

1 **[Supplementary materials]**

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3 **Performance evaluation of an *on-site* biocomplex textile as an**
4 **alternative daily cover in a sanitary landfill, South Korea**

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Supplementary Table S1. Metagenome analysis results of the biocomplex textile prototype

Sampling time (date)	Repl.	No. of reads ^a	No. of OTUs	Chao1 ^b	Diversity index		Good's coverage ^e
					Shannon ^c	Simpson ^d	
6 d	1	62,919	868	1041.91	4.32	0.77	0.997
	2	45,119	853	1018.19	4.93	0.83	0.996
39 d	1	83,307	559	680.69	4.78	0.89	0.999
	2	84,332	570	656.39	4.94	0.90	0.999
66 d	1	83,386	1,051	1172.40	6.11	0.94	0.998
	2	64,431	996	1073.41	5.80	0.92	0.998
89 d	1	65,393	981	1067.68	7.46	0.97	0.998
	2	74,858	947	1098.89	5.16	0.87	0.998
125 d	1	44,805	948	1055.10	6.28	0.94	0.997
	2	41,521	932	1040.39	6.15	0.94	0.996
151 d	1	52,270	1,065	1151.01	6.73	0.96	0.997
	2	82,315	1,100	1165.58	7.01	0.97	0.999

^a No. of reads is the number of sequences after trimming.

^b Chao1 is an index of bacterial population richness.

^c Shannon index of diversity within the bacterial population.

^d Simpson index represents probability that two randomly selected individuals in the habitat will belong to the same species.

^e Coverage is calculated as $C=1-(s/n)$, where s is the number of unique OTUs and n is the number of individuals in the sample. This index gives a relative measure of how well the sample represents the larger environment.

