Supplementary Material

Table S1 The sequence amount of different types of saprotroph fungi from different landfill samples, classified by FUNGuild

Samples	Undefined Saprotroph	Wood Saprotroph	Soil Saprotroph	Plant Saprotroph	Leaf Saprotroph	Dung Saprotroph	Litter Saprotroph
A03	4766	13	7	2	0	2	0
A06	2627	261	16	3	1	2	2
A09	644	125	5	1	0	2	0
A12	2875	47	9	3	0	2	0
A15	5114	544	78	3	0	4	0
B03	3696	585	5	3	0	2	11
B06	2116	1452	46	4	1	3	33
B09	402	1602	24	1	0	1	0
B12	6476	503	9	2	487	2	6
B15	1267	128	4	2	0	3	0
C03	2475	1186	220	3	0	392	0
C06	3674	68	12	3	0	3	0
C09	3632	191	1095	191	0	134	0
C12	5004	195	6	0	0	1	0
C15	6292	972	424	52	0	30	1

Notes: The OTU numbers of undefined saprotroph, wood saprotroph, soil saprotroph, plant saprotroph, leaf saprotroph, dung saprotroph and litter saprotroph detected in all samples are 105, 24, 3, 6, 2, 4, and 4 respectively

Table S2 Functional information of top 20 genera* of fungi in landfill

Genera	Taxon	Taxon Level	Trophic Mode	Guild	Confidence Ranking
f_Hypocreaceae_unclassified	Hypocreales	order	Saprotroph	**Undefined Saprotroph**	Possible
Fusarium	Fusarium	genus	Pathotroph-Saprotroph-Symbiotroph	Animal Pathogen-Endophyte-Lichen Parasite-Plant Pathogen-**Soil Saprotroph-Wood Saprotroph**	Possible
Aspergillus	Eurotiales	order	Saprotroph	**Undefined Saprotroph**	Possible
	Aspergillus niger	species	Pathotroph-Saprotroph	Plant Pathogen-**Wood Saprotroph**	Probable
	Aspergillus flavus	species	Pathotroph-Saprotroph	Animal Pathogen-Plant Pathogen-**Wood Saprotroph**	Probable
	Aspergillus terreus	species	Pathotroph-Saprotroph	Animal Pathogen-**Wood Saprotroph**	Probable
	Aspergillus ustus	species	Saprotroph	**Wood Saprotroph**	Highly probable
	Aspergillus aculeatus	species	Pathotroph	Plant Pathogen	Probable
Talaromyces	Talaromyces	genus	Saprotroph	**Undefined Saprotroph**	Probable
Gibberella	Gibberella	genus	Pathotroph	Plant Pathogen	Probable
Penicillium	Eurotiales	order	Saprotroph	**Undefined Saprotroph**	Possible
	Penicillium digitatum	species	Pathotroph	Plant Pathogen	Probable
	Penicillium oxalicum	species	Pathotroph	Plant Pathogen	Probable
	Penicillium purpurogenum	species	Pathotroph	Plant Pathogen	Probable
	Penicillium citrinum	species	Pathotroph	Plant Pathogen	Probable
Malassezia	Malassezia	genus	Pathotroph-Saprotroph	Animal Pathogen-**Undefined Saprotroph**	Probable
Meyerozyma	Saccharomycetales	order	Saprotroph	**Undefined Saprotroph**	Possible
g_unclassified_Ustilaginaceae	Ustilaginaceae	family	Pathotroph	Plant Pathogen	Probable

Trichoderma	Hypocreales	order	Saprotroph	**Undefined Saprotroph**	Possible
	Trichoderma longibrachiatum	species	Pathotroph-Symbiotroph	Endophyte-Plant Pathogen	Probable
Pseudallescheria	Pseudallescheria	genus	Saprotroph	**Undefined Saprotroph**	Probable
Trichothecium	Trichothecium	genus	Pathotroph	Plant Pathogen	Probable
Pseudeurotium	Pseudeurotium	genus	Saprotroph	**Undefined Saprotroph**	Probable
Guehomyces	Guehomyces	genus	Saprotroph	**Undefined Saprotroph**	Probable
Candida	Saccharomycetales	order	Saprotroph	**Undefined Saprotroph**	Possible
Cladosporium	Cladosporium sphaerospermum	species	Symbiotroph	Endophyte	Highly probable
	Cladosporium	genus	Pathotroph-Saprotroph-Symbiotroph	Animal Pathogen-Endophyte-Lichen Parasite-Plant Pathogen-**Wood Saprotroph**	Possible
g__unclassified_Pezizaceae	Peziza	genus	Saprotroph-Symbiotroph	Dung Saprotroph-Ectomycorrhizal-**Litter Saprotroph**-**Undefined Saprotroph**	Possible

Note: *There is no functional information of *p_Ascomycota_unclassified*, *g_unclassified_Fungi* and *g_unclassified_Ustilaginaceae*.

Fig. S1 Sampling sites (A, B and C) and their horizontal distance

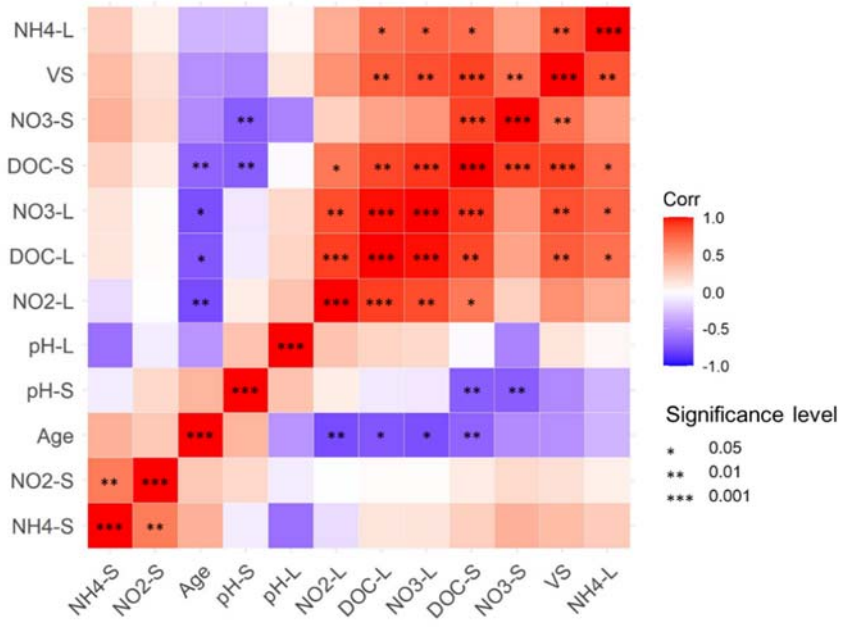


Fig. S2 Spearman correlation analysis among the properties of refuse and leachate samples, including landfilled age and physiochemical parameters (pH, DOC, VS, ammonia, nitrite, and nitrate). S means solid samples, i.e. refuse; L means leachate samples

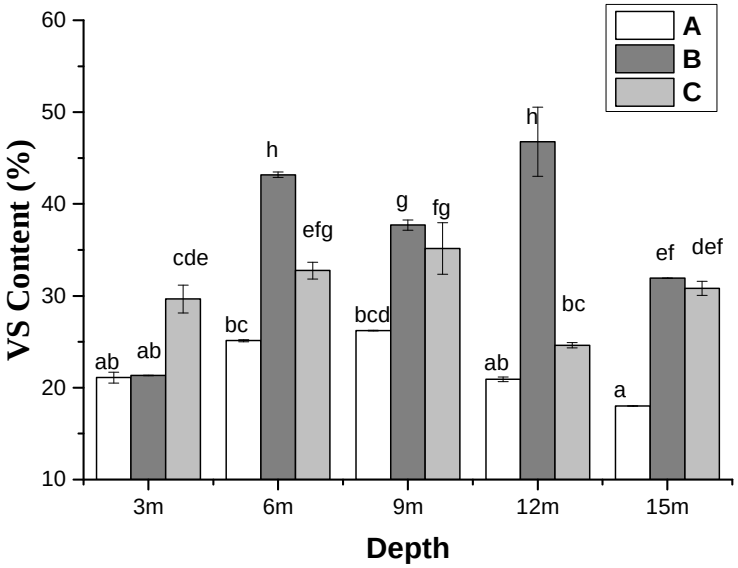


Fig. S3 Volatile solid (VS) content variation of refuse samples (A, B, C) from different depth in landfill. Small letters above bars indicate significant difference among VS values observed in different refuse samples

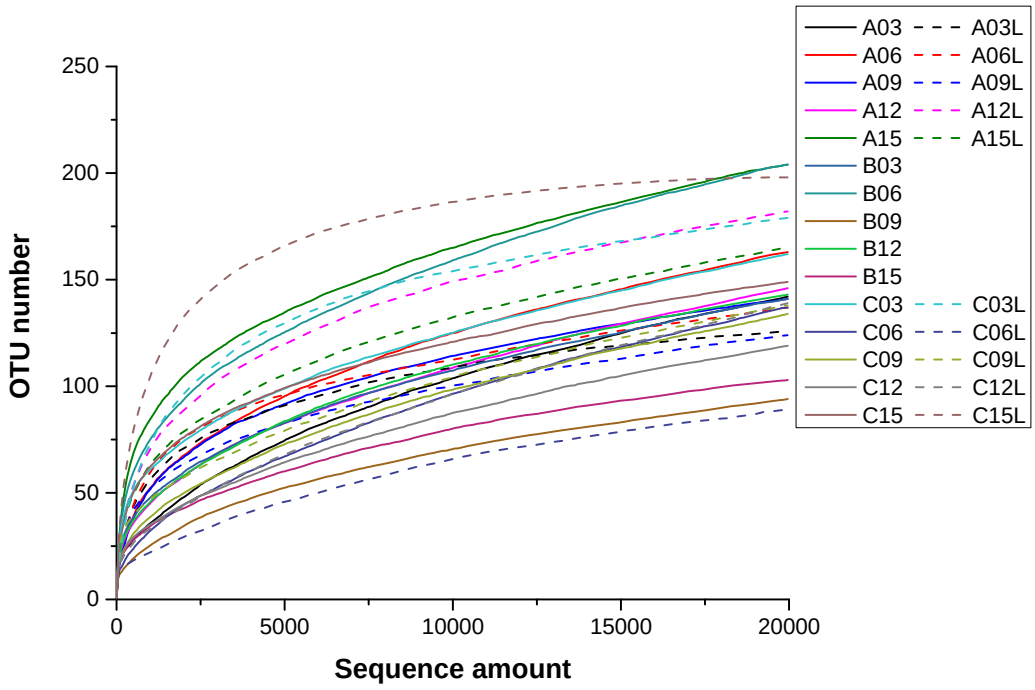
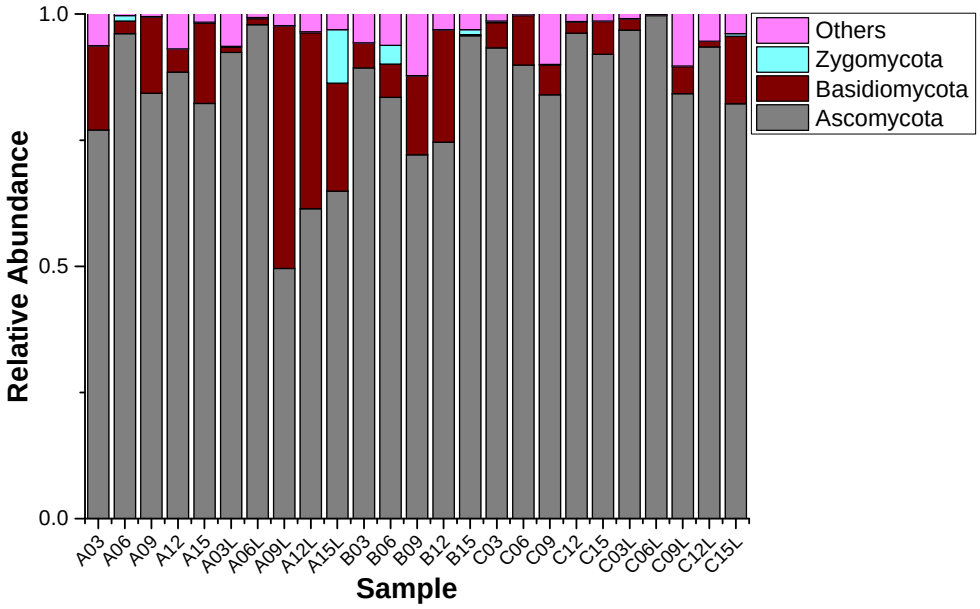
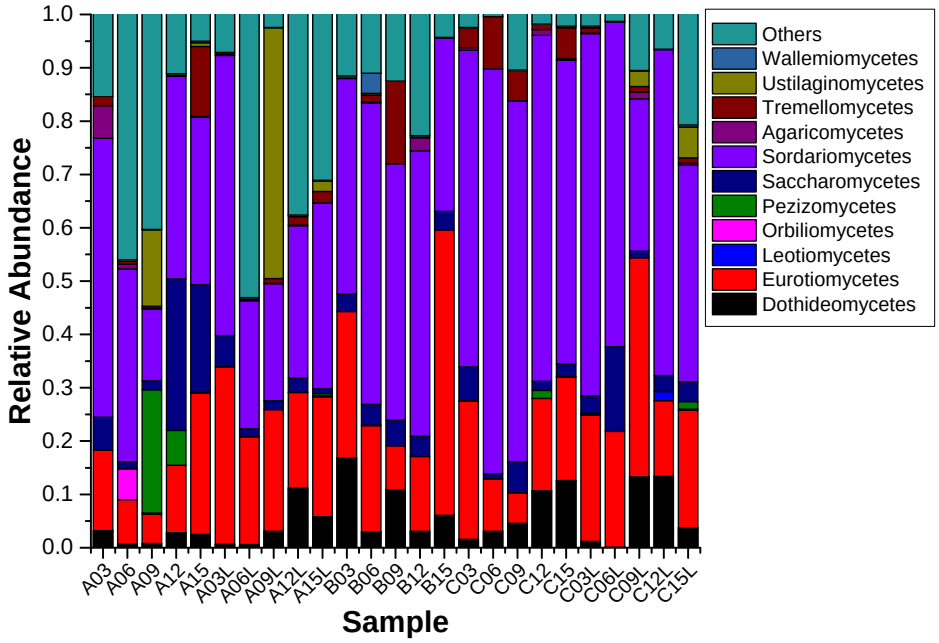


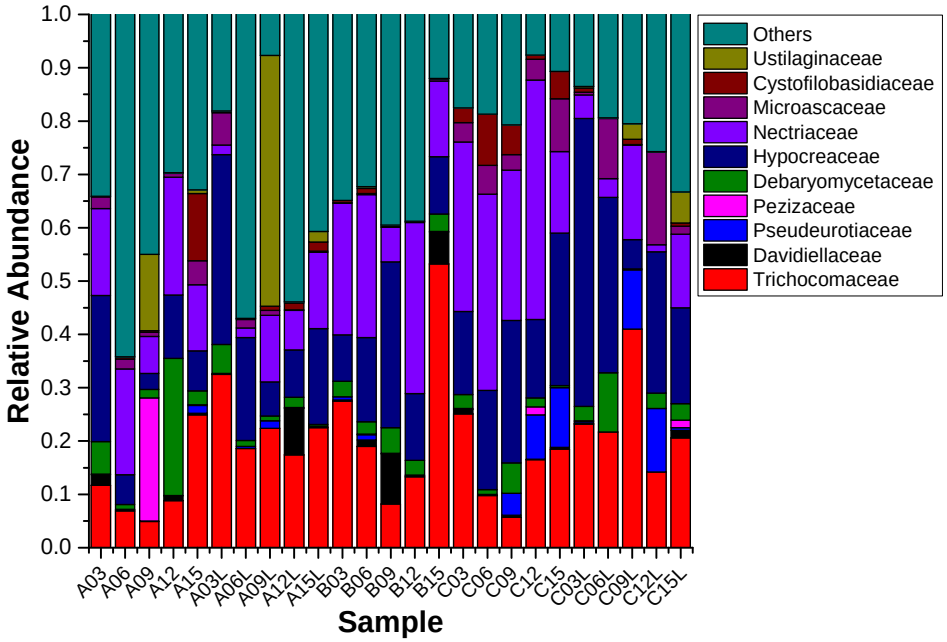
Fig. S4 Rarefaction curve of observed fungal OTUs to assess sequencing depth


Relative Abundance
1.0
0.5
0.0
Others
Zygomycota
Basidiomycota
Ascomycota
A03
A06
A09
A12
A15
A03L
A06L
A09L
A12L
A15L
B03
B06
B09
B12
B15
C03
C06
C09
C12
C15
C03L
C06L
C09L
C12L
C15L
Sample

(a)


Relative Abundance
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Others
Wallemiomycetes
Ustilaginomycetes
Tremellomycetes
Agaricomycetes
Sordariomycetes
Saccharomycetes
Pezizomycetes
Orbiliomycetes
Leotiomycetes
Eurotiomycetes
Dothideomycetes
A03
A06
A09
A12
A15
A03L
A06L
A09L
A12L
A15L
B03
B06
B09
B12
B15
C03
C06
C09
C12
C15
C03L
C06L
C09L
C12L
C15L
Sample

(b)



(c)

Fig. S5 Relative abundance of different phyla (a), classes (b) and families (c) among fungal communities from landfill samples