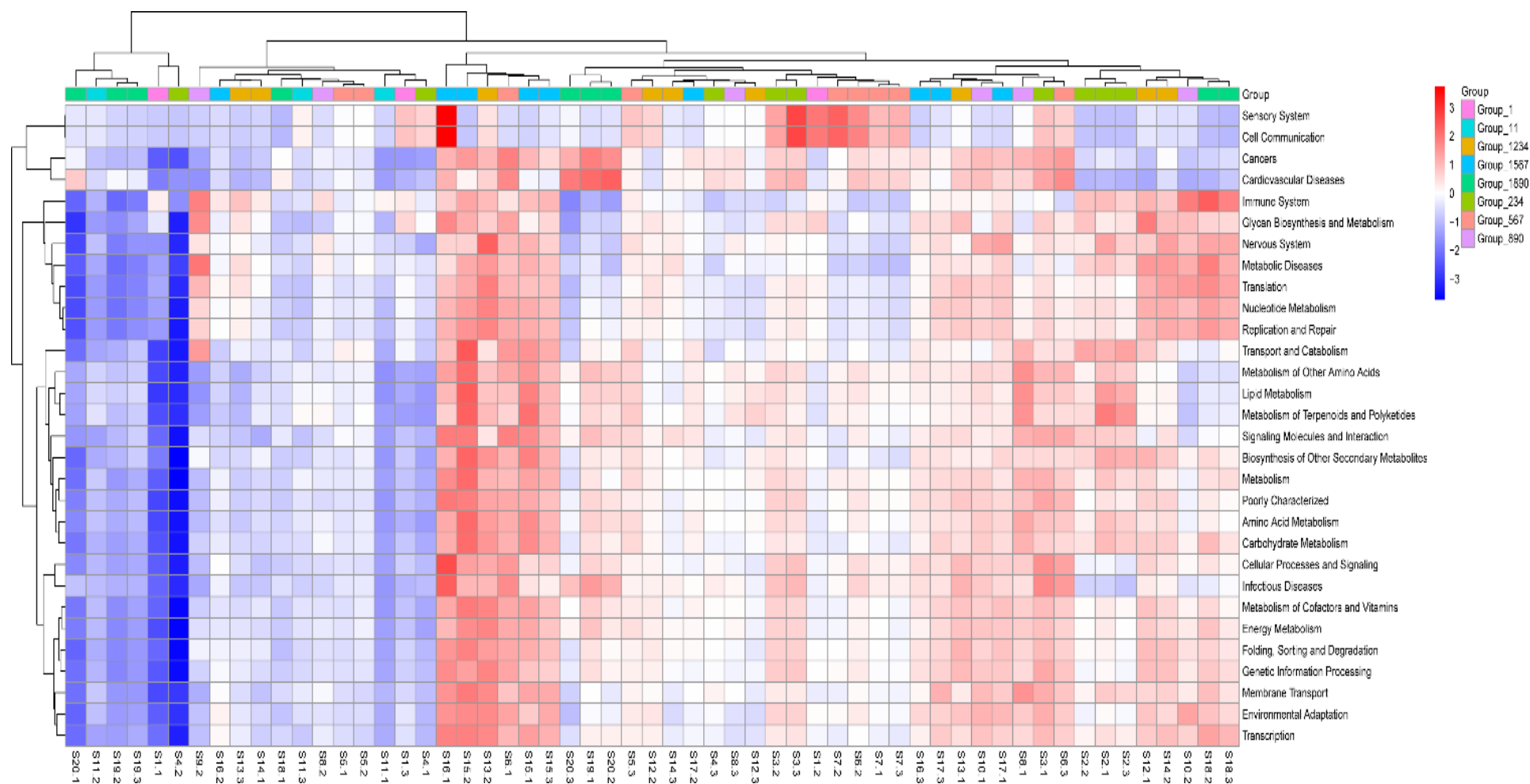


Figure S6. The significant KEGG pathways among the groups. CK at 0 and 30 d named as group 1 and 11, HcT1 at 0 and 30 d named as group 234 and 1234, HcT1 at 0 and 30 d named as group 567 and 1567, and Jr at 0 and 30 d named as group 890 and 1890.