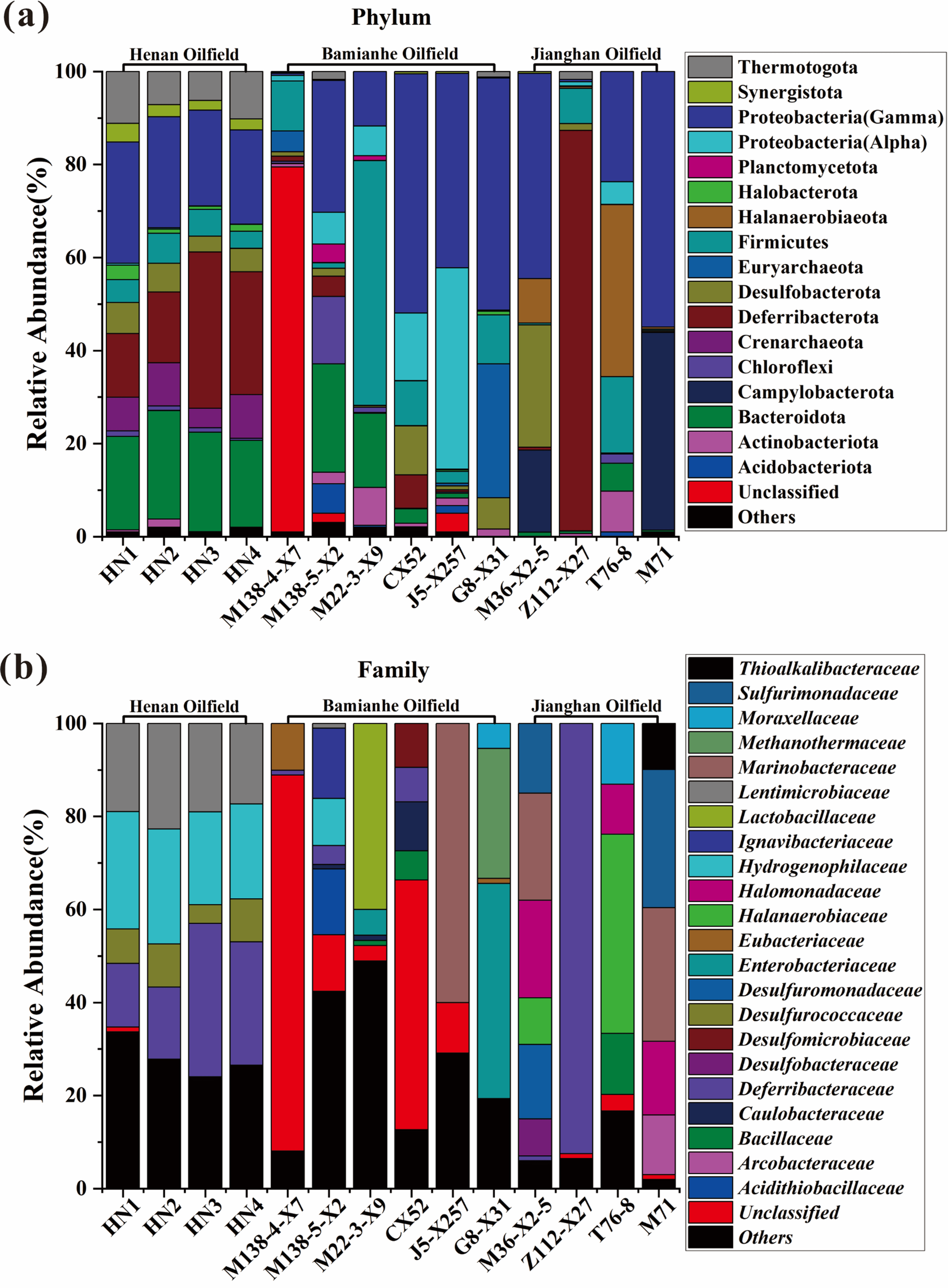


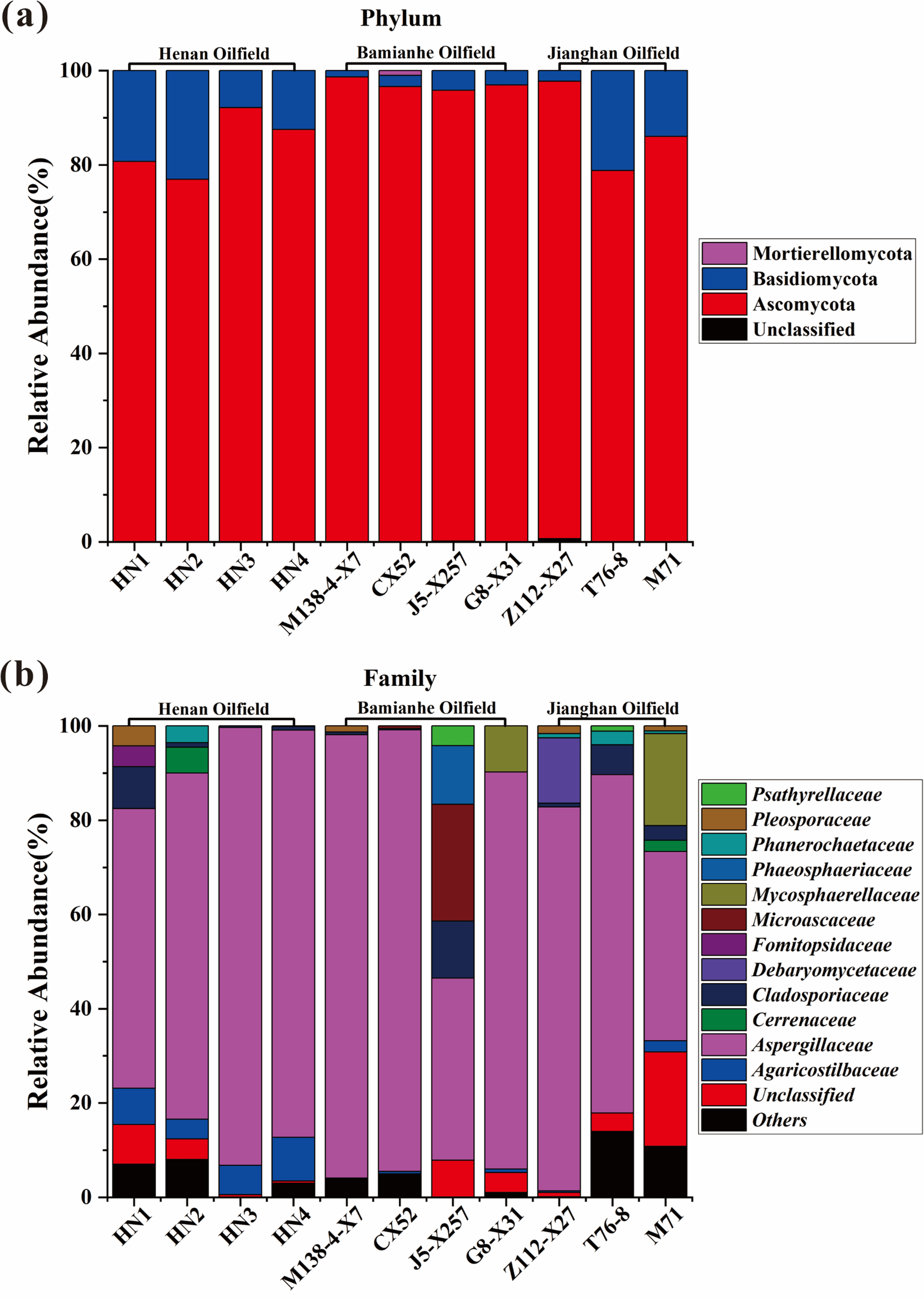


**S1** **The typical GC traces of whole oils and molecular biomarker compositions of crude oils with different biodegradation levels**



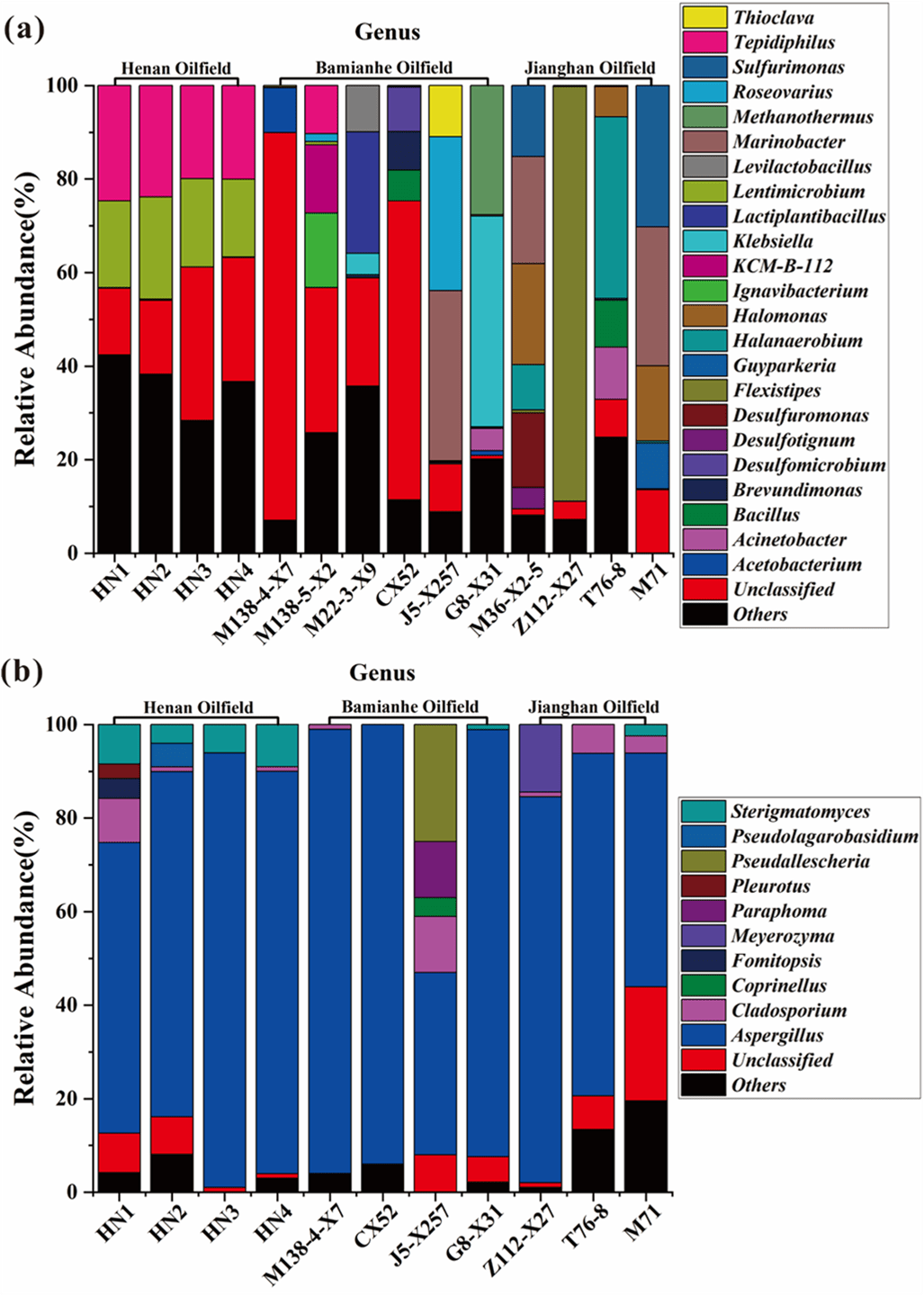
**S2** **Prokaryotic community members of the crude oils at the phylum and family level**

Relative abundance of the most abundant genera. (a) Phylum；(b) Family



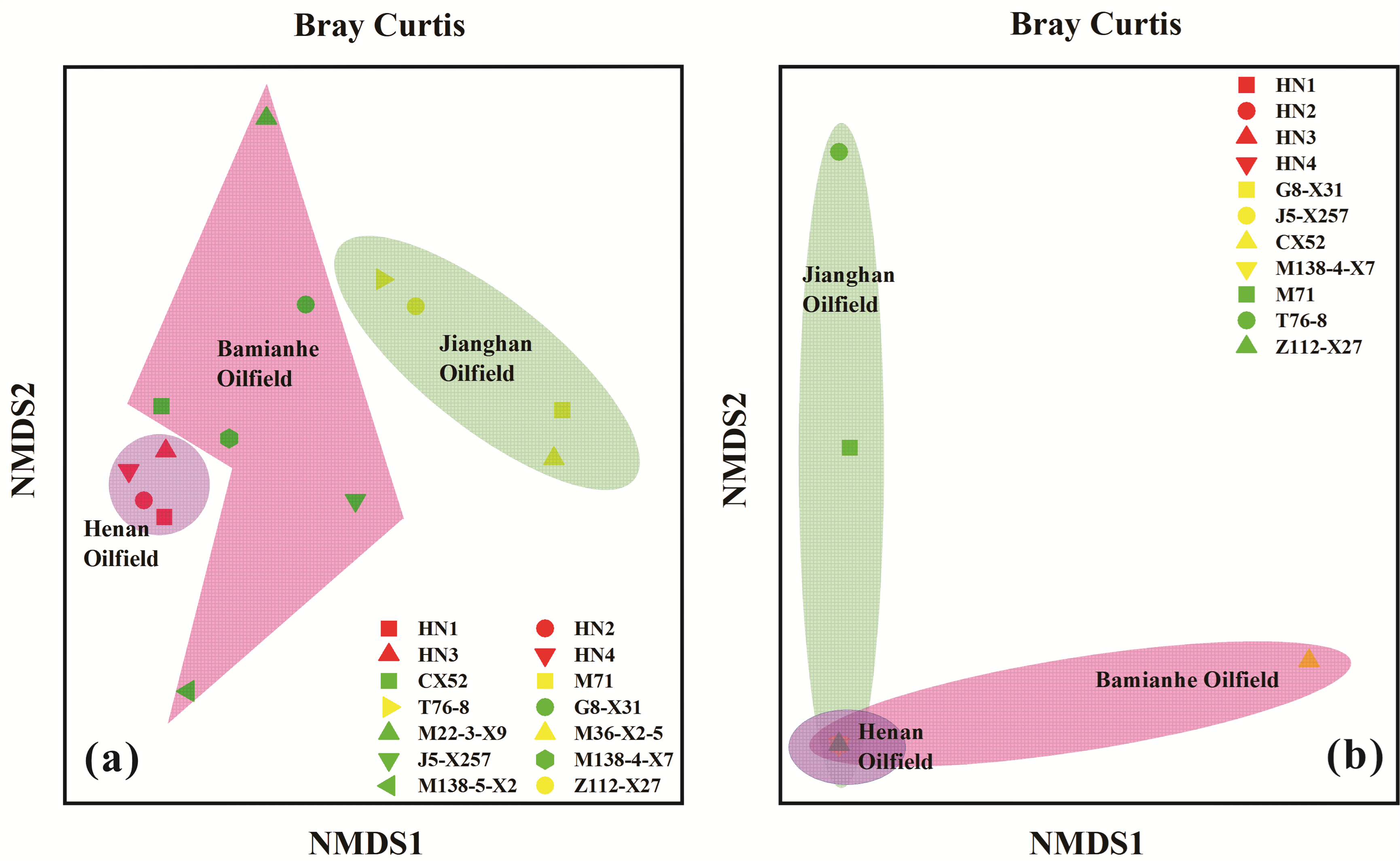
**S3 Fungal community members of the crude oils at the phylum and family level**

Relative abundance of the most abundant genera. (a) Phylum；(b) Family



**S4 Microbial community members of the crude oils at the genus level**

Relative abundance of the most abundant genera. (a) Prokaryotic communities；(b) Fungal communities



**S5 NMDS analysis of prokaryotic and fungal community structure in three oilfields**

NMDS shows the relationship among three oilfields that these crude oil samples have significant differences. (a) Prokaryotic communities；(b) Fungal communities

Plots in (a,b) were calculated based on Bray-Curtis distance.

**S6** **Three non-parametric multivariate statistical results of prokaryotic communities from three oilfields**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Reigon | | MRPP | | ANOSIM | | PERMANOVA | |
| *P* | Delta | *P* | r | *P* | Pseudo-F |
| Bray-Curtis  distance | Henan-  Bamianhe | 0.007 | 0.66 | 0.047 | 0.31 | 0.011 | 3.99 |
| Henan-  Jianghan | 0.034 | 0.55 | 0.019 | 0.99 | 0.04 | 5.88 |
| Bamianhe-  Jinghan | 0.038 | 0.96 | 0.017 | 0.50 | 0.045 | 1.26 |

**S7 Three non-parametric multivariate statistical results of crude oil fungal communities in three oilfields**

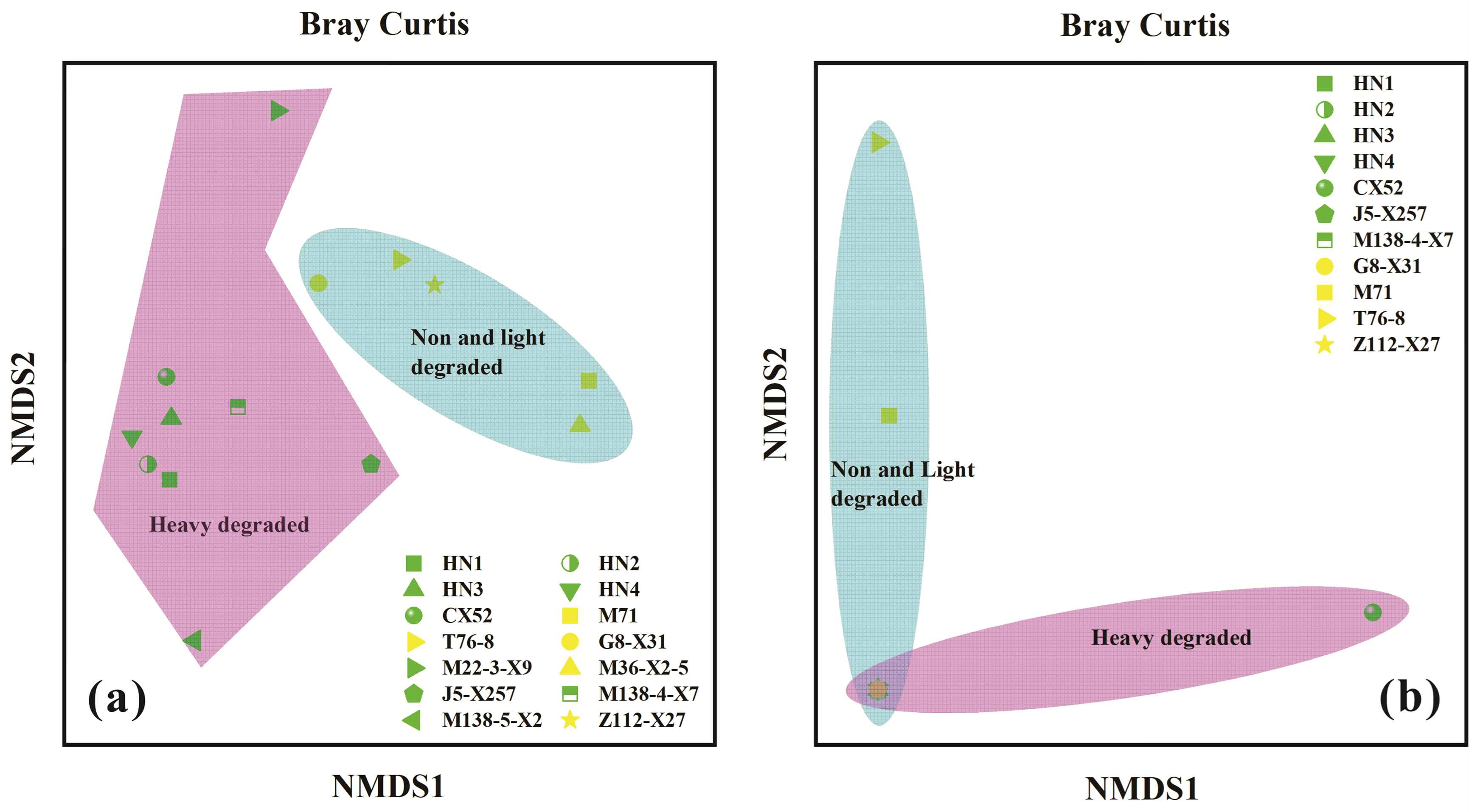
|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Reigon | | MRPP | | ANOSIM | | PERMANOVA | |
| *P* | Delta | *P* | r | *P* | Pseudo-F |
| Bray-Curtis  distance | Henan-  Bamianhe | 0.42 | 0.57 | 0.61 | 0.042 | 0.30 | 1.069 |
| Henan-  Jianghan | 0.48 | 0.49 | 0.28 | 0.12 | 0.57 | 0.91 |
| Bamianhe-Jinghan | 0.84 | 0.69 | 0.93 | -0.19 | 0.89 | 0.65 |

**S8 Three non-parametric multivariate statistical results of prokaryotic communities from three oilfields**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Reigon | | MRPP | | ANOSIM | | PERMANOVA | |
| *p* | Delta | *p* | r | *p* | Pseudo-F |
| Jaccard  distance | Henan-Bamianhe | 0.005 | 0.74 | 0.13 | 0.14 | 0.009 | 3.10 |
| Henan-Jianghan | 0.031 | 0.67 | 0.038 | 1.00 | 0.04 | 4.56 |
| Bamianhe-Jinghan | 0.007 | 0.92 | 0.017 | 0.52 | 0.008 | 1.47 |

**S9 Three non-parametric multivariate statistical results of crude oil fungal communities in three oilfields**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Reigon | | MRPP | | ANOSIM | | PERMANOVA | |
| *p* | Delta | *p* | r | *p* | Pseudo-F |
| Jaccard  distance | Henan-Bamianhe | 0.033 | 0.69 | 0.033 | 0.38 | 0.04 | 1.49 |
| Henan-Jianghan | 0.029 | 0.71 | 0.028 | 0.41 | 0.03 | 1.45 |
| Bamianhe-Jinghan | 0.067 | 0.77 | 0.077 | 0.03 | 0.03 | 1.23 |



**S10 NMDS analysis of prokaryotic and fungal community structure with different degradation degrees**

NMDS shows the relationship among different biodegradation levels that these crude oil samples have significant differences. (a) Prokaryotic communities；(b) Fungal communities Plots in (a,b) were calculated based on Bray-Curtis distance.

**S11 Three non-parametric multivariate statistical results of prokaryotic communities with different degrees of degradation crude oil**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Heavy-degraded vs  Non and Light degraded | MRPP | | ASOSIM | | PERMANOVA | |
| *p* | Delta | *p* | r | *p* | Pseudo-F |
| Bray-Curtis distance | 0.017 | 0.88 | 0.002 | 0.64 | 0.013 | 2.08 |

**S12 Three non-parametric multivariate statistical results of fungal communities with different degrees of degradation crude oil**

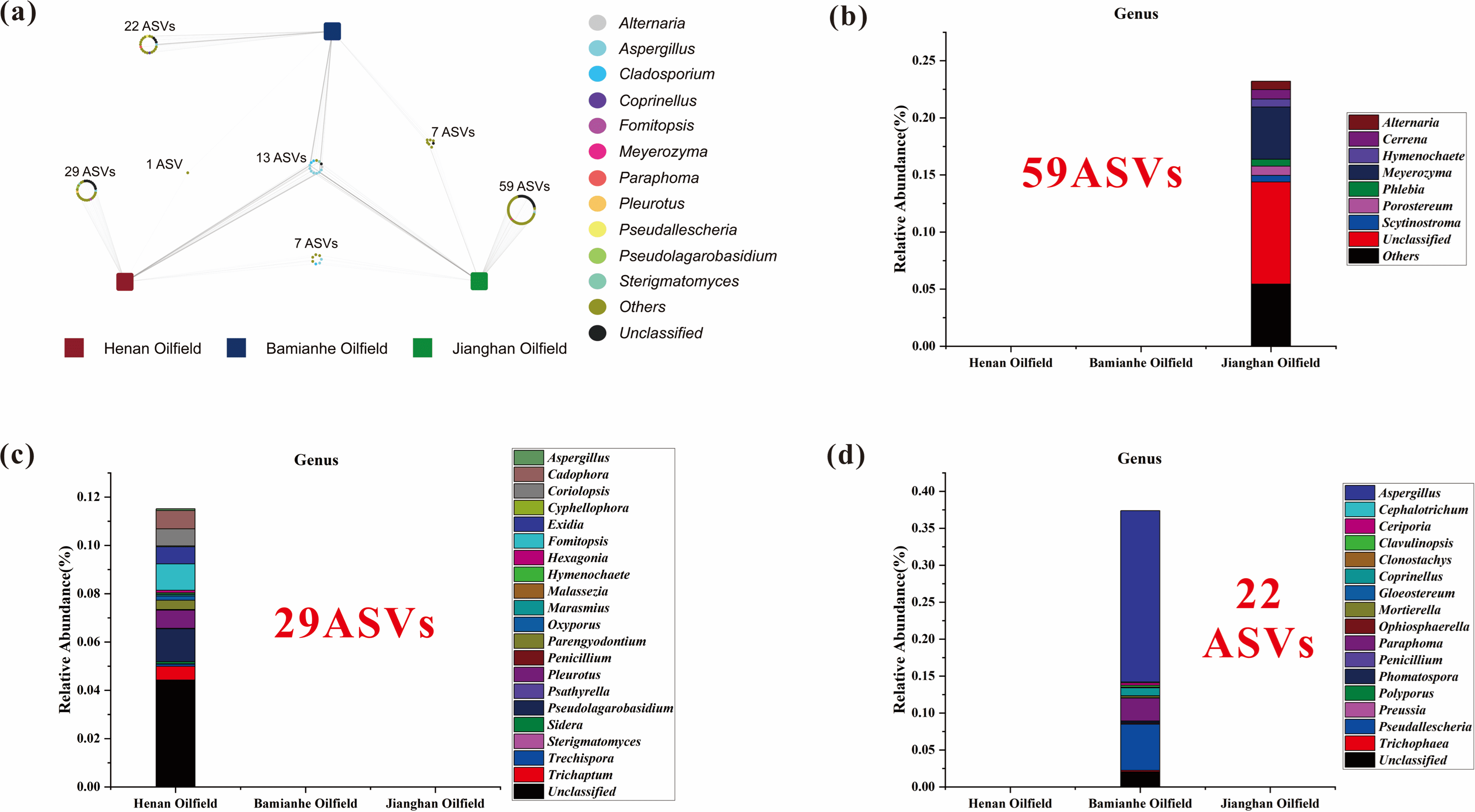
|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Heavy-degraded vs  Non and Light degraded | MRPP | | ASOSIM | | PERMANOVA | |
| *p* | Delta | *p* | r | *p* | Pseudo-F |
| Bray-Curtis distance | 0.82 | 0.58 | 0.64 | -0.075 | 0.8 | 0.70 |

**S13 Three non-parametric multivariate statistical results of prokaryotic communities with different degrees of degradation crude oil**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Heavy-degraded vs  Non and Light degraded | MRPP | | ASOSIM | | PERMANOVA | |
| *p* | Delta | *p* | r | *p* | Pseudo-F |
| Jaccard distance | 0.007 | 0.87 | 0.005 | 0.62 | 0.007 | 2.21 |

**S14 Three non-parametric multivariate statistical results of fungal communities with different degrees of degradation crude oil**

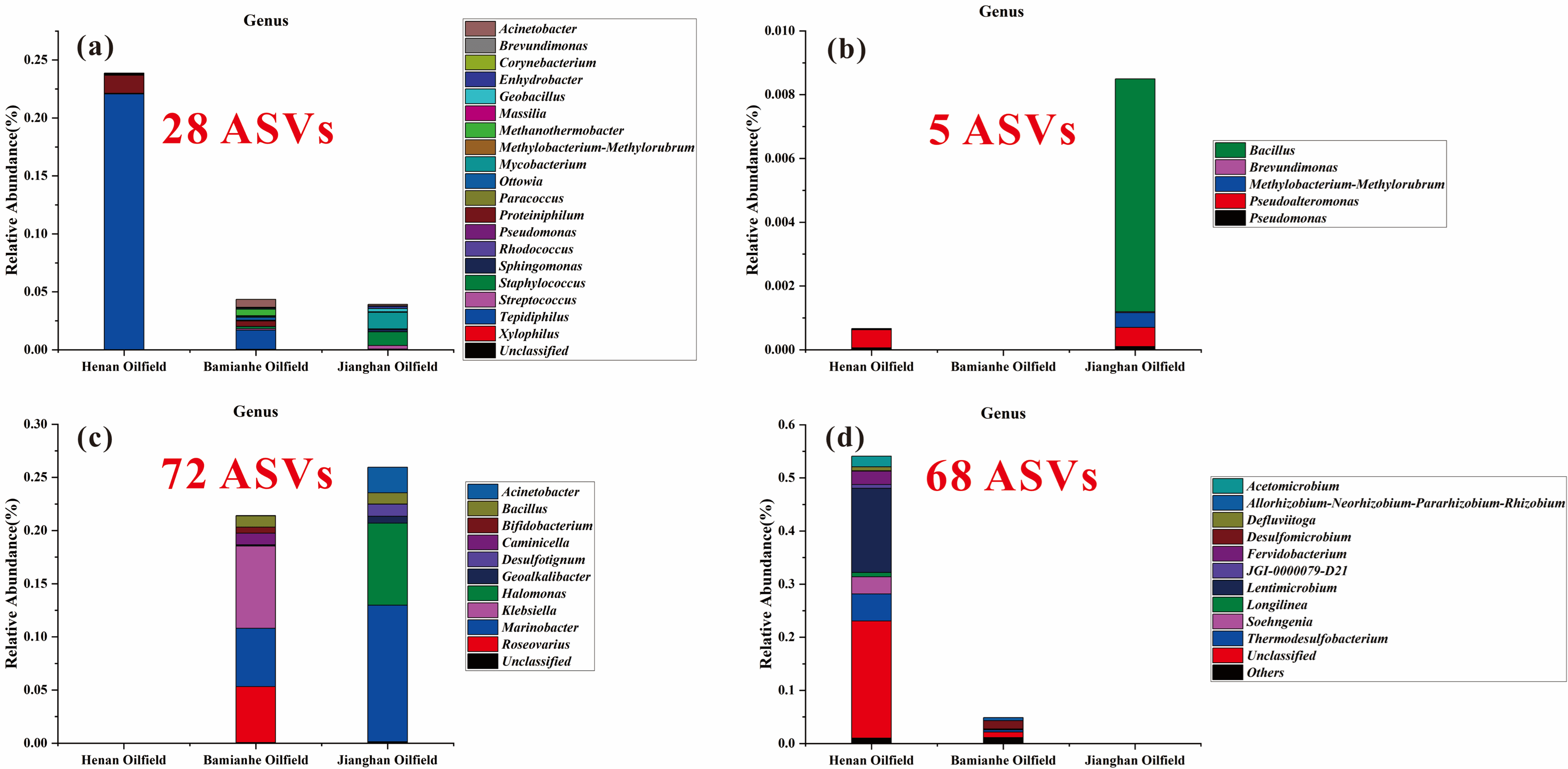
|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Heavy-degraded vs  Non and Light degraded | MRPP | | ASOSIM | | PERMANOVA | |
| *p* | Delta | *p* | r | *p* | Pseudo-F |
| Jaccard distance | 0.036 | 0.74 | 0.027 | 0.34 | 0.01 | 1.34 |



**S15 ASVs results of fungal communities compared with oil samples from three oilfields**

The Henan oilfield was clustered into 29 ASVs alone. TheBamianhe Oilfield gathers into 22 ASVs alone. The Jianghan Oilfield has clustered into 59 ASVs alone. Henan and Bamianhe oilfields were together to form 1 ASVs. The Henan and Jianghan oilfields were together to form 7ASVs. The Bamianhe and Jianghan oilfield are together to form 7ASVs. The three oilfields aggregated into 13 ASVs.

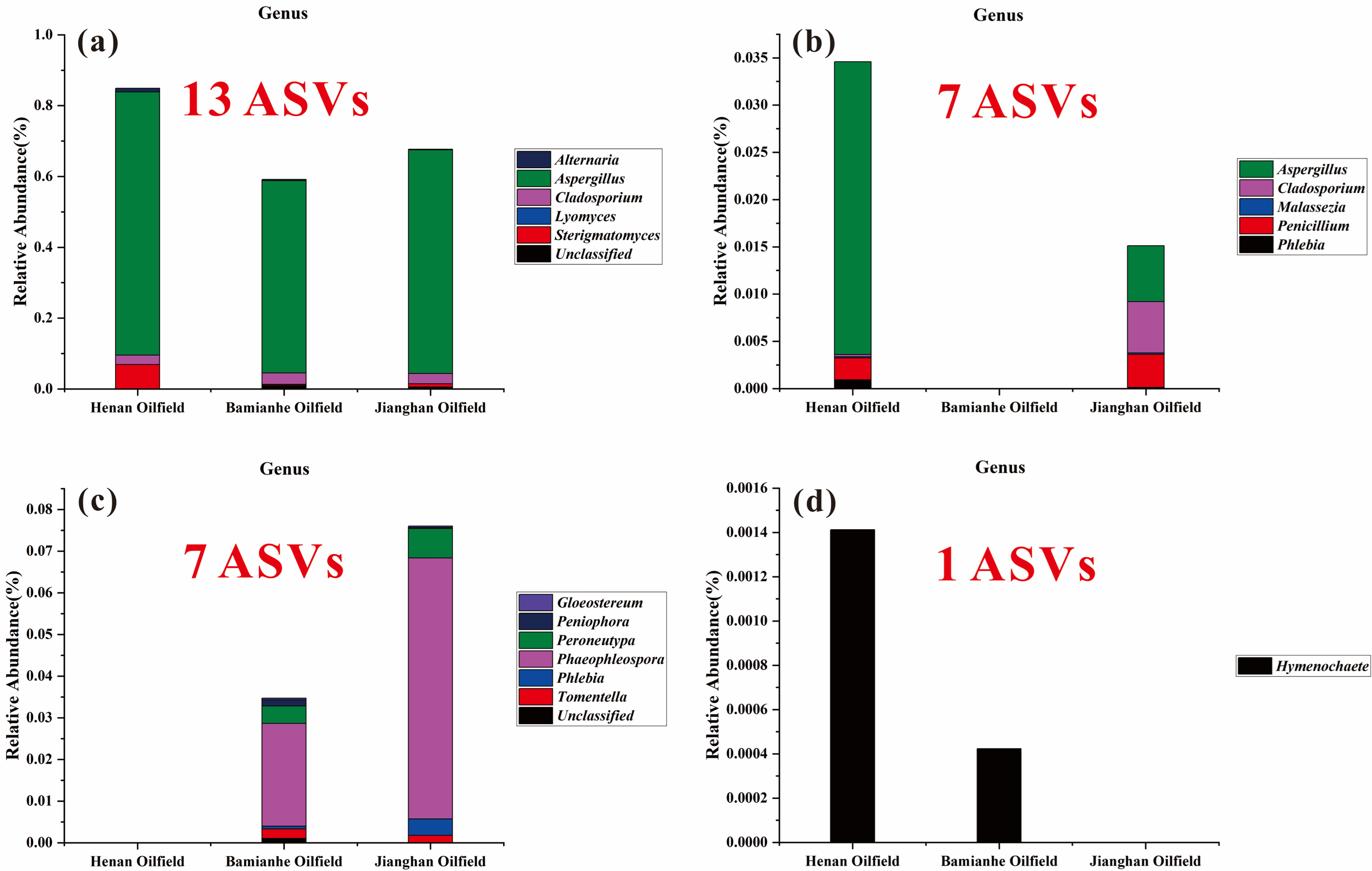
(a) ASVs results of three oilfields at genus level；(b) Jianghan Oilfield unique fungi at genus level；(c) Henan Oilfield unique fungi at genus level；(d) Bamianhe Oilfield unique fungi at genus level



**S16 ASVs results of prokaryotic communities compared with oil samples from three oilfields**

Among the 68 ASVs shared between the Henan and Bamianhe oilfield. 5 ASVs were shared between Henan and Jianghan oilfield. 72 ASVs shared between the Bamianhe and Jianghan oilfield. The three oilfields were clustered into 28 ASVs.

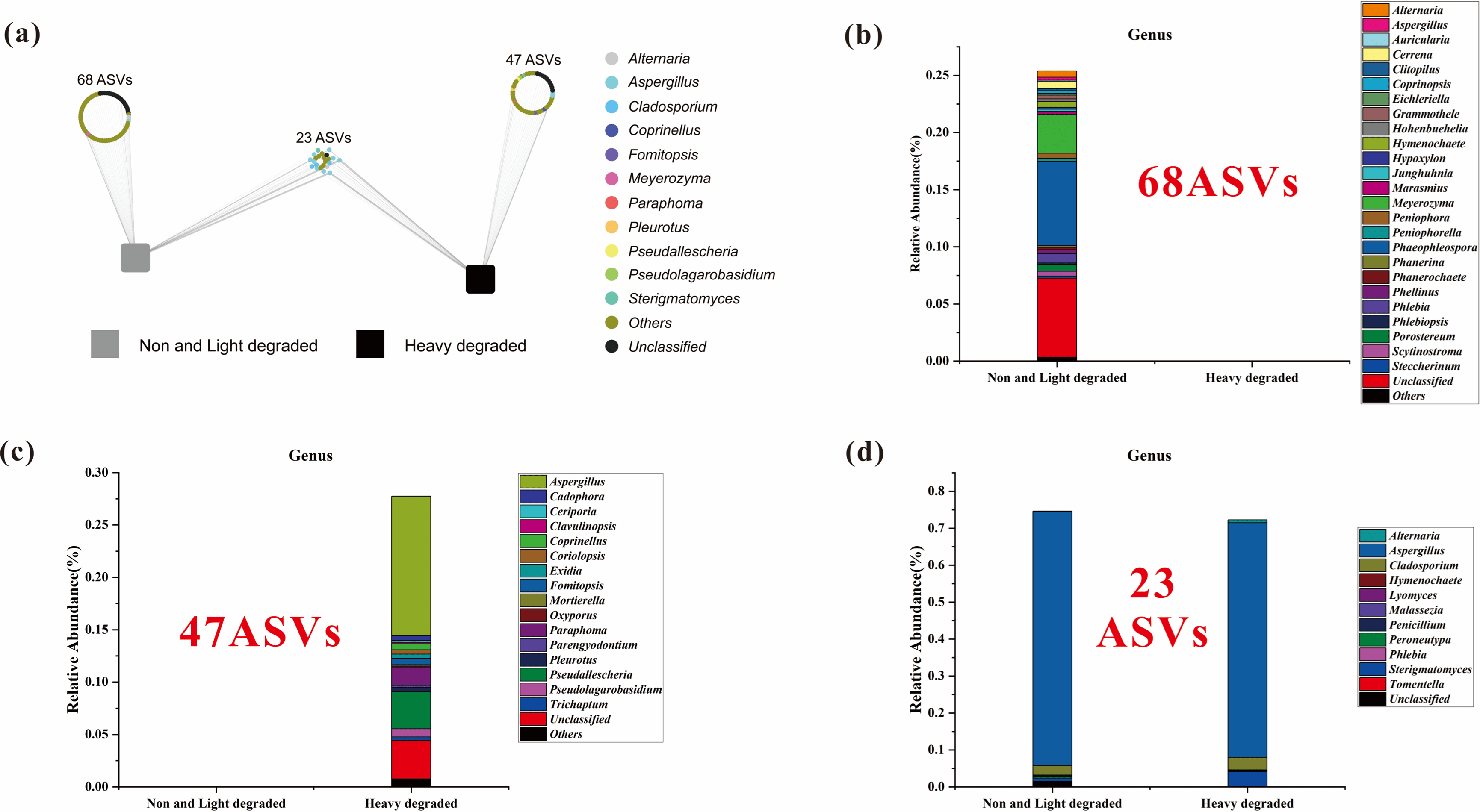
(a) Three oilfields shared prokaryotes at genus level；(b) Henan oilfield and Jianghan oilfield shared prokaryotes at genus level；(c) Bamianhe oilfield and Jianghan oilfield shared prokaryotes at genus level; (d) Henan oilfield and Bamianhe oilfield shared prokaryotes at genus level



**S17**  **ASVs results of fungal communities compared with oil samples with oil samples from three oilfields**

Henan and Bamianhe oilfields were together to form 1 ASVs. The Henan and Jianghan oilfields were together to form 7ASVs. The Bamianhe and Jianghan oilfield are together to form 7ASVs. The three oilfields aggregated into 13 ASVs.

(a) Three oilfields shared fungi at genus level；(b) Henan oilfield and Jianghan oilfield shared fungi at genus level；(c) Bamianhe oilfield and Jianghan oilfield shared fungi at genus level; (d) Henan oilfield and Bamianhe oilfield shared fungi at genus level



**S18 ASVs results of fungal communities compared with oil samples with different degrees of degradation**

The non and light degraded groups included 68 unique ASVs. The heavy-degraded group had 47 unique ASVs. These two groups had a total of 23 ASVs**.**

(a) Two kinds of degradation genus level ASVs results；(b) Non and Light samples particular fungi at genus level；(c) Heavy degraded samples particular fungi at genus level；(d) The two kinds of degradation degree shared fungi at genus level