

Table S1. Number of reads and alpha diversity indices of sea cucumbers (*H. polii*, HP and *H. tubulosa*, HT) under different processing situations (Raw-R, Boiled-B, Frozen-F, Final Product-FP and salted Final Product-FPS).

Sample	Raw reads	Filtered/denoised/non-chimeric reads	Observed Features	Shannon
HP.F	40,156	21,592	161	4.66
HT.F	42,250	22,208	50	3
HP.FP	40,229	21,413	77	4.31
HT.FP	40,346	18,919	339	6.65
HP.B	42,637	23,999	57	2.56
HT.B	45,056	17,312	71	3.87
HP.SFP	47,375	22,249	447	6.85
HT.SFP	47,232	23,538	375	6.83
HP.R	36,131	16,032	76	4.57
HT.R	43,393	19,791	57	3.94

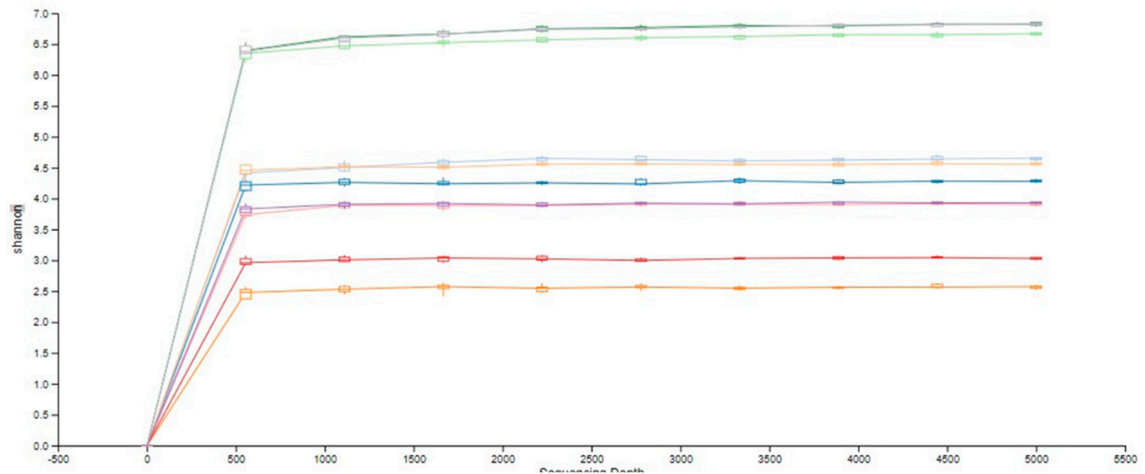


Figure S1. Shannon-Wiener rarefaction curves of sea cucumbers (*H. polii*, HP and *H. tubulosa*, HT) under different processing situations (Raw-R, Boiled-B, Frozen-F, Final Product-FP and salted Final Product-SFP).

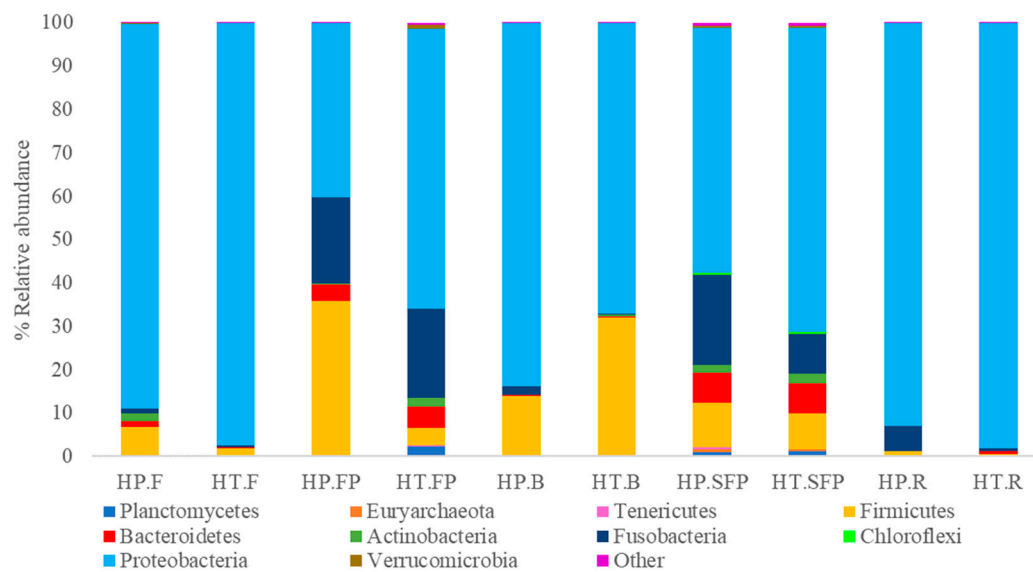


Figure S2. Relative abundance (%) of bacterial phyla of sea cucumbers (*H. polii*, HP and *H. tubulosa*, HT) under different processing situations (Raw-R, Boiled-B, Frozen-F, Dehydrated Final Product-FP and Salted Final Product-SFP), as revealed by 16S rRNA metabarcoding analysis.

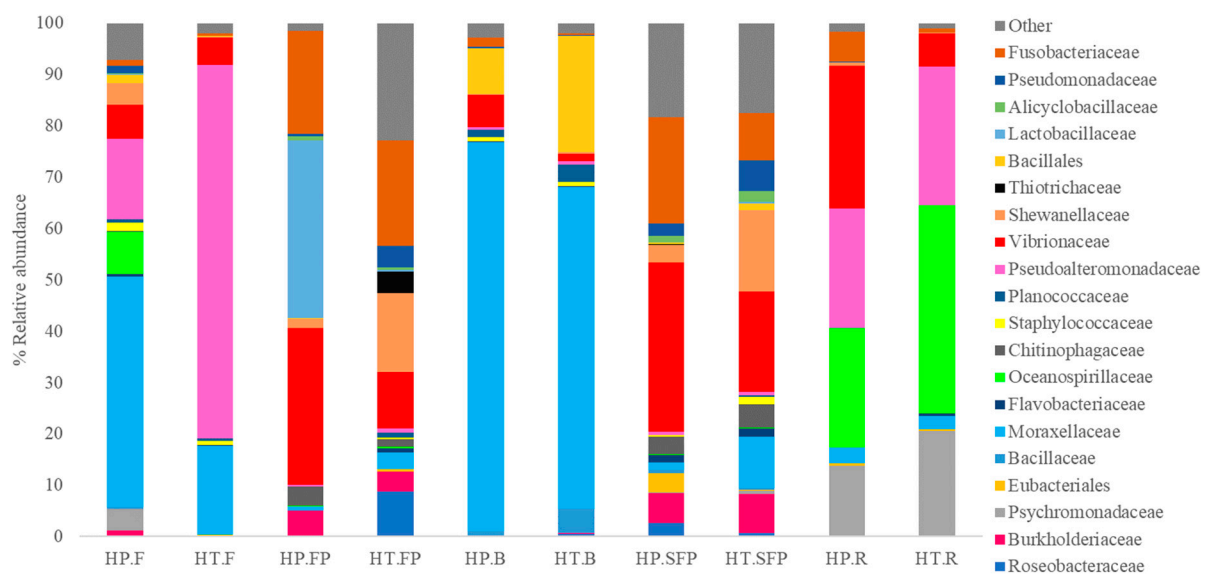


Figure S3. Relative abundance (%) of bacterial families of sea cucumbers (*H. polii*, HP and *H. tubulosa*, HT) under different processing situations (Raw-R, Boiled-B, Frozen-F, Dehydrated Final Product-FP and Salted Final Product-SFP), as revealed by 16S rRNA metabarcoding analysis.