Table S1: HuNoV changes the diversity of gut microbiota in oysters

| Group     | Reads       | Good's coverage | OTUs  | Abundance | Diversity |
|-----------|-------------|-----------------|-------|-----------|-----------|
|           |             |                 |       | Chao      | ACE       | Shannon   | Simpson   |
| Control   | 40954±2808  | 0.9985±0.0004   | 324±37| 363±47    | 2.28±0.21 | 0.34±0.05 |
| C6h       | 40872±2179  | 0.9982±0.0004   | 285±27| 327±43    | 2.01±0.18 | 0.38±0.05 |
| C24h      | 40578±2568  | 0.9987±0.0003   | 312±32| 362±38    | 2.17±0.22 | 0.36±0.04 |
| D6h       | 39194±3072  | 0.9984±0.0004   | 306±25| 359±39    | 1.75±0.23 | 0.43±0.04 |
| D24h      | 40295±2109  | 0.9989±0.0003   | 177±14| 221±25    | 1.16±0.17 | 0.52±0.05 |

Fig. S1: GO annotation analysis of DEGs affected with HuNoV