

Table S1: The forward primer and reverse primer for qRT-PCR.

Gene	Gene Accession Number	Primer Sequences 5'-3'	Product size (bp)
GAPDH	NM_001289726.1	F: AGGTCGGTGTGAACGGATTTG R: TGTAGACCATGTAGTTGAGGTC	123
TNF- α	NM_013693.3	F: ATGTCTCAGCCTCTTCTCATTC R: GCTTGTCACCTCGAATTTTGAG	179
IL-6	NM_031168.2	F: CTCCCAACAGACCTGTCTATAC R: ACTCCAGGTAGCTATGGTACTC	258
IL-1 β	NM_008361.4	F: TCGCAGCAGCACATCAACAAGAG R: CTAATGGGAACGTCACACACCAGC	209

Table S2: Summary of OTUs sequencing data attained.

Samples	OTUs Number	Sequences	Sample Size (bases)	OTUs Reads
NC1	530	113100	48110474	92903
NC2	396	102491	43723810	92756
NC3	315	83974	35713510	81194
M1	529	105648	44717689	75885
M2	495	89582	37974126	73128
M3	444	114530	48503613	105717
HWH-L1	636	99086	41894229	68860
HWH-L2	573	92149	39212706	74834
HWH-L3	548	117577	50019073	89014
HWH-H1	700	123618	52255791	95562
HWH-H2	555	98554	41610830	74018
HWH-H3	643	98316	41376776	73812
PC1	370	85293	35983737	83487
PC2	613	121490	51381017	91173
PC3	678	118720	50295278	89909
NH1	771	122252	51543743	84554
NH2	576	75637	31728517	57439
NH3	614	97212	41045291	66304

Table S3: Summary of alpha diversity indices estimation via 16S rRNA gene sequencing.

Samples	ACE	Chao 1	Shannon	Simpson	Coverage
NC1	583	571	3.52	0.0689	0.999
NC2	432	492	2.77	0.1913	0.999
NC3	344	345	2.75	0.17	0.999
M1	585	576	4.07	0.0317	0.998
M2	536	534	3.95	0.0374	0.999

M3	484	489	3.75	0.0414	0.999
HWH-L1	696	695	4.29	0.0355	0.998
HWH-L2	646	653	3.95	0.043	0.998
HWH-L3	612	596	3.88	0.0435	0.999
HWH-H1	763	753	4.27	0.035	0.999
HWH-H2	617	616	3.69	0.0906	0.998
HWH-H3	690	673	4.35	0.0356	0.998
PC1	380	378	4.07	0.0368	0.999
PC2	685	683	3.99	0.0372	0.998
PC3	734	721	3.94	0.0534	0.999
NH1	827	807	4.64	0.0205	0.998
NH2	646	648	4.37	0.0309	0.998
NH3	686	670	4.23	0.0287	0.998

Table S4: Percentage of bacterial phyla in different treatment groups.

Groups	NC	M	HWH-L	HWH-H	PC	NH
<i>Bacteroidetes</i>	18.3	69.25	63.10	45.82	68.19	65.48
<i>Firmicutes</i>	74.18	28.34	34.23	50.51	28.88	31.18
<i>Proteobacteria</i>	4.21	0.98	0.80	2.54	1.12	1.39
<i>Actinobacteria</i>	0.49	0.71	0.89	0.18	0.62	1.41
<i>Deferribacteres</i>	1.81	0.15	0.56	0.35	0.52	0.06
<i>Chloroflexi</i>	0	0	0	0	0	0
<i>Cyanobacteria</i>	0.01	0	0.08	0.15	0	0.01
<i>Gemmatimonadetes</i>	0	0	0	0	0	1.39
<i>Saccharibacteria</i>	0.15	0.09	0.06	0.06	0.13	0.18
<i>Tenericutes</i>	0.63	0.38	0.11	0.14	0.4	0.14
<i>Verrucomicrobia</i>	0.01	0	0.01	0.01	0.01	0

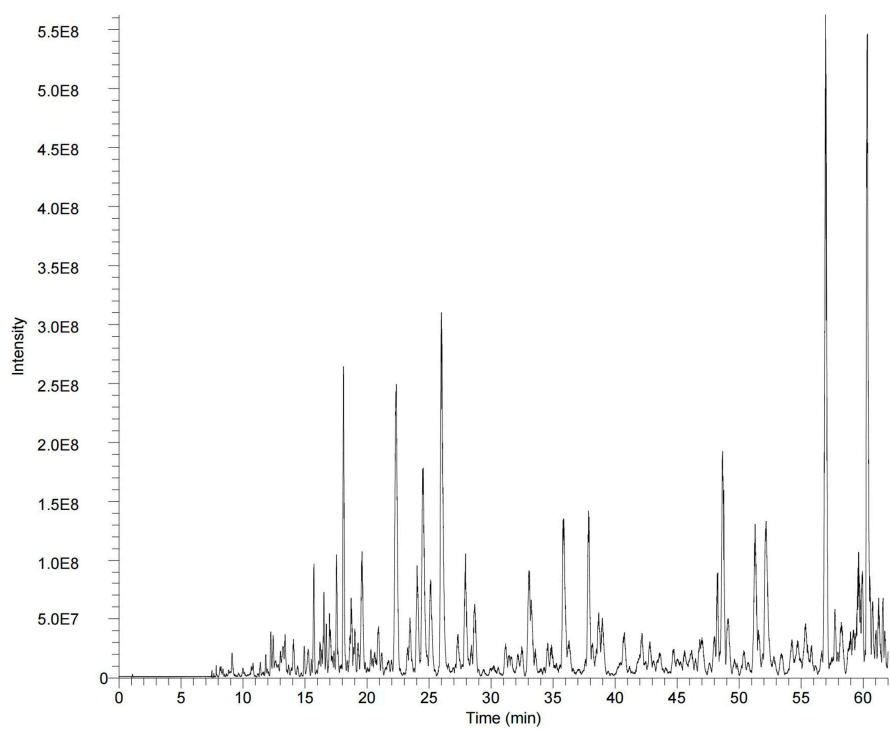


Figure S1. Total ion current diagram of HWH. Scanning range: 300-1400 m/z.